

Result	Query	Score	Match	Length	DB	ID	Description
No.							
1	342	95.3	352	1	00CVC1	00CVC1	Al1 protein - toman
2	242	67.4	361	1	00CVC1	00CVC1	Al1 protein - pota
3	229	63.8	358	2	S07594	S07594	hypothetical prote
4	222	61.8	362	1	J01887	J01887	Al1 protein - toman
5	216	60.2	349	2	J02300	J02300	replicase - pepper
6	216	60.2	349	2	S31875	S31875	Al1 protein - pepper
7	215	59.9	359	2	S39211	S39211	gene C1 protein -
8	212	59.1	385	2	S28360	S28360	Al1 protein - beet
9	211	58.8	359	2	S22593	S22593	hypothetical prote
10	210	58.5	355	1	00CVC1	00CVC1	AV1 protein - abut
11	207	57.7	358	1	J01870	J01870	Al1 protein - toman
12	205	57.1	351	2	J02327	J02327	Al1 protein - Indi
13	205	57.1	359	2	S39335	S39335	gene C1 protein -
14	195	54.3	360	2	S59885	S59885	replication-associ
15	193	53.8	357	1	00CVC1	00CVC1	Al1 protein - toman
16	120	33.4	131	2	S45059	S45059	AC1 protein (clone
17	107	29.8	347	1	00CVC1	00CVC1	Al1 protein
18	70	19.5	567	2	JC1419	JC1419	Fe gamma (Irg) rec
19	68	18.9	447	2	T12544	T12544	hypothetical prote
20	64	17.8	316	2	C82085	C82085	conserved hypothe
21	63.5	17.7	1259	2	T48959	T48959	kinesin-like prote
22	63.5	17.7	1610	2	A46227	A46227	voltage-dependent
23	63.5	17.7	1646	2	JH0422	JH0422	voltage-dependent
24	63.5	17.7	2161	2	JH0564	JH0564	calcium channel al
25	63.5	17.7	2181	2	A38198	A38198	calcium channel al
26	63.5	17.7	2203	2	T42742	T42742	voltage-dependent
27	62	17.3	2265	2	S76632	S76632	hypothetical prote
28	61	16.9	1502	1	RGBYH1	RGBYH1	CYC1/CY3 transcri
29	60.5	16.9	840	2	T36175	T36175	probable large ATP

30	59.5	16.6	224	2	I40474	pro-sigma-E process
31	59.5	16.6	4465	1	S17653	pro-sigma beta heavy
32	59	16.4	370	2	T34050	hypothetical prote
33	59	16.4	384	1	W2W41	E2 protein - human
34	58.5	16.3	136	2	T22240	hypothetical protea
35	58.5	16.3	299	2	B71967	probable peptidyl-i-
36	58.5	16.3	354	2	A75087	acetyl ornithine d
37	58.5	16.3	1402	2	F84480	probable retrotransl
38	58	16.2	390	2	T30020	hypothetical proteaf
39	57.5	16.0	230	2	S45332	homeotic protein G
40	57.5	16.0	234	2	D84075	hypothetical proteaf
41	57.5	16.0	343	2	D83718	glycoprotein endop
42	57.5	16.0	311	2	B69502	alcohol dehydrogen
43	57.5	16.0	419	2	T08683	hypothetical proteaf
44	57.5	16.0	1852	2	A37860	calcium channel pr
45	57.5	16.0	2137	2	T05244	hypothetical proteaf

ALIGNMENTS

RESULT

All protein - tomato golden mosaic virus
 C:Species: tomato golden mosaic virus
 A:Note: host Nicotiana sp. (tobacco)
 C:Date: 28-Aug-1985 #sequence,revision 28-Aug-1985 #text,change 08-Apr-1994
 C:Accession: A04170
 R:Hamilton, W.D.O.; Stein, V.E.; Coutts, R.H.A.; Buck, K.W.
 EMBL J. 3, 2197-2205, 1984
 A:Title: Complete nucleotide sequence of the infectious cloned DNA components of tomato
 A:Reference number: A04163
 A:Accession: A04170
 A:Molecule type: DNA
 A:Residues: 1-352 <HAM>
 C:Comment: The genome consists of two circular, single-stranded DNA components, DNA A
 C:Genetics:
 A:Map position: segment A
 C:Superfamily: tomato golden mosaic virus All protein

	Query Match	95.3%	Score 342	DB 1	Length 352
	Best Local Similarity	95.7%	Pred. No. 2.3e-31		
	Matches 67	Conservative	0	Mismatches 3	Indels 0
QY	1 TLVWEFPOVDGSAAGGCGTSDNDAAEALNASSKKEALQIREKIPEKYLFOFHNLSAL	60			
DB	111 TLVWEFPOVDGSAAGGCGTSDNDAAEALNASSKKEALQIREKIPEKYLFOFHNLSNL	170			
QY	61 AAFDKTPEP 70				
DB	171 DRIFDKTPEP 180				

RESULT 2
00CVPY
A: protein - potato yellow mosaic virus (isolate Venezuela)
C: Species: potato yellow mosaic virus
C: Date: 30-Jun-1992 #sequence: revision 30-Jun-1992 #text: change 16-Jun-2000
C: Accession: J00364
R: Coutts, R.H.A.; Coffin, R.S.; Roberts, E.J.F.; Hamilton, W.D.O.
J. Gen. Virol. 72, 1515-1520, 1991
A: title: The nucleotide sequence of the infectious cloned DNA components of potato yellow mosaic virus
A: Reference number: J00362; MUID: 91311403
A: Accession: J00364
A: Status: translation not shown
A: Molecule type: DNA
A: Residues: 1361 <COU>
A: Cross-references: GB: D000940; NID: g222458; PIDN: BAA00782.1; PID: g222459
C: GenElcs:
A: Map position: segment A
A: Superfamily: tomato golden mosaic virus A1 protein

RESULT 7
S39211
gene CI protein - tomato yellow leaf curl virus

C:Species: tomato yellow leaf curl virus
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Sep-1999
C:Accession: S39211
R:Norris, E.; Hidalgo, E.; Accotto, G.; Moriones, E.
submitted to the EMBL Data Library, August 1993
A:Description: High similarity among the tomato yellow leaf curl virus isolates from the
A:Reference number: S39209
A:Accession: S39211
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-359 <NOR>
A:Cross-references: EMBL:Z25751; NID:9433655; PIDN:CAA81026.1; PID:9433658
C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match 59.9%; Score 215; DB 2; Length 359;
Best Local Similarity 58.0%; Pred. No. 7.1e-17;
Matches 40; Conservative 9; Mismatches 20; Indels 0; Gaps 0;

OY 2 LVMGEFQVDSARGCGCOTSDNDAAEALNASSKEEALQIIRKIPKYLFOFHNLSALA 61
DB 111 LEMGTFQIDGSRARGGQOTANDAYAKAINAGSKSEALDVYIKELAPRDYTLHFHNINSMD 170

OY 62 AIFDKTPEP 70
DB 171 KVFQVPPAP 179

RESULT 8
S28360
A1: protein - beet curly top virus
C:Species: beet curly top virus
C:Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 20-Sep-1999
C:Accession: S28360
R:Stanley, J.; Markham, P.G.; Callis, R.J.; Pinner, M.S.
EMBO J. 5, 1761-1767, 1986
A:Title: The nucleotide sequence of an infectious clone of the geminivirus beet curly to
A:Reference number: S28360
A:Accession: S28360
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-385 <STA>
A:Cross-references: GB:M24597; EMBL:X04144; NID:9210678; PIDN:AAA42751.1; PID:9210679
C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match 59.1%; Score 212; DB 2; Length 385;
Best Local Similarity 55.7%; Pred. No. 1.7e-16;
Matches 39; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

OY 1 TLVMGEFQVDSARGCGCOTSDNDAAEALNASSKEEALQIIRKIPKYLFOFHNLSAL 60
DB 137 TIEWGEFQIDGSRARGGQOTANDSYAKALNATSDQALIKKEQPKDYFLQHNHNLNNA 196

OY 61 AIFDKTPEP 70
DB 197 QKIFGRPPDP 206

RESULT 9
S22593
A1: hypothetical protein C4 - tomato yellow leaf curl virus
C:Species: tomato yellow leaf curl virus
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Sep-1999
C:Accession: S22593
R:Kheyr-Pour, A.; Bendahmane, M.; Matzeit, V.; Accotto, G.P.; Crespi, S.; Gronenborn, B.
Nucleic Acids Res. 19, 6763-6769, 1991
A:Title: Tomato yellow leaf curl virus from Sardinia is a whitefly-transmitted monopartit
A:Reference number: S22588; MUID:92107660
A:Accession: S22593
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-359 <KHE>

A:Cross-references: EMBL:X61153; NID:962211; PIDN:CAA43466.1; PID:962217
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1991
C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match 58.8%; Score 211; DB 2; Length 359;
Best Local Similarity 56.5%; Pred. No. 2e-16;
Matches 39; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

OY 2 LVMGEFQVDSARGCGCOTSDNDAAEALNASSKEEALQIIRKIPKYLFOFHNLSALA 61
DB 111 LEMGTFQIDGSRARGGQOTANDAYAKAINAGSKSOALDVYIKELAPRDYTLHFHNINSMD 170

OY 62 AIFDKTPEP 70
DB 171 KVFQVPPAP 179

RESULT 10
OCCVW1
A1: protein - abutilon mosaic virus (isolate West India)
C:Species: abutilon mosaic virus
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 08-Apr-1994
C:Accession: A36214
R:Friscimuth, T.; Zimmat, G.; Jeske, H.
Virology 178, 461-468, 1990
A:Title: The nucleotide sequence of the abutilon mosaic virus reveals prokaryotic as
A:Reference number: A36214; MUID:91020984
A:Accession: A36214
A:Molecule type: DNA
A:Residues: 1-355 <FRI>
A:Cross-references: EMBL:X15983
C:Genetics:
A:Map position: segment A
C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match 58.5%; Score 210; DB 1; Length 355;
Best Local Similarity 57.1%; Pred. No. 2.6e-16;
Matches 40; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

OY 1 TLVMGEFQVDSARGCGCOTSDNDAAEALNASSKEEALQIIRKIPKYLFOFHNLSAL 60
DB 110 TAEWGEFQIDGSRARGGQOTANDSYAKALNAGDVQALNLIKEDPKDYVLQHNHNSRL 169

OY 61 AIFDKTPEP 70
DB 170 ERIFAKPEP 179

RESULT 11
J01870
A1: protein - tomato mottle virus (isolate Florida)
C:Species: tomato mottle virus
C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 07-May-1999
C:Accession: J01870
R:Abouzid, A.M.; Polston, J.E.; Hiebert, E.
J. Gen. Virol. 73, 3225-3229, 1992
A:Title: The nucleotide sequence of tomato mottle virus, a new geminivirus isolated f
A:Reference number: J01869; MUID:93107858
A:Accession: J01870
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-358 <ABO>
A:Cross-references: GB:L14460
C:Genetics:
A:Map position: segment A
C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match 57.7%; Score 207; DB 1; Length 358;
Best Local Similarity 54.3%; Pred. No. 5.8e-16;
Matches 38; Conservative 15; Mismatches 17; Indels 0; Gaps 0;

```

QY      1 TLWGEFFOVDGSSAGCGGCGOTSDNDAAAEALNNSKKEEALQIIREKIPEKYVLPQFNHUNSL 60
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db     107 TIEMCDPFIDGRSANGGGQSANDSYAKLNMGSYGSAVLAVEEQPKDFVLGNHNIRSNL 166
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

RESULT  12
QJ02327
ALI protein - Indian cassava mosaic virus
N:Alternate names: replication-associated protein
C:Species: Indian cassava mosaic virus
C>Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 20-Sep-1999
C:Accession: J02327; S35883
R:Hong, Y.G.; Robinson, D.J.; Harrison, B.D.
J. Gen. Virol. 74, 2437-2443, 1993
A>Title: Nucleotide sequence evidence for the occurrence of three distinct whitefly-tran
A:Reference number: J02326; MUID:94065670
A:Accession: J02327
A:Molecule type: DNA
A:Residues: 1-351 <HON>
C:Cross-references: EMBL:Z24758; NID:g395351; PIDDN:CA80891.1; PID:g584046
C:Superfamily: Tomato golden mosaic virus ALI protein

```

Query Match	57.1%	Score 205;	DB 2;	length 351;
Best Local Similarity	59.7%	Pred. No. 9.6e-16;		
Matches 40;	Conservative	9;	Mismatches 18;	Indels 0;
			Gaps	0

QY	4	WGEFQVDDSRARGCGOTSDNDAALNLSNSKEEALQITREKIPKYLFOQFINLSALAAI	63
		: : : : : : : : : : : : : :	
Db	113	WGTFQIDRSRARGCGQSDNDAVAALNLSNGSRSEALKITRELAFLADYLDLDFHHSNLDRI	172
QY	64	FDKTPPEP	70
		: : : : : : : : : : : : :	
Db	173	FTKPPPP	179

RESULT	13
S39235	gene C1 protein - tomato yellow leaf curl virus
C:Species:	tomato yellow leaf curl virus
C:Date:	06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 08-Sep-1997
C:Accession:	S39235
R:Crespi, S.; Norris, E.; Valira, A.; Bosco, D.; Accotto, G.	
A:Submitted to:	the EMBL Data Library, December 1993
A:Description:	A cloned DNA from a TYLCV isolate from Sicily showing low infectivity
A:Reference number:	S39233
A:Accession:	S39235
A:Status:	preliminary
A:Molecule type:	DNA
A:Residues:	1-359 <CDD>
A:Cross-references:	EMBL:Z28390; NID:91041671; PID:g1334964
C:Superfamily:	tomato golden mosaic virus A11 protein

Query Match	57.1%	Score 205	DB 2	length 359
Best Local Similarity	55.1%	Pred. No. 9.8e-16		
Matches 38	Conservative 11	Mismatches 20	Indels 0	Gaps 0

QY 2 LVWGEFQVUGRSARGGCQTSDNAAAEALNASSKEEALQITREKIDPKYLFGFHNLNSALA 61
| | | : | | | | | : | | | : | | : | : | : | : | : | : |
Db 111 LEMGTFQIDGRSARSGOQTANDAYAKALINARSSEALDVIKQLAPRDYVLHFHNISMD 170

```
QY      62 AIFDKTPEP 70
      :| | |
Db      171 KVFQVPPAP 179
```

RESULT 14

S59885
replication-associated protein C1 - tomato yellow leaf curl virus
C:Species: tomato yellow leaf curl virus
C:Date: 14-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 20-Sep-1999
C:Accession: S59885
R:Hong, Y.; Harrison, B.D.
submitted to the EMBL Data Library, February 1995
A:Description: Nucleotide sequences from tomato leaf curl viruses from different countries and geminiviruses.
A:Reference number: S58346
A:Accession: S59885
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-360 <HON>
A:Cross-references: EMBL:Z48182; NID:G944838; PIDN:CAAB80229.1; PID:G974211
C:superfamily: tomato golden mosaic virus A1 protein

Query Match	54.38;	Score 195;	DB 2;	Length 360;
Best Local Similarity	57.68;	Pred. NO. 1.4e-14;		
Matches 38;	Conservative 12;	Mismatches 16;	Indels 0;	Gaps 0;

[illegible]

RESULT 15

AL1 protein -tomato yellow leaf curl virus
 N:Alternate names: CI protein
 C:Species: tomato yellow leaf curl virus
 C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
 C:Accession: D40779
 R:Navot, N.; Pichersky, E.; Zeidan, M.; Zamir, D.; Czosnek, H.
 Virology 185, 151-161, 1991
 A:Title: Tomato yellow leaf curl virus: a whitefly-transmitted geminivirus with a sin-
 A:Reference number: A40779; MUID:92024070
 A:Accession: D40779
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-357 <NAV>
 A:Cross-references: GB:X15656; NID:g62204; PIDN:CA33688.1; PID:g62207
 C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match	53.8%	Score 193;	DB 1;	Length 357;
Best Local Similarity	62.3%;	Pred. No. 2.3e-14;		
Matches 38;	Conservative 10;	Mismatches 13;	Indels 0;	Gaps 0;

```
OY      4 MGCFVQDRSRARGCGQTSDNDAAAEALNLNASSKEEALOJIREKIPERYLFOPHILNSATAAI    63  
         | : ||| |||||   ||| ||| ||||| : || ||| : ||| : ||| : ||| : ||  
Db     111 FGVSIDRSRARGGQSNDAYAEALNLNGSSSEALNILKERAPDYI LLOGFINLSSNDRI    170
```

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OY      QY          6A F        64  
         ↓  
db       171 F 171
```

Search completed: January 3, 2002, 15:40:11
Job time: 307 sec

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```
ID VAL1_PYMV STANDARD; PRT; 361 AA.
AC P27258;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE AL1 PROTEIN.
OS Potato yellow mosaic virus (isolate Venezuela).
OC Viruses: ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10828;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-91311403; PubMed-1856690;
RA Coutts R.H.A.; Coffin R.S.; Roberts E.J.F.; Hamilton W.D.O.;
RT "The nucleotide sequence of the infectious cloned DNA components of
RT potato yellow mosaic virus";
RL J. Gen. Virol. 72:1515-1520(1991).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: D00940; BAA00782.1; -
CC PIR: J00364; OOCVPT.
DR InterPro: IPR001191; Gemin1_AL1.
DR Pfam: PF00799; Gemin1_AL1; 1.
DR PRINTS: PR00227; GEMCOATL1.
DR PRINTS: PR00228; GEMCOATCLV1.
DR ProDom: PD000736; Gemin1_AL1; 1.
KW ATP-binding. 229
KW NP_BIND
SQ SEQUENCE 361 AA; 40850 MW; 5627A33BF1264383 CRC64;

Query Match
Best Local Similarity: 67.4%; Score 242; DB 1; Length 361;
Matches 46; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 1 TLWGEFQVYDGRSARGGCQTSNDAAEALNASSKEEALQIREKIEKYLFQPHNLSAL 60
   1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 110 TIVMGCFQIDGRSARGGCQTVNDAAEALNASTGKKAAMKIKREKLFQYHNLSNL 169
   1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 AAFDKTPE 69
   1:|||||
DB 170 DRIFMKAPE 178

RESULT 3
VAL1_CLVX STANDARD; PRT; 358 AA.
ID VAL1_CLVX STANDARD; PRT; 358 AA.
AC P14982;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 PROTEIN (40.4 KDA PROTEIN).
GN AC1
OS Cassava latent virus (strain West Kenyan 844).
OC Viruses: ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10818;
RN [1]
RP SEQUENCE FROM N.A.
RA Stanley J.; Gay M.R.;
RT "Nucleotide sequence of cassava latent virus DNA.";
RL Nature 301:260-262(1983).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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CC -----
CC EMBL: J02057; -; NOT_ANNOTATED_CDS.
DR InterPro: IPR001191; Gemin1_AL1.
DR Pfam: PF00799; Gemin1_AL1; 1.
DR PRINTS: PR00227; GEMCOATL1.
DR PRINTS: PR00228; GEMCOATCLV1.
DR ProDom: PD000736; Gemin1_AL1; 1.
KW ATP-binding.
KW NP_BIND
SQ SEQUENCE 358 AA; 40346 MW; ED173EF53BE92D69 CRC64;

Query Match
Best Local Similarity: 63.8%; Score 229; DB 1; Length 358;
Matches 42; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 TLWGEFQVYDGRSARGGCQTSNDAAEALNASSKEEALQIREKIEKYLFQPHNLSAL 60
   1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 109 TIVMGCFQIDGRSARGGCQTSNDAAEALNASSKEEALQIREKIEKYLFQPHNLSNL 168
   1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 AAFDKTPE 70
   1:|||||
DB 169 DRIFORPPAP 178
```

```
RESULT 4
VAL1_CLVX STANDARD; PRT; 358 AA.
ID VAL1_CLVX STANDARD; PRT; 358 AA.
AC P14972;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 PROTEIN (40.4 KDA PROTEIN).
GN AC1
OS Cassava latent virus (strain Nigerian).
OC Viruses: ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10819;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-90174930; PubMed-2308831;
RA Morris B.; Coates L.; Lowe S.; Richardson K.; Eddy P.;
RT "Nucleotide sequence of the infectious cloned DNA components of
RT African cassava mosaic virus (Nigerian strain)".
RL Nucleic Acids Res. 18:197-198(1990).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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CC -----
CC EMBL: X17095; CAA34953.1; -
CC PIR: S07594; S07594.
DR InterPro: IPR001191; Gemin1_AL1.
DR Pfam: PF00799; Gemin1_AL1; 1.
DR PRINTS: PR00227; GEMCOATL1.
DR PRINTS: PR00228; GEMCOATCLV1.
DR ProDom: PD000736; Gemin1_AL1; 1.
KW ATP-binding.
KW NP_BIND
SQ SEQUENCE 358 AA; 40435 MW; 1DB16B0CB2D5E2C CRC64;

Query Match
Best Local Similarity: 63.8%; Score 229; DB 1; Length 358;
Matches 42; Conservative 13; Mismatches 15; Indels 0; Gaps 0;
```

```

OY 1 TLWGEFQVDGSRAGGCGTSDNDAAEALNASSKEALQIIREKIPEKYLFOFHNLNSAL 60
   1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 109 TVEMGEFQIDGSRAGGCGSANDAYAKALNASSKEALNVLRELVPKDFLOFHNLSNL 168
OY 61 AAIPEKTPPEP 70
   1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 169 DRIFQEPPEP 178

RESULT 5
VAL1_TYLCU STANDARD: PRT: 362 AA.
AC P36279;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE A1 PROTEIN (C1 PROTEIN).
GN C1.
OS Tomato yellow leaf curl virus (strain Australia) (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=36447;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE-93139778; PubMed-8423446;
RA Dry I.B., Rigden J.E., Krake L.R., Mullineaux P.M., Rezaian M.A.;
RT "Nucleotide sequence and genome organization of tomato leaf curl
   geminivirus."
RL J. Gen. Virol. 74:147-151(1993).
CC -1 SIMILARITY: BELONGS TO GEMINIVIRUSES A1 PROTEIN FAMILY.
DR PIR: J01887; J01887.
DR InterPro: IPR001191; Gemin1_AL1.
DR Pfam: PF00799; Gemin1_AL1; 1.
DR PRINTS: PR00227; GEMCOATL1.
DR PRINTS: PR00228; GEMCOATLVL.
DR Prodom: PD000736; Gemin1_AL1; 1.
KW ATP-binding.
NP_BIND 221 228 ATP (POTENTIAL).
FT SEQUENCE 362 AA; 41197 MW; 343E7184B4704098 CRC64;
SQ

Query Match 61.8%; Score 222; DB 1; Length 362;
Best Local Similarity 52.9%; Pred. No. 7e-18;
Matches 45; Conservative 9; Mismatches 15; Indels 16; Gaps 1;

OY 1 TLWGEFQVDGSRAGGCGTSDNDAAEALNASSKEALQIIREKIPEKYLFOFHNLNSAL 60
   1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 110 TLEMGEFQIDGSRAGGCGSANDAYAKALNASSKEALNVLRELVPKDFLOFHNLSNL 169
OY 61 AAIPEKTPPEP 69
   1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 170 DRIFPELVVVSPLSSSDFRPE 194

RESULT 6
VAL1_PHVU STANDARD: PRT: 349 AA.
AC Q06923;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE A1 PROTEIN.
GN A1.
OS Pepper huasteco virus (PHV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=28349;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE-94015007; PubMed-8409944;
RA Torres-Pacheco I., Garzon-Riznado J.A., Herrera-Estrella L.,
RA Rivera-Bustamante R.F.;
RT "Complete nucleotide sequence of pepper huasteco virus: analysis and
   comparison with bipartite geminiviruses."

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RL J. Gen. Virol. 74:2225-2231(1993).
CC -1 SIMILARITY: BELONGS TO GEMINIVIRUSES A1 PROTEIN FAMILY.
CC -----
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CC -----
DR EMBL: X70418; CAA49856.1; -
DR PIR: S31875; S31875.
DR PIR: J02300; J02300.
DR InterPro: IPR001191; Gemin1_AL1.
DR Pfam: PF00799; Gemin1_AL1; 1.
DR PRINTS: PR00227; GEMCOATL1.
DR PRINTS: PR00228; GEMCOATLVL.
DR Prodom: PD000736; Gemin1_AL1; 1.
KW ATP-binding.
NP_BIND 221 228 ATP (BY SIMILARITY).
FT SEQUENCE 349 AA; 39722 MW; D5F4E76CD56370F4 CRC64;
SQ

Query Match 60.2%; Score 216; DB 1; Length 349;
Best Local Similarity 58.6%; Pred. No. 3.2e-17;
Matches 41; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

OY 1 TLWGEFQVDGSRAGGCGTSDNDAAEALNASSKEALQIIREKIPEKYLFOFHNLNSAL 60
   1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 110 TVEMGEFQIDGSRAGGCGSANDAYAKALNASSKEALQIIREKQPHFLFOFHNLVNSA 169
OY 61 AAIPEKTPPEP 70
   1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 170 NRIFQPEP 179

RESULT 7
VAL1_TYLCU STANDARD: PRT: 359 AA.
AC P38609;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE A1 PROTEIN (C1 PROTEIN).
GN C1.
OS Tomato yellow leaf curl virus (strain Murcia) (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=37139;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE-94256836; PubMed-8198442;
RA Norris E., Hidalgo E., Accotto G., Moriones E.;
RT "High similarity among the tomato yellow leaf curl virus isolates
   from the west Mediterranean basin: the nucleotide sequence of an
   infectious clone from Spain."
RL Arch. Virol. 135:165-170(1994).
CC -1 SIMILARITY: BELONGS TO GEMINIVIRUSES A1 PROTEIN FAMILY.
CC -----
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CC -----
DR EMBL: Z25751; CAA81026.1; -
DR PIR: S39211; S39211.
DR InterPro: IPR001191; Gemin1_AL1.
DR Pfam: PF00799; Gemin1_AL1; 1.
DR PRINTS: PR00227; GEMCOATL1.
DR PRINTS: PR00228; GEMCOATLVL.

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DR PRODOM; PD000736; Gemin1_AL1; 1.
 KW ATP-binding. 221 228 ATP (POTENTIAL).
 FT NP-BIND 221 228
 SQ SEQUENCE 359 AA: 41065 MW; 2D170A51EF80A3EC CRC64;

Query Match
 Best Local Similarity 59.9%; Score 215; DB 1; Length 359;
 Matches 40; Conservative 9; Mismatches 20; Indels 0; Gaps 0;

QY 2 LVMGEFQVDSARSGCOTSDNDAAEALNASSKEALQIREKIPKYLFOFHNLSAL 61
 DB 111 LEMGFQIDGRSARSGQOTANDAYAKAINAGSKSEALDYIKELAPRDYILFHNNISNL 170

QY 62 AAFDKTPPEP 70
 DB 171 RVFQVPPAP 179

RESULT 8
 VAL1_BCTV STANDARD; PRT; 358 AA.

AC P14991:
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 01-AUG-1992 (Rel. 23, Last annotation update)
 DE AL1 PROTEIN (40.8 KDA PROTEIN).
 OS Beet curly top virus (BCTV).
 CC Viruses; ssDNA viruses; Geminiviridae; Curtovirus.

OC NCBI_TaxId=10840;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Stanley J., Markham P.G., Callis R.J., Pinner M.S.;
 RT "The nucleotide sequence of an infectious clone of the geminivirus
 RT beet curly top virus.";
 RL EMBL J. 5:1761-1767(1986).

-1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.

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CC EMBL; X04144; -; NOT_ANNOTATED_CDS.

DR InterPro: IPR001191; Gemin1_AL1.

DR Pfam: PF00799; Gemin1_AL1; 1.

DR PRINTS: PR00227; GEMCOATAL1.

DR PRINTS: PR00228; GEMCOATCLV1.

DR PRODOM: PD000736; Gemin1_AL1; 1.

KW ATP-binding. 222
 FT NP-BIND 222
 SQ SEQUENCE 358 AA: 40889 MW; 39A45FE3C0B9C333 CRC64;

Query Match
 Best Local Similarity 59.1%; Score 212; DB 1; Length 358;
 Matches 39; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSARSGCOTSDNDAAEALNASSKEALQIREKIPKYLFOFHNLSAL 60
 DB 110 TLVWGEFQVDSARSGCOTSDNDAAEALNASSKEALQIREKIPKYLFOFHNLSAL 169

QY 61 AAFDKTPPEP 70
 DB 170 QKIFQRPDP 179

RESULT 9
 VAL1_BGMV STANDARD; PRT; 353 AA.

AC P05175;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE AL1 PROTEIN (40.2 KDA PROTEIN).

OS Bean golden mosaic virus.
 CC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OC NCBI_TaxId=10839;

RN [1]
 RP SEQUENCE FROM N.A.
 RA Howarth A.J., Cation J., Bossert M., Goodhan R.M.;
 RT "Nucleotide sequence of bean golden mosaic virus and a model for gene
 RT regulation in geminiviruses.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:3572-3576(1985).

-1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.

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CC EMBL; M10070; AAA46318.1; -.

DR InterPro: IPR001191; Gemin1_AL1.

DR Pfam: PF00799; Gemin1_AL1; 1.

DR PRINTS: PR00227; GEMCOATAL1.

DR PRODOM: PD000736; Gemin1_AL1; 1.

KW ATP-binding. 222

FT NP-BIND 222
 SQ SEQUENCE 353 AA: 40190 MW; 80FA779DFE029A34 CRC64;

Query Match
 Best Local Similarity 58.8%; Score 211; DB 1; Length 353;
 Matches 41; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSARSGCOTSDNDAAEALNASSKEALQIREKIPKYLFOFHNLSAL 60
 DB 110 TLVWGEFQVDSARSGCOTSDNDAAEALNASSKEALQIREKIPKYLFOFHNLSAL 169

QY 61 AAFDKTPPEP 70
 DB 170 ERIFFKVPPEP 179

RESULT 10

VAL1_TYLCM STANDARD; PRT; 359 AA.

AC P27260;

DT 01-AUG-1992 (Rel. 23, Created)

DT 01-AUG-1992 (Rel. 23, Last sequence update)

DT 01-JUN-1994 (Rel. 29, Last annotation update)

DE AL1 PROTEIN (C1 PROTEIN).

GN Cl.

OS Tomato yellow leaf curl virus (strain Marmande) (TYLCV).

OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.

OC NCBI_TaxId=10833;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=92107660; PubMed=1840676;

RA Kheyr-Pour A., Bendahmane M., Matzeit V., Accotto G.P., Crespi S.,

RA Groenborn B.;

RT "Tomato yellow leaf curl virus from sardina is a

RT whitefly-transmitted monopartite geminivirus.";

RL Nucleic Acids Res. 19:6763-6769(1991).

-1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.

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DR EMBL: X61153; CAA43466.1; .
DR PIR: S22593; S22593.
DR InterPro: IPR001191; Gemini_AL1.
DR Pfam: PF00799; Gemini_AL1; 1.
DR PRINTS: PR00227; GEMCOATAL1.
DR PRINTS: PR00228; GEMCOATCIVL1.
DR Prodom: PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP_BIND 220 ATP (POTENTIAL).
SQ SEQUENCE 359 AA; 40733 MW; 9717B4A07C93EFA7 CRC64;

Query Match 58.8%; Score 211; DB 1; Length 359;
Best Local Similarity 56.5%; Pred. No. 1.2e-16;
Matches 39; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

QY 2 LVWGEFOVYDGRSARGCGCOTSDNDAAEALNASSKEEALQITREKPEKYLFOFHNLNSALA 61
DB 111 LEMGTFTQIDGRSARGCGGTANDAYAKAINAGSKSQAIDYIKELAPDYLVHFNHNSNLD 170
QY 62 AAFDKTPPEP 70
DB 171 KVFQVPPAP 179

RESULT 11
VAL1_ABMVW

ID VAL1_ABMVW STANDARD; PRT; 355 AA.
AC P21947;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 PROTEIN.
GN AC1.
OS Abutillon mosaic virus (Isolate West India).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10816;

RP SEQUENCE FROM N.A.
RX MEDLINE-91020984; PubMed-2219703;
RA Frischmuth T.; Zimmat G.; Jeske H.;
RT "The nucleotide sequence of abutillon mosaic virus reveals prokaryotic
RT as well as eukaryotic features."
RL Virology 178:461-468(1990).
CC -i- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.

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CC EMBL: X15983; -; NOT_ANNOTATED_CDS.
DR PIR: A36214; QOCVW1.
DR InterPro: IPR001191; Gemini_AL1.
DR Pfam: PF00799; Gemini_AL1; 1.
DR PRINTS: PR00227; GEMCOATAL1.
DR PRINTS: PR00228; GEMCOATCIVL1.
DR Prodom: PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP_BIND 221 228 ATP (POTENTIAL).
SQ SEQUENCE 355 AA; 40257 MW; 16A2CA8A6525IE95 CRC64;

Query Match 58.5%; Score 210; DB 1; Length 355;

Best Local Similarity 57.1%; Pred. No. 1.6e-16;
Matches 40; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

QY 1 TLWGEFOVYDGRSARGCGCOTSDNDAAEALNASSKEEALQITREKPEKYLFOFHNLNSAL 60
DB 110 FAWGEFOVYDGRSARGCGGTANDSAYAKAINAGVGSALNILEKEQKDYLVQHNHNSNL 169
QY 61 AAFDKTPPEP 70
DB 170 ERIFAKAPPEP 179

RESULT 12
VAL1_TMOV

ID VAL1_TMOV STANDARD; PRT; 361 AA.
AC Q06657;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 PROTEIN.
GN AL1.
OS Tomato mottle virus (Isolate Florida) (TMOV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=36449;

RP SEQUENCE FROM N.A.
RX MEDLINE-93107858; PubMed-1469361;
RA Abouzid A.M., Polston J.E., Hiebert E.;
RT "The nucleotide sequence of tomato mottle virus, a new geminivirus
RT isolated from tomatoes in Florida."
RL J. Gen. Virol. 73:3225-3229(1992).
CC -i- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.

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DR EMBL: L14460; AAC32414.1; .
DR PIR: J01870; J01870.
DR InterPro: IPR001191; Gemini_AL1.
DR Pfam: PF00799; Gemini_AL1; 1.
DR PRINTS: PR00227; GEMCOATAL1.
DR PRINTS: PR00228; GEMCOATCIVL1.
DR Prodom: PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP_BIND 222 229 ATP (BY SIMILARITY).
SQ SEQUENCE 361 AA; 40516 MW; 8138B65CEBAC6950 CRC64;

Query Match 57.7%; Score 207; DB 1; Length 361;
Best Local Similarity 54.3%; Pred. No. 3.5e-16;
Matches 38; Conservative 15; Mismatches 17; Indels 0; Gaps 0;

QY 1 TLWGEFOVYDGRSARGCGCOTSDNDAAEALNASSKEEALQITREKPEKYLFOFHNLNSAL 60
DB 110 TLEWGEFOVYDGRSARGCGGSANDSAYAKAINAGSVGSALAVLREGEKDFVLQHNHNSNL 169
QY 61 AAFDKTPPEP 70
DB 170 ERIFAKAPPEP 179

RESULT 13
VAL1_TYLCV

ID VAL1_TYLCV STANDARD; PRT; 357 AA.
AC P27259;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)

```

DE AL1 PROTEIN (C1 PROTEIN).
GN C1.
OS Tomato yellow leaf curl virus (TYLCV).
OC Viruses: ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10832;
RN (1)
RP SEQUENCE FROM N.A.
RA MEDLINE-92024070; PubMed-1926771;
RA Navot N., Pichersky E., Zeidan M., Zamir D., Czosnek H.;
RT "Tomato yellow leaf curl virus: a whitefly-transmitted geminivirus
RT with a single genomic component.";
RT Virology 185:151-161(1991).
CC -1 SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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CC -----
DR EMBL: X15656; CA33688.1;
DR PIR: D40779; Q0CVCL;
DR InterPro: IPR001191; Geminl_AL1.
DR Pfam: PF00799; Geminl_AL1; 1.
DR PRINTS: PR00227; GEMCOATP.L.
DR PRINTS: PR00228; GEMCOATCLV.L.
DR ProDom: PD000736; Geminl_AL1; 1.
KW ATP-binding.
KW NP_BIND.
FT SEQUENCE 357 AA; 40678 MW; 939AB68E1AB3B2A7 CRC64;
QY 4 MGFEVDGRSARGCQTSNDAAEALNASSKEPALQITIREKIPKYLFOFHNLSALAAIP 63
DB 111 FGVSQIDGRSARGCOOSANDAYAEALNAGSKSEALNILEKAPKDYILLOPHNLSSLDRI 170
QY 64 F 64
DB 171 F 171
RESULT 14
VAL1 SLICV
ID VAL1_SLICV STANDARD: PRT: 347 AA.
AC P29048;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE AL1 PROTEIN.
OS Squash leaf curl virus.
OC Viruses: ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10829;
RN (1)
RP SEQUENCE FROM N.A.
RA MEDLINE-91082449; PubMed-1984668;
RA Lazarowitz S.G., Lazdins J.B.;
RT "Infectivity and complete nucleotide sequence of the cloned genomic
RT components of a bipartite squash leaf curl geminivirus with a broad
RT host range phenotype.";
RT Virology 180:58-69(1991).
CC -1 SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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CC -----
DR EMBL: M38183; AAC32410.1; ALT_INIT.
DR PIR: C36785; Q0CVSL.
DR InterPro: IPR001191; Geminl_AL1.
DR Pfam: PF00799; Geminl_AL1; 1.
DR PRINTS: PR00227; GEMCOATP.L.
DR PRINTS: PR00228; GEMCOATCLV.L.
DR ProDom: PD000736; Geminl_AL1; 1.
KW ATP-binding.
KW NP_BIND.
FT SEQUENCE 347 AA; 39110 MW; AFDAEBDE122110E CRC64;
QY 5 GFQVDGRSARGCQTSNDAAEALNASSKEPALQITIREKIPKYLFOFHNLSALAAIP 64
DB 116 GQKVGSG---GSKSNKDDVYHNAVNAAGSAGEALDIKADPKFTLVYHNLNLANVERLF 171
QY 65 DKTRPEP 70
DB 172 QKPEP 177
RESULT 15
TBL2_HUMAN
ID TBL2_HUMAN STANDARD: PRT: 447 AA.
AC Q9Y4P3; Q9Q0E2;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE TRANSDUCIN BETA-LIKE 2 PROTEIN (WS BETA-TRANSDUCIN REPEATS PROTEIN)
DE (WS-BETA-TRP).
GN TBL2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=20044626; PubMed=10575226;
RA Perez Jurado L.A., Wang Y.-K., Francke U., Cruces J.;
RT TBL2, a novel transducin family member in the WBS deletion;
RT characterization of the complete sequence, genomic structure,
RT transcriptional variants and the mouse ortholog.";
RT Cytogenet. Cell Genet. 86:277-284(1999).
RN (2)
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=21154917; PubMed=11230166;
RA Wiemann S., Well B., Wellenreuther R., Gassenhuber J., Glassl S.,
RA Ansorge W., Boecker M., Bloecker H., Bauersachs S., Blum H.,
RA Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strick N.,
RA Mewes H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D.,
RA Wambutt R., Korn B., Klein M., Pouskka A.;
RT "Towards a catalog of human genes and proteins: sequencing and
RT analysis of 500 novel complete protein coding human cDNAs.";
RL Genome Res. 11:422-435(2001).
RN (3)
RP SEQUENCE OF 14-447 FROM N.A.
RX MEDLINE=99075645; PubMed=9860302;
RA Meng X., Lu X., Li Z., Green E.D., Massa H., Trask B.J., Morris C.A.,
RA Keating M.T.;
RT "Complete physical map of the common deletion region in Williams
RT syndrome and identification and characterization of three novel
RT genes.";
RL Hum. Genet. 103:590-599(1998).
CC -1 SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
CC -----

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DR EMBL: AF097484; AAF06823.1; -.
DR EMBL: AF097485; AAF06824.1; -.
DR EMBL: AL080162; CAB45751.1; -.
DR EMBL: AF056183; AAD28083.1; ALT_INIT.
DR InterPro: IPR001680; WD40.
DR Pfam: PF00400; WD40; 5.
DR PRINTS: PRO0320; GPROTEINBRPT.
DR SMART: SM00320; WD40; 5.
DR PROSITE: PS00676; WD_REPEATS_1; 1.
DR PROSITE: PS50082; WD_REPEATS_2; 3.
DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.
FT REPEAT 88 127 WD 1.
FT REPEAT 134 174 WD 2.
FT REPEAT 186 226 WD 3.
FT REPEAT 228 267 WD 4.
FT REPEAT 277 316 WD 5.
FT REPEAT 329 367 WD 6.
FT REPEAT 371 409 WD 7.
SQ SEQUENCE 447 AA; 49797 MW; R260087E1A71D3F9 CRC64;

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Query Match 18.9%; Score 68; DB 1; Length 447;
Best Local Similarity 32.7%; Pred. NO. 2.6;
Matches 16; Conservative 11; Mismatches 22; Indels 0; Gaps 0;

QY 12 KSAAGCCQTSDAAAEALNASKKEEALÖIREKIPEKYLFGFHNUNLSA 600
|| | : | : | : | : | : | : | : ||
Db 38 RSGRPACQKANGFPDPDKSSGSKQKQYQRIRKEKPQGHNFTHRLAAL 866

Search completed: January 3, 2002, 15:57:17
Job time: 1103 sec

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009727
ID 009727 PRELIMINARY: PRT: 226 AA.
AC 009727:
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE REP PROTEIN (FRAGMENT).
GN REP.
OS Leornurus mosaic virus.
OC Viruses: ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=58177;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LEWY-BRAZIL 1;
RA Faria J.C., Maxwell D.P.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: 092532; AAB5157.1;
DR InterPro: IPRO01191; Geminl_AL1.
DR Pfam: PF00799; Geminl_AL1.
DR PRINTS: PR00227; GEMCOATALL.
DR Prodom: PD000736; Geminl_AL1: 1.
FT NON_TER 226
SQ SEQUENCE 226 AA: 25617 MW: 73CDB6E766083FC5 CRC64:

Query Match 76.3%; Score 274; DB 12; Length 226;
Best Local Similarity 77.1%; Pred. No. 2.3e-23;
Matches 54; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

OY 1 TLVGEFQVDSRGSGCOTSDNDAEALNASSKEPALQITREKPEKYLFGFHNSAL 60
1: |||||
DB 111 TVMGFEQVDSRGSGCOTSDNDAEALNAPKRTALQITREKPEKYLFGFHNSNL 170
1: |||||
OY 61 AATFDKTPP 70
1: |||||
DB 171 DRLFAKAPP 180
1: |||||

RESULT 3
O9WHF6 PRELIMINARY: PRT: 226 AA.
AC O9WHF6:
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE REPLICATION-ASSOCIATED PROTEIN (FRAGMENT).
GN REP.
OS tomato mild mottle geminivirus.
OC Viruses: ssDNA viruses; Geminiviridae; Unclassified Geminiviridae.
OX NCBI_TaxID=92943;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HN96-HSKW;
RA Nakhta M.K., Mejia L., Ramirez P., Karkashian J.P., Doyle M.M.,
RA Maxwell D.P.;
RL "Molecular characterization and DNA-based detection methods for
vegetable-infecting geminiviruses in Central America."
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: A131071; A033471.1;
DR InterPro: IPRO01191; Geminl_AL1.
DR Pfam: PF00799; Geminl_AL1.
DR PRINTS: PR00227; GEMCOATALL.
DR Prodom: PD000736; Geminl_AL1: 1.
FT NON_TER 226
SQ SEQUENCE 226 AA: 25941 MW: 2EA4116712871A23 CRC64:

Query Match 76.3%; Score 274; DB 12; Length 226;
Best Local Similarity 72.9%; Pred. No. 2.3e-23;
Matches 51; Conservative 12; Mismatches 7; Indels 0; Gaps 0;
OY 1 TLVGEFQVDSRGSGCOTSDNDAEALNASSKEPALQITREKPEKYLFGFHNSAL 60
1: |||||

DB 111 TVMGFEQVDSRGSGCOTSDNDAEALNASSKEPALQITREKPEKYLFGFHNSNL 170
OY 61 AATFDKTPP 70
1: |||||
DB 171 DRLFAKAPP 180
1: |||||

RESULT 4
O67574 PRELIMINARY: PRT: 361 AA.
ID O67574:
AC O67574:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE PUTATIVE REPLICATIVE PROTEIN.
GN AL1.
OS Bean golden mosaic virus.
OC Viruses: ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10839;
RN [1]
RP SEQUENCE FROM N.A.
RA Gilbertson R.L., Faria J.C., Hanson S.F., Morales F.J., Ahlquist P.G.,
RA Maxwell D.P., Russell D.R.;
RL Phytopathology 81:980-985(1991).
RN [2]
RP SEQUENCE FROM N.A.
RA Gilbertson R.L., Hidayat S.H., Martinez R.T., Leong S.A., Faria J.C.,
RA Morales F.J., Maxwell D.P.;
RL Plant Dis. 75:336-342(1991).
RN [3]
RP SEQUENCE FROM N.A.
RA Gilbertson R.L., Faria J.C., Ahlquist P.G., Maxwell D.P.;
RL Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.
DR EMBL: M88686; AAA46312.1;
DR InterPro: IPRO01191; Geminl_AL1.
DR Pfam: PF00799; Geminl_AL1.
DR PRINTS: PR00227; GEMCOATALL.
DR Prodom: PD000736; Geminl_AL1: 1.
FT SEQUENCE 361 AA: 41041 MW: 0094C7ACAF06B788 CRC64:

Query Match 75.8%; Score 272; DB 12; Length 361;
Best Local Similarity 76.1%; Pred. No. 6.7e-23;
Matches 51; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

OY 4 WGEFQVDSRGSGCOTSDNDAEALNASSKEPALQITREKPEKYLFGFHNSALAI 63
1: |||||
DB 113 WGEFQVDSRGSGCOTSDNDAEALNASSKEPALQITREKPEKYLFGFHNSLMDRI 172
1: |||||
OY 64 FDKTPP 70
1: |||||
DB 173 FTKAPP 179
1: |||||

RESULT 5
O9QDB1 PRELIMINARY: PRT: 225 AA.
ID O9QDB1:
AC O9QDB1:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE REPLICATION ASSOCIATED PROTEIN (FRAGMENT).
GN REP.
OS cowpea golden mosaic geminivirus.
OC Viruses: ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=69263;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CGW-BR;
RA Faria J.C.;
RL "Partial nucleotide sequence of cowpea golden mosaic geminivirus from
Brazil."
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF188708; AAF06318.1; -.
DR InterPro: IPR001191; Gemini_AL1.
DR Pfam: PF00799; Gemini_AL1.
DR PRINTS: PR00227; GEMCOATALL.
DR ProDom: PD000736; Gemini_AL1.
FT NON_TER 225 225
SQ SEQUENCE 225 AA; 25766 MW; 1089CB8BD8D15B5D CRC64;

Query Match 75.2%; Score 270; DB 12; Length 225;
Best Local Similarity 76.1%; Pred. No. 6, 6e-23;
Matches 51; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 4 TCGEFOVDGSRAGCGCOTSDNAAAEALNASSKEEALQIREKIPKYLFOFHNLSALAI 63
DB 113 TCGEFOVDGSRAGCGCOTSDNAAAEALNASSKEEALQIREKIPKYLFOFHNLSALAI 172
QY 64 FDKTPEP 70
DB 173 FKRPPEP 179

RESULT 6
Q9ELT8 PRELIMINARY; PRT; 314 AA.
AC Q9ELT8:
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE REPLICATION ASSOCIATION PROTEIN.
GN AC1.
OS sweet potato leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=100755;
RN [1]
RP SEQUENCE FROM N.A.
RA Lotrakul P., Valverde R.A., Clark C.A., Sim J., De la Torre R.;
RT "Detection of a geminivirus infecting sweet potato in the United
RT States.";
RL Plant Dis. 82:1253-1257(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Lotrakul P., Valverde R.A.;
RT Submitted (JUL-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF288227; AAG01006.1; -.
DR InterPro: IPR001191; Gemini_AL1.
DR Pfam: PF00799; Gemini_AL1.
DR PRINTS: PR00227; GEMCOATALL.
DR ProDom: PD000736; Gemini_AL1.
SQ SEQUENCE 314 AA; 35153 MW; 686220613046943F CRC64;

Query Match 75.2%; Score 270; DB 12; Length 314;
Best Local Similarity 79.4%; Pred. No. 9, 7e-23;
Matches 54; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 1 TLWGEFOVDGSRAGCGCOTSDNAAAEALNASSKEEALQIREKIPKYLFOFHNLSAL 60
DB 110 TLWGEFOVDGSRAGCGCOTSDNAAAEALNASSKEEALQIREKIPKYLFOFHNLSAL 169
QY 61 AATFDKTP 68
DB 170 DRIFSPPEP 177

RESULT 7
Q9QS55 PRELIMINARY; PRT; 364 AA.
AC Q9QS55:
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE REPLICATION INITIATION PROTEIN AC1.

GN AC1.
OS sweet potato leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=100755;
RN [1]
RP SEQUENCE FROM N.A.
RA Lotrakul P., Valverde R.A., Clark C.A., Sim J., De la Torre R.;
RT "Detection of a geminivirus infecting sweet potato in the United
RT States.";
RL Plant Dis. 82:1253-1257(1998).
DR EMBL: AF104036; AAD47173.1; -.
DR InterPro: IPR001191; Gemini_AL1.
DR Pfam: PF00799; Gemini_AL1.
DR PRINTS: PR00227; GEMCOATALL.
DR ProDom: PD000736; Gemini_AL1.
SQ SEQUENCE 364 AA; 40680 MW; 5F79752431A09D6E CRC64;

Query Match 75.2%; Score 270; DB 12; Length 364;
Best Local Similarity 79.4%; Pred. No. 1, 1e-22;
Matches 54; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 1 TLWGEFOVDGSRAGCGCOTSDNAAAEALNASSKEEALQIREKIPKYLFOFHNLSAL 60
DB 110 TLWGEFOVDGSRAGCGCOTSDNAAAEALNASSKEEALQIREKIPKYLFOFHNLSAL 169
QY 61 AATFDKTP 68
DB 170 DRIFSPPEP 177

RESULT 8
Q98693 PRELIMINARY; PRT; 185 AA.
AC Q98693:
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE REP PROTEIN (FRAGMENT).
GN AC1.
OS sida golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=51034;
RN [1]
RP SEQUENCE FROM N.A.
KC STRAIN=JAMAICA.
RA Roye M.E., McLaughlin W.A., Nakhla N.K., Maxwell D.P.;
RL Plant Dis. 81:1251-1258(1997).
DR EMBL: U67926; AAB97865.1; -.
DR InterPro: IPR001191; Gemini_AL1.
DR Pfam: PF00799; Gemini_AL1.
DR PRINTS: PR00227; GEMCOATALL.
DR ProDom: PD000736; Gemini_AL1.
FT NON_TER 1 1
FT NON_TER 185 185
SQ SEQUENCE 185 AA; 20975 MW; 3913850A025A5BE1 CRC64;

Query Match 74.4%; Score 267; DB 12; Length 185;
Best Local Similarity 70.0%; Pred. No. 1, 2e-22;
Matches 49; Conservative 12; Mismatches 9; Indels 0; Gaps 0;

QY 1 TLWGEFOVDGSRAGCGCOTSDNAAAEALNASSKEEALQIREKIPKYLFOFHNLSAL 60
DB 89 TLWGEFOVDGSRAGCGCOTSDNAAAEALNASSKEEALQIREKIPKYLFOFHNLSAL 148
QY 61 AATFDKTP 70
DB 149 DRIFSKPEP 158

RESULT 9
P88975

Fri Jan 4 09:39:30 2002

us-09-289-346a-7.rspt

Page 6

Job time: 1121 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 3, 2002, 15:38:50 ; Search time 65.28 Seconds
(without alignments)
24.130 Million cell updates/sec

Title: US-09-289-346A-7

Perfect score: 359
Sequence: 1 TLVWGEFGYDGRSARGCCT.....PQHNLSALATFDKTPPE 70

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*

- 1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
- 2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
- 3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
- 4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
- 5: /cgn2_6/ptodata/2/1aa/PCITUS.COMB.pep:*
- 6: /cgn2_6/ptodata/2/1aa/backfilest1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	213	59.3	353	4	US-08-838-151A-44
2	213	59.3	353	4	US-08-838-151A-46
3	213	59.3	353	4	US-08-838-151A-49
4	213	59.3	353	4	US-08-838-151A-52
5	213	59.3	353	4	US-08-838-151A-55
6	211	58.8	359	4	US-08-809-103B-2
7	211	58.8	359	4	US-08-809-103B-4
8	211	58.8	359	4	US-08-809-103B-6
9	211	58.8	359	4	US-08-809-103B-8
10	211	58.8	361	4	US-08-838-151A-2
11	211	58.8	361	4	US-08-838-151A-4
12	211	58.8	361	4	US-08-838-151A-6
13	211	58.8	361	4	US-08-838-151A-8
14	193	53.8	357	4	US-08-838-151A-24
15	193	53.8	357	4	US-08-838-151A-27
16	193	53.8	357	4	US-08-838-151A-30
17	185	51.5	357	4	US-08-838-151A-20
18	63.5	17.7	2161	1	US-07-745-206A-2
19	63.5	17.7	2161	1	US-08-455-543A-49
20	63.5	17.7	2161	1	US-08-455-543A-51
21	63.5	17.7	2161	2	US-08-223-305C-49
22	63.5	17.7	2161	2	US-08-223-305C-51
23	63.5	17.7	2161	2	US-08-311-363-2
24	60.5	16.9	131	4	US-08-838-151A-14
25	58	16.2	374	2	US-08-928-692-51
26	57	15.9	454	3	US-08-446-100-26
27	57	15.9	454	3	US-08-446-100-27

28	57	15.9	454	3	US-08-446-100-28	Sequence 28, Appl
29	57	15.9	454	3	US-08-446-100-29	Sequence 29, Appl
30	57	15.9	454	3	US-08-446-100-30	Sequence 30, Appl
31	56	15.6	602	2	US-08-419-652-6	Sequence 6, Appl
32	56	15.6	771	1	US-07-923-976-6	Sequence 4, Appl
33	56	15.6	783	6	5422248-2	Sequence 6, Appl
34	56	15.6	836	1	US-07-923-976-4	Sequence 4, Appl
35	56	15.6	863	1	US-07-923-976-8	Sequence 8, Appl
36	55.5	15.5	860	1	US-08-117-362-3	Sequence 3, Appl
37	55.5	15.5	860	1	US-08-486-924-3	Sequence 3, Appl
38	55	15.3	432	1	US-08-167-919A-11	Sequence 11, Appl
39	55	15.3	432	3	US-08-715-106-11	Sequence 31, Appl
40	55	15.3	454	3	US-08-446-100-31	Sequence 24, Appl
41	54.5	15.2	1713	3	US-08-600-982-24	Sequence 24, Appl
42	54.5	15.2	1713	5	PCT-US94-10261A-24	Sequence 24, Appl
43	54	15.0	751	4	US-09-036-987A-24	Sequence 24, Appl
44	54	15.0	751	4	US-09-370-700-24	Sequence 24, Appl
45	53.5	14.9	373	3	US-08-258-287B-42	Sequence 42, Appl

ALIGNMENTS

RESULT 1
US-08-838-151A-44
; Sequence 44, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Lou, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminitovirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838.151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-44

Query Match 59.3%; Score 213; DB 4; Length 353;
Best Local Similarity 58.6%; Pred. No. 1.7e-20;
Matches 41; Conservative 12; Mismatches 17; Indels 0; Gaps 0;
QY 1 TLVWGEFGYDGRSARGCCTSDMAAEALNASSKEALQIREKIPKYLFPQHNLSAL 60

Db 110 TIEWGQFQVYDGRSARCGQGSANDSYAKALNADISALTLTKEOPKDYVLOHHNIRSNL 169
QY 61 AAIPTKPEP 70
Db 170 ERIYFKVPEP 179

RESULT 2

US-08-838-151A-46

Sequence 46, Application US/08838151A

Patent No. 6291743

GENERAL INFORMATION:

APPLICANT: Stout, John T

APPLICANT: Luu, Hang T

APPLICANT: Maxwell, Douglas

APPLICANT: Ahlquist, Paul

TITLE OF INVENTION: Transgenic Plants Expressing Geminitivirus

TITLE OF INVENTION: Genes

NUMBER OF SEQUENCES: 63

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/838,151A

FILING DATE:

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Mueller, Lisa V

REGISTRATION NUMBER: 38,978

REFERENCE/DOCKET NUMBER: SVS3801P0260

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-616-5460

TELEFAX: 312-616-5460

INFORMATION FOR SEQ ID NO: 46:

SEQUENCE CHARACTERISTICS:

LENGTH: 353 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-838-151A-46

Query Match 59.3%; Score 213; DB 4; Length 353;
Best Local Similarity 58.6%; Pred. No. 1.7e-20;
Matches 41; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

QY 1 TLWGEFQVYDGRSARCGQGSANDSYAKALNADISALTLTKEOPKDYVLOHHNIRSNL 60
Db 110 TIEWGQFQVYDGRSARCGQGSANDSYAKALNADISALTLTKEOPKDYVLOHHNIRSNL 169
QY 61 AAIPTKPEP 70
Db 170 ERIYFKVPEP 179

RESULT 3

US-08-838-151A-49

Sequence 49, Application US/08838151A

Patent No. 6291743

GENERAL INFORMATION:

APPLICANT: Stout, John T

APPLICANT: Luu, Hang T

APPLICANT: Maxwell, Douglas

APPLICANT: Ahlquist, Paul

TITLE OF INVENTION: Transgenic Plants Expressing Geminitivirus

TITLE OF INVENTION: Genes

NUMBER OF SEQUENCES: 63

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/838,151A

FILING DATE:

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Mueller, Lisa V

REGISTRATION NUMBER: 38,978

REFERENCE/DOCKET NUMBER: SVS3801P0260

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-616-5460

TELEFAX: 312-616-5460

INFORMATION FOR SEQ ID NO: 49:

SEQUENCE CHARACTERISTICS:

LENGTH: 353 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-838-151A-49

APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminitivirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5460
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 353 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-838-151A-49

Query Match 59.3%; Score 213; DB 4; Length 353;
Best Local Similarity 58.6%; Pred. No. 1.7e-20;
Matches 41; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

QY 1 TLWGEFQVYDGRSARCGQGSANDSYAKALNADISALTLTKEOPKDYVLOHHNIRSNL 60
Db 110 TIEWGQFQVYDGRSARCGQGSANDSYAKALNADISALTLTKEOPKDYVLOHHNIRSNL 169
QY 61 AAIPTKPEP 70
Db 170 ERIYFKVPEP 179

RESULT 4

US-08-838-151A-52

Sequence 52, Application US/08838151A

Patent No. 6291743

GENERAL INFORMATION:

APPLICANT: Stout, John T

APPLICANT: Luu, Hang T

APPLICANT: Maxwell, Douglas

APPLICANT: Ahlquist, Paul

APPLICANT: Hanson, Steve

TITLE OF INVENTION: Transgenic Plants Expressing Geminitivirus

TITLE OF INVENTION: Genes

NUMBER OF SEQUENCES: 63

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/838,151A

FILING DATE:

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Mueller, Lisa V

REGISTRATION NUMBER: 38,978

REFERENCE/DOCKET NUMBER: SVS3801P0260

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-616-5460

TELEFAX: 312-616-5460

INFORMATION FOR SEQ ID NO: 52:

SEQUENCE CHARACTERISTICS:

LENGTH: 353 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-838-151A-52

```

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 353 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-838-151A-52

```

Query Match	59.3%	Score 213	DB 4	Length 353
Best Local Similarity	58.6%	Pred. No. 1.7e-20		
Matches 41	Conservative 12	Mismatches 17	Indels 0	Gaps 0

[illegible]

RESULT 5
 US-08-838-151A-55
 Sequence 55, Application US/08838151A
 Patent No. 6291743
 GENERAL INFORMATION:
 APPLICANT: Stout, John T
 APPLICANT: Liu, Hang T
 APPLICANT: Maxwell, Douglas
 APPLICANT: Ahlquist, Paul
 APPLICANT: Hanson, Steve
 TITLE OF INVENTION: Transgenic Plants Expressing GeminiVirus
 TITLE OF INVENTION: Genes
 NUMBER OF SEQUENCES: 63
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dressler, Rocky, Milnamow & Katz
 STREET: Two Prudential Plaza, Suite 4700
 CITY: Chicago
 STATE: Illinois
 COUNTRY: U.S.A.
 ZIP: 60601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/838,151A
 FILING DATE:
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Mueller, Lisa V
 REGISTRATION NUMBER: 38,978
 REFERENCE/DOCKET NUMBER: SVS3801P0260
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-616-5400
 TELEFAX: 312-616-5460
 INFORMATION FOR SEQ ID NO: 55:

```

;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 353 amino acids
;      TYPE: amino acid
;      TOPOLOGY: linear
;      MOLECULE TYPE: protein
US-08-838-151A-55

```

Query Match	59.3%	Score 213;	DB 4;	Length 353;
Best Local Similarity	58.6%	Pred. No. 1.7e-20;		
Matches 41;	Conservative 12;	Mismatches 17;	Indels 0;	Gaps 0;

[illegible]

RESULT 6
US-08-809-103B-2

Sequence 2, Application US/08809103B
Patent No. 6133505

APPLICANT: GRONENBORN, Bruno
TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:

ADDRESSEE: YOUNG & THOMPSON
STREET: 745 South 23rd Street
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.

```

1 COMPUTER READABLE FORM:
2 MEDIUM TYPE: Floppy disk
3 COMPUTER: IBM PC compatible
4 OPERATING SYSTEM: PC-DOS/MS-DOS
5 SOFTWARE: Patent In Release #1.0, Version #1.30
6 CURRENT APPLICATION DATA:
7 APPLICATION NUMBER: US/08/809,103B
8 FILING DATE: 17-MAR-1997
9 CLASSIFICATION: 800
10 PRIOR APPLICATION DATA:
11 APPLICATION NUMBER: FR 94.11040
12 FILING DATE: 15-SEP-1994
13 PRIOR APPLICATION DATA:
14 APPLICATION NUMBER: WO PCT/FR95/01192
15 FILING DATE: 15-SEP-1995
16 ATTORNEY/AGENT INFORMATION:
17 NAME: PATCH, Andrew J.
18 REGISTRATION NUMBER: 32,925
19 REFERENCE/DOCKET NUMBER: US94AL CNR TOM
20 TELECOMMUNICATION INFORMATION:
21 TELEPHONE: (703) 521-2297
22 TELEFAX: (703) 585-0573
23 TELEX: 248425 EMBON
24 INFORMATION FOR SEQ ID NO: 2:
25 SEQUENCE CHARACTERISTICS:
26 LENGTH: 359 amino acids
27 TYPE: amino acid
28 TOPOLOGY: linear
29 MOLECULE TYPE: protein
30 US-08-809-103B-2

```

Query Match	58.8%	Score 211;	DB 4;	Length 359;
Best Local Similarity	56.5%;	Pred. No. 3.1e-20;		
Matches	39;	Conservative	10;	Mismatches 20;
			Indels	0;
			Gaps	0;

ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/809.103B
FILING DATE: 17-MAR-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94.11040
FILING DATE: 15-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR95/01192
FILING DATE: 15-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: PATCH, Andrew J.
REGISTRATION NUMBER: 32,925
REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 521-2297
TELEFAX: (703) 685-0573
TELEX: 248425 EMBON
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-809-103B-8

Query Match 58.8%; Score 211; DB 4; Length 359;
Best Local Similarity 56.5%; Pred. No. 3.1e-20;
Matches 39; Conservative 10; Mismatches 20; Indels 0; Gaps 0;
QY 2 LWMGEFOVDRGSRAGCGCOTSDNAAAEALNASSKEFALQIREKIPEKYLFOFHINLSAL 61
DB 111 LWMGEFOVDRGSRAGCGCOTSDNAAAEALNASSKEFALQIREKIPEKYLFOFHINLSAL 170
QY 62 AAFDRTPEP 70
DB 171 KVFQVPPAP 179
RESULT 10
US-08-838-151A-2
Sequence 2, Application US/08838151A
Patent No. 6291743
GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminitivirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CURRENT APPLICATION DATA:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rocky, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838.151A

FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 361 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-838-151A-2

Query Match 58.8%; Score 211; DB 4; Length 361;
Best Local Similarity 55.7%; Pred. No. 3.2e-20;
Matches 39; Conservative 15; Mismatches 16; Indels 0; Gaps 0;
QY 1 TLWGEFOVDRGSRAGCGCOTSDNAAAEALNASSKEFALQIREKIPEKYLFOFHINLSAL 60
DB 110 TLWGEFOVDRGSRAGCGCOTSDNAAAEALNASSKEFALQIREKIPEKYLFOFHINLSAL 169
QY 61 AAFDRTPEP 70
DB 170 ERIFAKAPAP 179

RESULT 11
US-08-838-151A-4
Sequence 4, Application US/08838151A
Patent No. 6291743
GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminitivirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CURRENT APPLICATION DATA:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rocky, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838.151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 361 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein


```
XX WPI: 2000-618851/59.
DR
XX Transgenic plants with increased resistance to geminivirus infection
PT comprise a nucleic acid construct containing a nucleic acid sequence
PT encoding a mutant AL1 protein with a mutation in the Rb binding region
PS
XX Claim 52: Page 45: 73pp: English.
XX
CC The present sequence represents a mutant peptide, derived from a
CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
CC protein are used to produce transgenic plants. The mutation in AL1 is
CC present in a ribosome binding region, and expression of mutant AL1
CC protein imparts increased resistance to geminivirus infection in the
CC plant. Mutant AL1 proteins are useful for producing plants having
CC increased resistance or reduced sensitivity to a geminivirus such as
CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
CC virus, cotton leaf curl virus or beet curly top virus.
SQ Sequence 70 AA:

Query Match 100.0%; Score 361; DB 21; Length 70;
Best Local Similarity 100.0%; Pred. No. 4,2e-38;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TLWGEAANVDGSRAGCGCOTSDNAAAEALNASSKEEALQITREKIPEKYLFOFHNLSNL 60
DB 1 tlwgeaavdgfsarggcqtlnadaaaalnasskeaalqitrekipekylfqfhnlnsl 60
OY 61 DRIFDKTPEP 70
DB 61 drifdktp 70

RESULT 2
AAB18677
ID AAB18677 standard; peptide: 70 AA.
XX
AC AAB18677;
XX
DT 22-JAN-2001 (first entry)
XX
DE Peptide fragment from Rep protein of TGMV (amino acids 110-179).
XX
KM Geminivirus: replication protein; Rep protein; AL1; transgenic plant;
KM ribosome binding region; resistance; geminivirus infection.
XX
OS Tomato golden mosaic virus.
XX
PN WO200054573-A1.
XX
PD 21-SEP-2000.
XX
PF 15-MAR-2000; 2000WO-US06759.
XX
PR 18-MAR-1999; 99US-0125004.
PR 09-APR-1999; 99US-0289346.
XX
PA (UYNC-) UNIV NORTH CAROLINA STATE.
XX
PI Hanley-Bowdoin L, Orozco BM, Kong L;
XX
DR WPI: 2000-618851/59.
XX
PT Transgenic plants with increased resistance to geminivirus infection
PT comprise a nucleic acid construct containing a nucleic acid sequence
```

```
PT encoding a mutant AL1 protein with a mutation in the Rb binding region
PT
PS Disclosure: Page 18: 73pp: English.
XX
XX The present sequence is derived from a geminivirus replication (Rep)
XX protein, which is also known as AL1. AL1 binds double-stranded DNA,
XX catalyses cleavage and ligation of single-stranded DNA, and interacts
XX with other viral and host proteins. Mutants of the AL1 protein are used
XX to produce transgenic plants. The mutation in AL1 is present in a
XX ribosome binding region, and expression of mutant AL1 protein imparts
XX increased resistance to geminivirus infection in the plant. Mutant AL1
XX proteins are useful for producing plants having increased resistance or
XX reduced sensitivity to a geminivirus such as tomato golden mosaic virus,
XX tomato mottle virus, tomato yellow leaf curl virus, tomato leaf curl
XX virus, African cassava mosaic virus, Indian cassava mosaic virus, potato
XX yellow mosaic virus, bean golden mosaic virus, bean dwarf mosaic virus,
XX squash leaf curl virus, Texas pepper virus, cotton leaf curl virus or
XX beet curly top virus.
SQ Sequence 70 AA:

Query Match 97.0%; Score 350; DB 21; Length 70;
Best Local Similarity 97.1%; Pred. No. 1e-36;
Matches 68; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 TLWGEAANVDGSRAGCGCOTSDNAAAEALNASSKEEALQITREKIPEKYLFOFHNLSNL 60
DB 1 tlwgeafgvdgsarggcqtlnadaaaalnasskeaalqitrekipekylfqfhnlnsl 60
OY 61 DRIFDKTPEP 70
DB 61 drifdktp 70

RESULT 3
AAB18687
ID AAB18687 standard; peptide: 356 AA.
XX
AC AAB18687;
XX
DT 22-JAN-2001 (first entry)
XX
DE Amino acid sequence of a geminivirus replication protein of TGMV.
XX
KM Geminivirus: replication protein; Rep protein; AL1; transgenic plant;
KM ribosome binding region; resistance; geminivirus infection.
XX
OS Tomato golden mosaic virus.
XX
FH Key Location/Qualifiers
FT Misc-difference 354 /note= "unspecified amino acid"
XX
PN WO200054573-A1.
XX
PD 21-SEP-2000.
XX
PF 15-MAR-2000; 2000WO-US06759.
XX
PR 18-MAR-1999; 99US-0125004.
PR 09-APR-1999; 99US-0289346.
XX
PA (UYNC-) UNIV NORTH CAROLINA STATE.
XX
PI Hanley-Bowdoin L, Orozco BM, Kong L;
XX
DR WPI: 2000-618851/59.
XX
XX Transgenic plants with increased resistance to geminivirus infection
PT comprise a nucleic acid construct containing a nucleic acid sequence
PT encoding a mutant AL1 protein with a mutation in the Rb binding region
```

PT -
XX
PS Disclosure; Page 47-48; 73pp; English.
XX
CC The present sequence represents a geminivirus replication (Rep)
CC protein, which is also known as AL1. AL1 binds double-stranded DNA,
CC catalyzes cleavage and ligation of single-stranded DNA, and interacts
CC with other viral and host proteins. Mutants of the AL1 protein are used
CC to produce transgenic plants. The mutation in AL1 is present in a
CC ribosome binding region, and expression of mutant AL1 protein imparts
CC increased resistance to geminivirus infection in the plant. Mutant AL1
CC proteins are useful for producing plants having increased resistance or
CC reduced sensitivity to a geminivirus such as tomato golden mosaic virus,
CC tomato mottle virus, tomato yellow leaf curl virus, tomato leaf curl
CC virus, African cassava mosaic virus, Indian cassava mosaic virus, potato
CC yellow mosaic virus, bean golden mosaic virus, bean dwarf mosaic virus,
CC squash leaf curl virus, Texas pepper virus, cotton leaf curl virus or
CC beet curly top virus.
XX
SQ Sequence 356 AA;

Query Match 97.0%; Score 350; DB 21; Length 356;
Best Local Similarity 97.1%; Pred. No. 8.1e-36;
Matches 68; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 TLVWGEAIVDGRSARCGCOTSDNDAAEALNASSKEEALQIIREKIPERYLQFHNLSNL 60
Db 110 flvwgefivdgrsargcqtstndaaealnasskeeaqlirekipekyltqfhnlnsl 169
|||
OY 61 DRIFDKTPEP 70
|||
Db 170 drifdktp 179
|||

RESULT 4
AAB18685
ID AAB18685 standard; peptide: 70 AA.
XX
AC AAB18685;
XX
DT 22-JAN-2001 (first entry)
XX
DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX
KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
KM ribosome binding region; resistance; geminivirus infection.
XX
OS Synthetic.
OS Tomato golden mosaic virus.
XX
FH Key Location/Qualifiers
FT Misc-difference 10
FT Misc-difference /note= "wild type residue replaced with Ala"
XX
PN WO200054573-A1.
XX
PD 21-SEP-2000.
XX
PF 15-MAR-2000; 2000WO-US06759.
XX
PR 18-MAR-1999; 99US-0125004.
PR 09-APR-1999; 99US-0289346.
XX
PA (UYNC-) UNIV NORTH CAROLINA STATE.
XX
PI Hanley-Bowdoin L, Orozco BM, Kong L;
XX
DR WPI: 2000-618851/59.
XX
PT Transgenic plants with increased resistance to geminivirus infection
PT comprise a nucleic acid construct containing a nucleic acid sequence
PT encoding a mutant AL1 protein with a mutation in the Rb binding region

PT -
XX
PS Claim 53; Page 46; 73pp; English.
XX
CC The present sequence represents a mutant peptide, derived from a
CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
CC protein are used to produce transgenic plants. The mutation in AL1 is
CC present in a ribosome binding region, and expression of mutant AL1
CC protein imparts increased resistance to geminivirus infection in the
CC plant. Mutant AL1 proteins are useful for producing plants having
CC increased resistance or reduced sensitivity to a geminivirus such as
CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
CC virus, cotton leaf curl virus or beet curly top virus.
XX
SQ Sequence 70 AA;

Query Match 94.7%; Score 342; DB 21; Length 70;
Best Local Similarity 95.7%; Pred. No. 1e-35;
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 TLVWGEAIVDGRSARCGCOTSDNDAAEALNASSKEEALQIIREKIPERYLQFHNLSNL 60
Db 1 flvwgefivdgrsargcqtstndaaealnasskeeaqlirekipekyltqfhnlnsl 60
|||
OY 61 DRIFDKTPEP 70
|||
Db 61 drifdktp 70
|||

RESULT 5
AAB18688
ID AAB18688 standard; peptide: 70 AA.
XX
AC AAB18688;
XX
DT 22-JAN-2001 (first entry)
XX
DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX
KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
KM ribosome binding region; resistance; geminivirus infection.
XX
OS Synthetic.
OS Tomato golden mosaic virus.
XX
FH Key Location/Qualifiers
FT Misc-difference 19
FT Misc-difference /note= "wild type residue replaced with Ala"
FT Misc-difference 20
FT Misc-difference /note= "wild type residue replaced with Ala"
XX
PN WO200054573-A1.
XX
PD 21-SEP-2000.
XX
PF 15-MAR-2000; 2000WO-US06759.
XX
PR 18-MAR-1999; 99US-0125004.
PR 09-APR-1999; 99US-0289346.
XX
PA (UYNC-) UNIV NORTH CAROLINA STATE.
XX
PI Hanley-Bowdoin L, Orozco BM, Kong L;
XX
DR WPI: 2000-618851/59.
XX
PT Transgenic plants with increased resistance to geminivirus infection


```
XX
DR WPI: 2000-618851/59.
XX
XX Transgenic plants with increased resistance to geminivirus infection
PT comprise a nucleic acid construct containing a nucleic acid sequence
PT encoding a mutant AL1 protein with a mutation in the Rb binding region
PT
PS Disclosure: Page 49; 73pp; English.
XX
XX The present sequence represents a mutant peptide, derived from a
XX geminivirus replication (Rep) protein, also known as AL1. AL1 binds
XX double-stranded DNA, catalyses cleavage and ligation of single-stranded
XX DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX protein are used to produce transgenic plants. The mutation in AL1 is
XX present in a ribosome binding region, and expression of mutant AL1
XX protein imparts increased resistance to geminivirus infection in the
XX plant. Mutant AL1 proteins are useful for producing plants having
XX increased resistance or reduced sensitivity to a geminivirus such as
XX tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX virus, tomato leaf curl virus, African cassava mosaic virus, Indian
XX cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX virus, cotton leaf curl virus or beet curly top virus.
XX
SQ Sequence 70 AA:

Query Match 93.1%; Score 336; DB 21; Length 70;
Best Local Similarity 94.3%; Pred. No. 5.9e-35;
Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 TLVWGEAAVDSRGANGCCTSDNDAAEALNASSKEALQIIREKIPKYLFGPHNINSNL 60
Db 1 tlwvgefgydvsargqctsndaaaaalaasskealqlirekipekylfgphlnsnl 60
OY 61 DRIFDKTPEP 70
Db 61 drifdktpcp 70

RESULT 8
AAB18678
ID AAB18678 standard; peptide: 70 AA.
XX
XX AAB18678;
XX
XX 22-JAN-2001 (first entry)
XX
XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX
XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX
XX Synthetic.
XX
XX Tomato golden mosaic virus.
XX
XX Key Location/Qualifiers
XX FT Misc-difference 12 /note= "wild type residue replaced with Ala"
XX FT Misc-difference 13 /note= "wild type residue replaced with Ala"
XX FT Misc-difference 15 /note= "wild type residue replaced with Ala"
XX FT Misc-difference 15 /note= "wild type residue replaced with Ala"
XX
XX WO200054573-A1.
XX
XX 21-SEP-2000.
XX
XX 15-MAR-2000; 2000WO-US06759.
XX
XX 18-MAR-1999; 99US-0125004.
XX
XX 09-APR-1999; 99US-0289346.
XX
```

```
XX
PA (UYNC-) UNIV NORTH CAROLINA STATE.
XX
XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX
XX WPI: 2000-618851/59.
XX
XX Transgenic plants with increased resistance to geminivirus infection
PT comprise a nucleic acid construct containing a nucleic acid sequence
PT encoding a mutant AL1 protein with a mutation in the Rb binding region
PT
PS Claim 53; Page 42-43; 73pp; English.
XX
XX The present sequence represents a mutant peptide, derived from a
XX geminivirus replication (Rep) protein, also known as AL1. AL1 binds
XX double-stranded DNA, catalyses cleavage and ligation of single-stranded
XX DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX protein are used to produce transgenic plants. The mutation in AL1 is
XX present in a ribosome binding region, and expression of mutant AL1
XX protein imparts increased resistance to geminivirus infection in the
XX plant. Mutant AL1 proteins are useful for producing plants having
XX increased resistance or reduced sensitivity to a geminivirus such as
XX tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX virus, tomato leaf curl virus, African cassava mosaic virus, Indian
XX cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX virus, cotton leaf curl virus or beet curly top virus.
XX
SQ Sequence 70 AA:

Query Match 92.8%; Score 335; DB 21; Length 70;
Best Local Similarity 92.9%; Pred. No. 7.9e-35;
Matches 65; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 TLVWGEAAVDSRGANGCCTSDNDAAEALNASSKEALQIIREKIPKYLFGPHNINSNL 60
Db 1 tlwvgefgydvsargqctsndaaaaalaasskealqlirekipekylfgphlnsnl 60
OY 61 DRIFDKTPEP 70
Db 61 drifdktpcp 70

RESULT 9
AAB18686
ID AAB18686 standard; peptide: 70 AA.
XX
XX AAB18686;
XX
XX 22-JAN-2001 (first entry)
XX
XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX
XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX
XX Synthetic.
XX
XX Tomato golden mosaic virus.
XX
XX Key Location/Qualifiers
XX FT Misc-difference 24 /note= "wild type residue replaced with Leu"
XX FT Misc-difference 25 /note= "wild type residue replaced with Leu"
XX FT Misc-difference 26 /note= "wild type residue replaced with Leu"
XX FT Misc-difference 26 /note= "wild type residue replaced with Leu"
XX
XX WO200054573-A1.
XX
XX 21-SEP-2000.
XX
XX
```

PF 15-MAR-2000; 2000MO-US06759.
XX 18-MAR-1999; 99US-0125004.
PR 09-APR-1999; 99US-0289346.
XX
PA (UYNC-) UNIV NORTH CAROLINA STATE.
XX
PI Hanley-Bowdoin L, Orozco BM, Kong L;
XX WPI: 2000-618851/59.
DR
XX Transgenic plants with increased resistance to geminivirus infection
PT comprise a nucleic acid construct containing a nucleic acid sequence
PI encoding a mutant AL1 protein with a mutation in the Rb binding region
PT
XX
PS Claim 53; Page 46; 73pp; English.
XX
XX The present sequence represents a mutant peptide, derived from a
CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
CC protein are used to produce transgenic plants. The mutation in AL1 is
CC present in a ribosome binding region, and expression of mutant AL1
CC protein imparts increased resistance to geminivirus infection in the
CC plant. Mutant AL1 proteins are useful for producing plants having
CC increased resistance or reduced sensitivity to a geminivirus such as
CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
CC virus, cotton leaf curl virus or beet curly top virus.
XX
SQ Sequence 70 AA:

Query Match 92.8%; Score 335; DB 21; Length 70;
Best Local Similarity 92.9%; Pred. No. 7.9e-35;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLWGEEAADVGSARGCGCTSDNAAEALNASSKEBALQIREKIPEKYLFFPHNLNSNL 60
DB 1 tlwgeefgvdgsargcgctsdnlllelnasskealqirekipekylffghnlnsl 60
QY 61 DRIFDKTPEP 70
DB 61 drifdktp 70

RESULT 10
AAB18689
ID AAB18689 standard; peptide; 70 AA.
XX
AC AAB18689;
XX
DT 22-JAN-2001 (first entry)
XX
XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
DE Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX
XX Synthetic.
OS Tomato golden mosaic virus.
XX
XX
FH Key Location/Qualifiers
FH Misc-difference 22
FT /note= "wild type residue replaced with Ala"
FT Misc-difference 23
FT /note= "wild type residue replaced with Ala"
XX
XX WO200054573-A1.
XX
XX

PD 21-SEP-2000.
XX
XX 15-MAR-2000; 2000MO-US06759.
PF 18-MAR-1999; 99US-0125004.
XX 09-APR-1999; 99US-0289346.
XX
PA (UYNC-) UNIV NORTH CAROLINA STATE.
XX
PI Hanley-Bowdoin L, Orozco BM, Kong L;
XX WPI: 2000-618851/59.
DR
XX Transgenic plants with increased resistance to geminivirus infection
PT comprise a nucleic acid construct containing a nucleic acid sequence
PI encoding a mutant AL1 protein with a mutation in the Rb binding region
PT
XX
XX Disclosure; Page 48-49; 73pp; English.
XX
XX The present sequence represents a mutant peptide, derived from a
CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
CC protein are used to produce transgenic plants. The mutation in AL1 is
CC present in a ribosome binding region, and expression of mutant AL1
CC protein imparts increased resistance to geminivirus infection in the
CC plant. Mutant AL1 proteins are useful for producing plants having
CC increased resistance or reduced sensitivity to a geminivirus such as
CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
CC virus, cotton leaf curl virus or beet curly top virus.
XX
SQ Sequence 70 AA:

Query Match 92.5%; Score 334; DB 21; Length 70;
Best Local Similarity 94.3%; Pred. No. 1.1e-34;
Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TLWGEEAADVGSARGCGCTSDNAAEALNASSKEBALQIREKIPEKYLFFPHNLNSNL 60
DB 1 tlwgeefgvdgsargcgctsdnlllelnasskealqirekipekylffghnlnsl 60
QY 61 DRIFDKTPEP 70
DB 61 drifdktp 70

RESULT 11
AAB18680
ID AAB18680 standard; peptide; 70 AA.
XX
AC AAB18680;
XX
DT 22-JAN-2001 (first entry)
XX
XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
DE Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX
XX Synthetic.
OS Tomato golden mosaic virus.
XX
XX
FH Key Location/Qualifiers
FH Misc-difference 42
FT /note= "wild type residue replaced with Ala"
FT Misc-difference 43
FT /note= "wild type residue replaced with Ala"
XX
XX Misc-difference 44
XX

FT		/note= "wild type residue replaced with Ala"
XX		
PN	WO200054573-A1.	
PD	21-SEP-2000.	
XX		
PF	15-MAR-2000; 2000WO-US06759.	
XX		
PR	18-MAR-1999; 99US-0125004.	
PR	09-APR-1999; 99US-0289346.	
PA	(UYNC-) UNIV NORTH CAROLINA STATE.	
XX		
PI	Hanley-Bowdoin L, Orozco BM, Kong L;	
DR	WPI: 2000-618851/59.	
XX		
PT	Transgenic plants with increased resistance to geminivirus infection	
PT	comprise a nucleic acid construct containing a nucleic acid sequence	
PT	encoding a mutant AL1 protein with a mutation in the Rb binding region	
XX		
PS	Claim 52; Page 43-44; 73pp: English.	
XX		
CC	The present sequence represents a mutant peptide, derived from a	
CC	geminivirus replication (Rep) protein, also known as AL1. AL1 binds	
CC	double-stranded DNA, catalyses cleavage and ligation of single-stranded	
CC	DNA, and interacts with other viral and host proteins. Mutants of the AL1	
CC	protein are used to produce transgenic plants. The mutation in AL1 is	
CC	present in a ribosome binding region, and expression of mutant AL1	
CC	protein imparts increased resistance to geminivirus infection in the	
CC	plant. Mutant AL1 proteins are useful for producing plants having	
CC	increased resistance or reduced sensitivity to a geminivirus such as	
CC	tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl	
CC	virus, tomato leaf curl virus, African cassava mosaic virus, Indian	
CC	cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic	
CC	virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper	
CC	virus, cotton leaf curl virus or beet curly top virus.	
XX		
SQ	Sequence 70 AA:	
OY	Query Match 92.0%; Score 332; DB 21; Length 70;	
	Best Local Similarity 92.9%; Pred. No. 1.9e-34;	
	Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;	
OY	1 TLVMEAAVDGSSAGSGOTSNDAAALMASCKEALQIFREKYLPGFHNLSNL 60	
DB	1 tlvwefqydgfsargcgtsndaaaealnasskeaalqliaaipexyltqfhnlnsnl 60	
OY	61 DRIPDKTEP 70	
DB	61 drifdktep 70	
RESULT 12		
ID	AAB18691	
	AAB18691 standard; peptide: 70 AA.	
XX		
AC	AAB18691;	
XX		
DT	22-JAN-2001 (first entry)	
XX		
DE	Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.	
XX	Geminivirus; replication protein; Rep protein; AL1; transgenic plant;	
KM	ribosome binding region; resistance; geminivirus infection.	
XX		
OS	Synthetic.	
OS	Tomato golden mosaic virus.	
XX		
Key	Location/Qualifiers	
FT	Misc-difference 34	

```

FT      Misc-difference 35 /note= "wild type residue replaced with Ala"
FT      Misc-difference 36 /note= "wild type residue replaced with Ala"
FT      Misc-difference 36 /note= "wild type residue replaced with Ala"
XX      WO200054573-A1.
PN      21-SEP-2000.
PD      15-MAR-2000; 2000WO-US06759.
XX      18-MAR-1999; 99US-0125004.
PR      09-APR-1999; 99US-0289346.
XX      (UYNC-) UNIV NORTH CAROLINA STATE.
PA      Hanley-Bowdoin L, Orozco BM, Kong L.
PI      WPI; 2000-618851/59.
DR      Transgenic plants with increased resistance to geminivirus infection
XX      comprise a nucleic acid construct containing a nucleic acid sequence
XX      encoding a mutant AL1 protein with a mutation in the Rb binding region
XX      .
PS      Disclosure; Page 49; 73pp; English.
XX      The present sequence represents a mutant peptide, derived from a
XX      geminivirus replication (Rep) protein, also known as AL1. AL1 binds
XX      double-stranded DNA, catalyses cleavage and ligation of single-stranded
XX      DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX      protein are used to produce transgenic plants. The mutation in AL1 is
XX      present in a ribosome binding region, and expression of mutant AL1
XX      protein imparts increased resistance to geminivirus infection in the
XX      plant. Mutant AL1 proteins are useful for producing plants having
XX      increased resistance or reduced sensitivity to a geminivirus such as
XX      tomatato golden mosaic virus, tomatato mottle virus, tomatato yellow leaf curl
XX      virus, tomatato leaf curl virus, African cassava mosaic virus, Indian
XX      cassava mosaic virus, potatato yellow mosaic virus, bean golden mosaic
XX      virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX      virus, cotton leaf curl virus or beet curly top virus.
XX      Sequence 70 AA:
XX
XX      Query Match 92.0%; Score 332; DB 21; Length 70;
XX      Best Local Similarity 92.9%; Pred. No. 1.9e-34;
XX      Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XX
XX      QY 1 TLVGFPAVDGHSARGCGCTSTNDAAEAALNASKKEPALQITREKTPREKLFQFHNLSNU. 60
XX      ||||| ||||||||||||||||||||| |||||||||||||||||||||
XX      Db 1 TLVGFfyvdgfsatrgcgctsndaaeaalnassaaaaaqlitrekipekylfqlfnlnsnl 60
XX      ||||| ||||||||
XX      QY 61 DRIFDKTPEP 70
XX      ||||||||
XX      Db 61 drlfdktpep 70
XX
XX      RESULT 13
XX      AAB18681
XX      ID AAB18681 standard; peptide; 70 AA.
XX      AC AAB18681;
XX      DT 22-JAN-2001 (first entry)
XX      DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX      Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX      ribosome binding region; resistance; geminivirus infection.
XX      KW Synthetic.
XX

```

OS	Tomato golden mosaic virus.
XX	
FH	Key Location/Qualifiers
FT	Misc-difference 47 /note= "wild type residue replaced with Ala"
FT	Misc-difference 48 /note= "wild type residue replaced with Ala"
FT	Misc-difference 49 /note= "wild type residue replaced with Ala"
FT	Misc-difference 49 /note= "wild type residue replaced with Ala"
PM	WO200054573-A1.
PD	21-SEP-2000.
PP	15-MAR-2000; 2000WO-US06759.
PR	18-MAR-1999; 99US-0125004.
PR	09-APR-1999; 99US-0289346.
PA	(UYNC-) UNIV NORTH CAROLINA STATE.
PI	Hanley-Bowdoin L., Orozco BM, Kong L;
XX	WPI; 2000-618851/59.
XX	
PT	Transgenic plants with increased resistance to geminivirus infection
PT	comprise a nucleic acid construct containing a nucleic acid sequence
PT	encoding a mutant AL1 protein with a mutation in the Rb binding region
PS	-
PS	Claim 52; Page 44; 73pp; English.
XX	
CC	The present sequence represents a mutant peptide, derived from a
CC	geminivirus replication (Rep) protein, also known as AL1. AL1 binds
CC	double-stranded DNA, catalyses cleavage and ligation of single-stranded
CC	DNA, and interacts with other viral and host proteins. Mutants of the AL1
CC	protein are used to produce transgenic plants. The mutation in AL1 is
CC	present in a ribosome binding region, and expression of mutant AL1
CC	protein imparts increased resistance to geminivirus infection in the
CC	plant. Mutant AL1 proteins are useful for producing plants having
CC	increased resistance or reduced sensitivity to a geminivirus such as
CC	tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
CC	virus, tomato leaf curl virus, African cassava mosaic virus, Indian
CC	cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
CC	virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
CC	virus, cotton leaf curl virus or beet curly top virus.
SO	Sequence 70 AA;
	Query Match 91.1%; Score 329; DB 21; Length 70;
	Best Local Similarity 92.9%; Pred. No. 4.5e+34;
	Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY	1 TLVGEAAVDGASAGCGCCTSDNDAAEALANASSKEPFIQIREKIPKYLFOFHNLNSL 60
Db	1 tlwgeefydgdsatagggcqtndaaaealnasskeeaqlirekikpaalrfqfmlnsl 60
OY	61 DRIEDKTEPEP 70
Db	61 drifdktppep 70
	RESULT 14
AAB18683	AAB18683 standard; peptide: 70 AA.
XX	
AC	AAB18683;
XX	
DT	22-JAN-2001 (first entry)
XX	
DE	Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX	

KM	Geminivirus; replication protein; Rep protein; ALI; transgenic plant;
KW	Ribosome binding region; resistance; geminivirus infection.
OS	Synthetic.
XX	Tomato golden mosaic virus.
FH	Key Location/Qualifiers
FT	Misc-difference 59 /note= "wild type residue replaced with Ala"
FT	Misc-difference 61 /note= "wild type residue replaced with Ala"
FT	Misc-difference 62 /note= "wild type residue replaced with Ala"
PM	WO200054573-AL.
PD	21-SEP-2000.
PX	15-MAR-2000; 2000WO-US06759.
PR	18-MAR-1999; 99US-0125004.
PA	09-APR-1999; 99US-0289346.
PI	(UYNC-) UNIV NORTH CAROLINA STATE.
DR	Hanley-Bowdoin L, Orozco BM, Kong L;
XX	WPI: 2000-618851/59.
PT	Transgenic plants with increased resistance to geminivirus infection comprise a nucleic acid construct containing a nucleic acid sequence encoding a mutant ALI protein with a mutation in the Rb binding region
PS	Claim 53; Page 45; 73pp; English.
CC	The present sequence represents a mutant peptide, derived from a geminivirus replication (Rep) protein, also known as ALI. ALI binds double-stranded DNA, catalyzes cleavage and ligation of single-stranded DNA, and interacts with other viral and host proteins. Mutants of the ALI protein are used to produce transgenic plants. The mutation in ALI is present in a ribosome binding region, and expression of mutant ALI protein imparts increased resistance to geminivirus infection in the plant. Mutant ALI proteins are useful for producing plants having increased resistance or reduced sensitivity to a geminivirus such as tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl virus, tomato leaf curl virus, African cassava mosaic virus, Indian cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper virus, cotton leaf curl virus or beet curly top virus.
Sequence	70 AA:
Query Match	90.9%; Score 328; DB 21; Length 70;
Best Local Similarity	92.9%; Pred Mo. 6e-34;
Matches	65; Conservative 0; Mismatches 5; Indels 0; Gaps 0.
OY	1 TLVWGCAAVDGSARGCOTSDNDAAEALINASSKKEALOIIREKIPEKYTLFOPHNINSNL 60
DQ	1 TLVGefgydqysargycqtndaaaealnasskeaalqilrekipexylfqfmlnsal 60
OY	61 DNIIFDKTPPP 70
DQ	61 aaifdktppe 70
RESULT 15	
AABI8682	ID AABI8682 standard; peptide: 70 AA.
AC	AABI8682;
XX	

DT 22-JAN-2001 (first entry)

DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.

KM Geminivirus; replication protein; Rep protein; ALI; transgenic plant
KM ribosome binding region; resistance; geminivirus infection.

OS Synthetic.
OS Tomato golden mosaic virus.

FH	Key	Location/Qualifiers
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3	3	3
4	4	4
5	5	5
6	6	6
7	7	7
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12	12	12
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18	18	18
19	19	19
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21	21	21
22	22	22
23	23	23
24	24	24
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95	95	95
96	96	96
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98	98	98
99	99	99
100	100	100

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FT      Misc-difference 52
FT      /not a= "wild type residue replaced with Ala"
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FT	Misc-difference	54	7/1000	with cyte residue replaced with and
1				

FT	/note= "wild type residue replaced with Ala"
FT	55
Misc-difference	

PN W0200054573-A1.

PD 21-SEP-2000

PF 15-MAR-2000; 2000WO-US06759.

PR 18-MAR-1999; 99US-0125004.

PR 09-APR-1999; 99US-0289346.

PA (UYNC-) UNIV NORTH CAROLINA STATE

PI Hanley-Bowdoin L, Orozco BM, Kong L;

DR WPI; 2000-618851/59.

PT Transgenic plants with increased resistance to geminivirus infection
PT comprise a nucleic acid construct containing a nucleic acid sequence
PT encoding a mutant Al1 protein with a mutation in the Rb binding region

PS Claim 53; Page 44-45; 73pp; English.

CC The present sequence represents a mutant peptide, derived from a
CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
CC protein are used to produce transgenic plants. The mutation in AL1 is
CC present in a ribosome binding region, and expression of mutant AL1
CC protein imparts increased resistance to geminivirus infection in the
CC plant. Mutant AL1 proteins are useful for producing plants having
CC increased resistance or reduced sensitivity to a geminivirus such as
CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
CC virus, cotton leaf curl virus or beet curly top virus.

SQ Sequence 70 AA;

Query Match	Score	DB	length
Best local similarity	90.3%	326	70
Matches	92.9%	Pred. No. 1, le-33	
Matches	65	conservative	0
		Mismatches	5
		Indels	0
		Gaps	0

QY	1	TLVMEAAVDGASGAGCGCOTSDNDAAEALINASSKEEALQIREKIPKTLFPOFHINSL	60
Db	1	tlvwefgdydgsatrgcqtndaaaaaainasskeaalqltrekipexylafafaaInsl	60
QY	61	DRIFDKTPPEP	70
Db	61	drifdktppep	70

Fri Jan 4 09:39:42 2002

us-09-289-346a-8.rag

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OM protein - protein search, using sw model

Run on: January 3, 2002, 15:40:11 ; Search time 72.79 seconds
(without alignments)
73.255 Million cell updates/sec

Title: US-09-289-346a-8

Perfect score: 361
Sequence: 1 TLVWGEAAVVDGRSARGGCOT.....PDPHNLNSMLDRIFDKTPEP 70

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:*

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	350	97.0	352	1 OQCVC1	ALI protein - toma
2	250	69.3	361	1 OQCVP1	ALI protein - toma
3	237	65.7	358	2 S07594	hypothetical prote
4	230	63.7	362	1 J01887	ALI protein - toma
5	223	61.8	359	2 S39211	gene C1 protein -
6	219	60.7	349	2 J02300	replicase - pepper
7	219	60.7	349	2 S31875	ALI protein - pepp
8	216	59.8	359	2 S22593	hypothetical prote
9	213	59.0	351	2 J02327	ALI protein - indi
10	213	59.0	351	1 OQCVC1	AVI protein - abut
11	212	58.7	357	1 OQCVC1	ALI protein - toma
12	210	58.2	358	1 J01870	ALI protein - toma
13	210	58.2	359	2 S39235	gene C1 protein -
14	210	58.2	360	2 S28360	ALI protein - beet
15	203	56.2	380	2 S59885	replication-associ
16	142	39.3	131	2 S45059	ACI protein (clone
17	117	32.4	347	1 OQCVC1	ALI protein - squa
18	68.5	19.0	1713	2 A55347	adhesive ligand ep
19	68	18.8	587	2 UC1419	Fc gamma (19c) rec
20	67	18.6	180	2 DB4082	hypothetical prote
21	66.5	18.4	201	2 A81380	probable flagellin
22	64.5	17.9	299	2 B71967	probable peptidyl-
23	63.5	17.6	447	2 T12544	hypothetical prote
24	63.5	17.6	1610	2 A46227	voltage-dependent
25	63.5	17.6	1646	2 JH0422	voltage-dependent
26	63.5	17.6	2161	2 JH0564	calcium channel al
27	63.5	17.6	2181	2 A38158	calcium channel al
28	63.5	17.6	2203	2 T42742	voltage-dependent
29	62	17.2	295	2 D42452	C1 protein - tobac

30	61.5	17.0	481	2 A70091	probable phosphoe
31	61	16.9	1502	1 RCBYH1	CYCL1/CYP3 transcri
32	60	16.6	432	2 D75348	gamma-glutamyl pho
33	60	16.6	447	2 S52437	CDP-diacylglycerol
34	59.5	16.5	136	2 T22240	hypothetical prote
35	59.5	16.5	299	2 G64541	cell binding facto
36	59.5	16.5	388	2 C69196	hypothetical prote
37	59.5	16.5	2137	2 T05244	hypothetical prote
38	59	16.3	316	2 C82085	conserved hypothet
39	59	16.3	397	2 B71078	probable MDH oxid
40	58.5	16.2	297	1 MNVNRV	nonstructural prot
41	58.5	16.2	335	1 DEBSGF	glyceroldehydro-3-p
42	58.5	16.2	589	2 D64125	hypothetical prote
43	58.5	16.2	1044	2 T43800	protein kinase hub
44	58.5	16.2	1070	1 A54600	1-phosphatidylinos
45	58.5	16.2	1265	2 T47626	structural mainlen

ALIGNMENTS

```

RESULT 1
OQCVC1
ALI protein - tomato golden mosaic virus
C:Species: tomato golden mosaic virus
A:Note: host Nicotiana sp. (tobacco)
C:Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 08-Apr-1994
C:Accession: A04170
R:Hamilton, W.D.O.; Stein, V.E.; Coutts, R.H.A.; Buck, K.W.
EMBO J. 3, 2197-2205, 1984
A:Title: Complete nucleotide sequence of the infectious cloned DNA components of toma
A:Reference number: A04163
A:Accession: A04170
A:Molecule type: DNA
A:Residues: 1-352 <HAM>
C:Comment: The genome consists of two circular, single-stranded DNA components, DNA A
C:Genetics:
A:Map position: segment A
C:Superfamily: tomato golden mosaic virus ALI protein

Query Match 97.0% Score 350; DB 1; Length 352;
Best Local Similarity 97.1%; Pred. No. 1.4e-31;
Matches 68; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 TLVWGEAAVVDGRSARGGCOTSNDAAEALNASSKKEALQIREKIPKYLFPFHNLNSNL 60
||||| ||||||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
DB 11 TLVWGEFVVDGRSARGGCOTSNDAAEALNASSKKEALQIREKIPKYLFPFHNLNSNL 170

OY 61 DRIFDKTPEP 70
||||| |||||||||
DB 171 DRIFDKTPEP 180

RESULT 2
OQCVP1
ALI protein - potato yellow mosaic virus (isolate Venezuela)
C:Species: potato yellow mosaic virus
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Jun-2000
C:Accession: J00364
R:Coutts, R.H.A.; Coffin, R.S.; Roberts, E.J.F.; Hamilton, W.D.O.
J. Gen. Virol. 72, 1515-1520, 1991
A:Title: The nucleotide sequence of the infectious cloned DNA components of potato ye
A:Reference number: J00362; MUID:91311403
A:Accession: J00364
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-361 <COU>
A:Cross-references: GB:D00940; NID:g222458; PIDN:BAA00782.1; PID:g222459
C:Genetics:
A:Map position: segment A
C:Superfamily: tomato golden mosaic virus ALI protein

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Fri Jan 4 09:39:49 2002

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OM protein - protein search, using sw model

Run on: January 3, 2002, 15:57:17 : Search time 43.68 Seconds
(without alignments)
56.758 Million cell updates/sec

Title: US-09-289-346a-8
Perfect score: 361
Sequence: 1 TLWGEAAVDSARGGCOT.....FGFHNLSNLDRIPOKTPPEP 70

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues
Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	350	97.0	352	1 VAL1_TGMV	P03567 tomato gold
2	250	69.3	361	1 VAL1_PYMV	P27258 potato yell
3	237	65.7	358	1 VAL1_CLVK	P14982 cassava lat
4	237	65.7	358	1 VAL1_CLVN	P14972 cassava lat
5	230	63.7	362	1 VAL1_TYCA	P36279 tomato yell
6	223	61.8	359	1 VAL1_TYCU	P38609 tomato yell
7	219	60.7	349	1 VAL1_PHVU	P06923 pepper huas
8	216	59.8	359	1 VAL1_TYLCM	P27260 tomato yell
9	214	59.3	353	1 VAL1_BGMV	P05175 bean golden
10	213	59.0	355	1 VAL1_ABMVW	P21947 abutilon mo
11	212	58.7	357	1 VAL1_TYCV	P27259 tomato yell
12	210	58.2	358	1 VAL1_BCTV	P14991 beet curly
13	210	58.2	361	1 VAL1_TMOV	P06657 tomato molt
14	117	32.4	347	1 VAL1_SLCV	P29048 squash leaf
15	68.5	19.0	1713	2 LMA3_HUMAN	Q16787 homo sapien
16	64.5	17.9	299	1 Y175_HELPJ	Q92mq7 helicobacte
17	63.5	17.6	447	1 TBL2_HUMAN	Q947p3 homo sapien
18	63.5	17.6	1610	1 CCAD_MESAU	Q09244 mesocricetu
19	63.5	17.6	2161	1 CCAD_HUMAN	Q01668 homo sapien
20	63.5	17.6	2203	1 CCAD_RAT	P27732 rattus norv
21	62	17.2	295	1 VAL1_TYDVA	P16173 tobacco yel
22	61	16.9	1483	1 CYP1_YEAST	P12351 saccharomyc
23	60	16.6	432	1 PROA_DEIRA	Q94td9 deinoceccus
24	60	16.6	447	1 CDSA_DROME	P56079 d phosphati
25	59.5	16.5	136	1 Y452_CAEEL	O62250 caenorhabdi
26	59.5	16.5	299	1 Y175_HELPJ	P56112 helicobacte
27	59	16.3	640	1 DNAX_RHOMR	Q95cb1 rhodothermu
28	58.5	16.2	297	1 RRPB_RABYP	P06747 radies vitu
29	58.5	16.2	334	1 G3P_BACST	P00362 bacillus st
30	58.5	16.2	335	1 G3P_BACCO	P15115 bacillus co
31	58.5	16.2	428	1 GBAL1_CANAL	P28868 candida alb
32	58.5	16.2	589	1 Y667_HAEIN	P45221 haemophilus
33	58.5	16.2	1044	1 BUB1_SCHRO	O94751 schizosacch

34	58.5	16.2	1070	1 P11B_HUMAN	P42338 homo sapien
35	58	16.1	617	1 YACH_ECOLI	P36683 escherichia
36	58	16.1	874	1 SLAP_BACLI	P49053 bacillus li
37	57.5	15.9	439	1 XTLA_LACIA	Q9c1g7 lactococcus
38	57	15.8	200	1 VIP_CHICK	P48143 gallus gall
39	57	15.8	200	1 VIP_MELGA	P45644 meleagris g
40	57	15.8	247	1 YCP4_YEAST	P25349 saccharomyc
41	57	15.8	355	1 CRTB_RHOSH	P4905 rhodobacter
42	57	15.8	387	1 Y4PF_RHISN	P55615 rhizobium s
43	57	15.8	4639	1 DYHC_DROME	P37276 drosophila
44	56.5	15.7	470	1 RHSA_RHIME	Q9332 rhizobium m
45	56.5	15.7	511	1 HUTH_VIBCH	Q9ksq4 vibrio chol

ALIGNMENTS

RESULT	ID	VAL1_TGMV	STANDARD:	PRT:	352 AA.
AC	P03567;				
DP	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DE	01-JUN-1994 (Rel. 29, Last annotation update)				
DE	ALI PROTEIN.				
GN	AC1.				
OS	Tomato golden mosaic virus ('TGMV').				
OC	Viruses; ssDNA viruses; Gemintiviridae; Begomovirus.				
OX	NCBI_TaxID=10831;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Hamilton W.D.O., Stein V.E., Coutts R.H.A., Buck K.W.;				
RT	"Complete nucleotide sequence of the infectious cloned DNA components				
RT	of tomato golden mosaic virus: potential coding regions and regulatory				
RT	sequences."				
RL	EMBO J. 3:2197-2205(1984).				
CC	-1 SIMILARITY: BELONGS TO GEMINIVIRUSES ALI PROTEIN FAMILY.				
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CC	-----				
DR	EMBL; K02029; -; NOT_ANNOTATED_CDS.				
DR	PIR; A04170; QOCVL1.				
DR	InterPro: IPR001191; Gemini_AL1.				
DR	Pfam; PF00799; Gemini_AL1; 1.				
DR	PRINTS; PR00227; GEMCOATPALL.				
DR	PRINTS; PR00228; GEMCOATCVL1.				
DR	ProDom; PD000736; Gemini_AL1; 1.				
KW	ATP-binding.				
FT	NP_BIND 223				
FT	SEQUENCE 352 AA; 40332 MW; C33C938E9644B4A4 CMC64;				
SO	SEQUENCE				
Query Match	97.0%;	Score 350;	DB 1;	Length 352;	
Best local similarity	97.1%;	Pred. No. 8.2e-32;			
Matches 68;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;	
OY	1 TLWGEAAVDSARGGCOTSNDAAAEALNSSKEEALQIIREKIPERYLFGFHNLSNL 60				
DB	111 TLWGEAFVDSARGGCOTSNDAAAEALNSSKEEALQIIREKIPERYLFGFHNLSNL 170				
OY	. 61 DRIPKTPPEP 70				
DB	171 DRIPKTPPEP 180				
RESULT	2				
VAL1_PYMV					

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ID VAL1_PYMV STANDARD; PRT: 361 AA.
AC P27258;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE AL1 PROTEIN.
OS Potato yellow mosaic virus (isolate Venezuela).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10828;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=91311403; PubMed=1856690;
RA Coutts R.H.A., Coffin R.S., Roberts E.J.F., Hamilton W.D.O.;
RT "The nucleotide sequence of the infectious cloned DNA components of
RT potato yellow mosaic virus."
RL J. Gen. Virol. 72:1515-1520(1991).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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CC -----
CC EMBL: D00940; BAA00782.1; -.
CC PIR: J00364; OOCVPT.
CC InterPro: IPR001191; Gemin1_AL1.
CC Pfam: PF00799; Gemin1_AL1; 1.
CC PRINTS: PR00227; GEMCOAT1.
CC PRODOM: PD00228; GEMCOAT1.
CC DR PRINTS: PR00228; GEMCOAT1.
CC DR Prodom: PD000736; Gemin1_AL1; 1.
CC ARP-binding. 222
CC NP-BIND
CC FT SEQUENCE 361 AA; 40850 MW; 5627A33BF1264383 CRC64;
SQ

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Query Match 69.3%; Score 250; DB 1; Length 361;
 Best Local Similarity 68.1%; Pred. No. 1.2e-20;
 Matches 47; Conservative 11; Mismatches 11; Indels 0; Gaps 0;

```

OY 1 TLWGEAAVDCRSARGCGQTSNDAAEAALNSKKEALQIIREKIPEKYLFQFHNLSNL 60
   11 :||||| 11 :||||| 11 :||||| 11 :||||| 11 :||||| 11 :|||||
DB 110 TIEMCLFQIDGSARGGOQTVDAEAALNSGCKEAMKIKRLEKLPQYHNLSNL 169
   11 :||||| 11 :||||| 11 :||||| 11 :||||| 11 :||||| 11 :|||||
OY 61 DRIFDKTPE 69
   11 :||||| 11 :||||| 11 :||||| 11 :||||| 11 :||||| 11 :|||||
DB 170 DRIEKAPE 178

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RESULT 3

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VAL1_CLVK STANDARD; PRT: 358 AA.
AC P14982;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 PROTEIN (40.4 KDA PROTEIN).
GN AC1.
OS Cassava latent virus (strain West Kenyan 844).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10818;
RN [1]
RP SEQUENCE FROM N.A.
RA Stanley J., Gay M.R.;
RT "Nucleotide sequence of cassava latent virus DNA."
RL Nature 301:260-262(1983).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC -----
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CC -----
CC EMBL: X17095; CAA34953.1; -.
CC PIR: S07594; S07594.
CC InterPro: IPR001191; Gemin1_AL1.
CC Pfam: PF00799; Gemin1_AL1; 1.
CC PRINTS: PR00227; GEMCOAT1.
CC DR PRINTS: PR00228; GEMCOAT1.
CC DR Prodom: PD000736; Gemin1_AL1; 1.
CC ARP-binding. 220
CC NP-BIND
CC FT SEQUENCE 358 AA; 40435 MW; 1DB16B80CB2D5E2C CRC64;
SQ

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CC -----
CC EMBL: J02057; -. NOT_ANNOTATED_CDS.
CC InterPro: IPR001191; Gemin1_AL1.
CC Pfam: PF00799; Gemin1_AL1; 1.
CC PRINTS: PR00227; GEMCOAT1.
CC DR PRINTS: PR00228; GEMCOAT1.
CC DR Prodom: PD000736; Gemin1_AL1; 1.
CC ARP-binding. 220
CC NP-BIND
CC FT SEQUENCE 358 AA; 40435 MW; ED173E753ED2D69 CRC64;
SQ

```

Query Match 65.7%; Score 237; DB 1; Length 358;
 Best Local Similarity 61.4%; Pred. No. 3.4e-19;
 Matches 43; Conservative 13; Mismatches 14; Indels 0; Gaps 0;

```

OY 1 TLWGEAAVDCRSARGCGQTSNDAAEAALNSKKEALQIIREKIPEKYLFQFHNLSNL 60
   11 :||||| 11 :||||| 11 :||||| 11 :||||| 11 :||||| 11 :|||||
DB 109 TVEWQFQIDGSARGGOQTSNDAAEAALNSGCKEAMKIKRLEKLPQYHNLSNL 168
   11 :||||| 11 :||||| 11 :||||| 11 :||||| 11 :||||| 11 :|||||
OY 61 DRIFDKTPE 70
   11 :||||| 11 :||||| 11 :||||| 11 :||||| 11 :||||| 11 :|||||
DB 169 DRIEKAPE 178

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RESULT 4

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VAL1_CLVK STANDARD; PRT: 358 AA.
AC P14972;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 PROTEIN (40.4 KDA PROTEIN).
GN AC1.
OS Cassava latent virus (strain Nigerian).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10819;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=90174930; PubMed=2308831;
RA Morris B., Coates L., Lowe S., Richardson K., Eddy P.;
RT "Nucleotide sequence of the infectious cloned DNA components of
RT African cassava mosaic virus (Nigerian strain).";
RL Nucleic Acids Res. 18:197-198(1990).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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CC -----
CC EMBL: X17095; CAA34953.1; -.
CC PIR: S07594; S07594.
CC InterPro: IPR001191; Gemin1_AL1.
CC Pfam: PF00799; Gemin1_AL1; 1.
CC PRINTS: PR00227; GEMCOAT1.
CC DR PRINTS: PR00228; GEMCOAT1.
CC DR Prodom: PD000736; Gemin1_AL1; 1.
CC ARP-binding. 220
CC NP-BIND
CC FT SEQUENCE 358 AA; 40435 MW; 1DB16B80CB2D5E2C CRC64;
SQ

```

Query Match 65.7%; Score 237; DB 1; Length 358;
 Best Local Similarity 61.4%; Pred. No. 3.4e-19;
 Matches 43; Conservative 13; Mismatches 14; Indels 0; Gaps 0;

DR Prodom: PD000736; Gemini_AL1; 1.
 KM ATP-binding. 221 228 ATP (BY SIMILARITY).
 FT NP-BIND 349 AA: 39722 MW: D5E4E76CD56370F4 CRC64:
 SQ SEQUENCE

Query Match
 Best Local Similarity 58.6%; Score 219; DB 1; Length 349;
 Matches 41; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

OY 1 TLWGEAAVDSARGCGCOTSDNDAAEALNASSKEBALQIIREKIPKYLQFHNLSNLD 60
 DB 110 TLWGEAFDGRSARGGQGSANDTYAKALNASSAEALQIIREKQPOHFLOFHNLSNLD 169
 OY 61 DRIFDKTPEP 70
 DB 170 NRIFQTPPEP 179

RESULT 8

VAL1_TYLCM STANDARD: PRT: 359 AA.

AC P27260: 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DE 01-JUN-1994 (Rel. 29, Last annotation update)
 DE AL1 PROTEIN (C1 PROTEIN).
 GN C1.
 OS Tomato yellow leaf curl virus (strain Marmande) (TYLCV).
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OX NCBI_TaxID=10833;
 RN [1]
 RP MEDLINE=92107660; PubMed=1840676;
 RX kherr-Pour A., Bendahmane M., Matzeit V., Accotto G.P., Crespi S.,
 RA Gronenborn B.;
 RT "Tomato yellow leaf curl virus from Sardinia is a
 RT whitefly-transmitted monopartite geminivirus.";
 RL Nucleic Acids Res; 19:6763-6769(1991).

CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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CC
 CC EMBL: X61153; CAA43466.1; -;
 DR PIR: S22593; S22593.
 DR InterPro: IPR001191; Gemini_AL1.
 DR Pfam: PF00799; Gemini_AL1; 1.
 DR PRINTS: PR00227; GEMCOATFAL1.
 DR PRINTS: PR00228; GEMCOATFAL1.
 DR Prodom: PD000736; Gemini_AL1; 1.
 KW ATP-binding.
 FT NP-BIND 220 227 ATP (POTENTIAL).
 SQ SEQUENCE 359 AA: 40733 MW: 971784A07C93EFA7 CRC64:

Query Match
 Best Local Similarity 59.8%; Score 216; DB 1; Length 359;
 Matches 39; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

OY 2 TLWGEAAVDSARGCGCOTSDNDAAEALNASSKEBALQIIREKIPKYLQFHNLSNLD 61
 DB 111 LEMGTFOIDGRSARGGQGTANDAYAKALNASSKQALVDYIKRLARDVYLHFNHNSNLD 170
 OY 62 RIFDKTPEP 70
 DB 171 KVEQVPAP 179

RESULT 9
 VAL1_BGMV STANDARD: PRT: 353 AA.
 AC P05175:
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE AL1 PROTEIN (40.2 KDA PROTEIN).
 GN AC1.
 OS Bean golden mosaic virus.
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OX NCBI_TaxID=10839;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Howarth A.J., Caton J., Bossert M., Goodman R.M.;
 RT "Nucleotide sequence of bean golden mosaic virus and a model for gene
 RT regulation in geminiviruses.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:3572-3576(1985).
 CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.

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CC
 CC EMBL: M10070; AAA46318.1; -;
 DR InterPro: IPR001191; Gemini_AL1.
 DR Pfam: PF00799; Gemini_AL1; 1.
 DR PRINTS: PR00227; GEMCOATFAL1.
 DR PRINTS: PR00228; GEMCOATFAL1.
 DR Prodom: PD000736; Gemini_AL1; 1.
 KW ATP-binding.
 FT NP-BIND 222 229 ATP (POTENTIAL).
 SQ SEQUENCE 353 AA: 40190 MW: 80FA779DF6029A34 CRC64:

Query Match
 Best Local Similarity 59.3%; Score 214; DB 1; Length 353;
 Matches 41; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

OY 1 TLWGEAAVDSARGCGCOTSDNDAAEALNASSKEBALQIIREKIPKYLQFHNLSNLD 60
 DB 110 TLWGEAFDGRSARGGQGSANDTYAKALNASSAEALQIIREKQPOHFLOFHNLSNLD 169
 OY 61 DRIFDKTPEP 70
 DB 170 ERIFKVPPEP 179

RESULT 10
 VAL1_ABMV STANDARD: PRT: 355 AA.
 AC P21947:
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE AL1 PROTEIN.
 GN AC1.
 OS Abutilon mosaic virus (isolate West India).
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OX NCBI_TaxID=10816;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91020984; PubMed=2219703;
 RA Fritschnuth T., Zimmat G., Jeske H.;
 RT "The nucleotide sequence of abutilon mosaic virus reveals prokaryotic
 RT as well as eukaryotic features.";
 RL Virology 178:461-468(1990).
 CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.

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CC -----
DR EMBL; X15983; -. NOT_ANNOTATED_CDS.
DR PIR; A36214; QOCVWL.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1.1.
DR PRINTS; PR00227; GEMCOATFALL.
DR PRINTS; PR00228; GEMCOATCVLL.
DR ProDom; PD000736; Gemini_AL1.1.
DR ATP-binding.
DR NP_BIND.
DR FT SEQUENCE 355 AA; 40257 MW; 16A2CA8A63251E95 CRC64;

Query Match
Best Local Similarity 59.0%; Score 213; DB 1; Length 355;
Matches 40; Conservative 12; Mismatches 18; Indels 0; Gaps 0;

OY 1 TLVWGEAAVDRSARGCGGOTSNDAAAEALNASSKEEALQIIRKIPKYLEFQFHNLSNLT 60
DB 110 TAEWGEFQIDRSARGGQOTANDSYAKALNAGDYOSALNLIKKEPKDYVLQHNHNSRL 169
OY 61 DRIFDKTPEP 70
DB 170 ERIFAKAPEP 179

RESULT 11
VAL1_TYLCV STANDARD: PRT; 357 AA.
AC P27259;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 PROTEIN (C1 PROTEIN).
GN C1.
OS Tomato yellow leaf curl virus (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10832;
RN [1]
RP MEDLINE=92024070; PubMed=1926771;
RA Navot N., Pichersky E., Zaidan M., Zamir D., Czosnek H.;
RT "Tomato yellow leaf curl virus: a whitefly-transmitted geminivirus
RT with a single genomic component."
RL Virology 185:151-161(1991).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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CC -----
DR EMBL; X15656; CAA33688.1; -.
DR PIR; D40779; QOCVCL.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1.1.
DR PRINTS; PR00227; GEMCOATFALL.
DR PRINTS; PR00228; GEMCOATCVLL.
DR ProDom; PD000736; Gemini_AL1.1.
DR ATP-binding.
DR NP_BIND.
DR FT SEQUENCE 357 AA; 40678 MW; 939AB68E1AB3B2A7 CRC64;
```

```
OY 4 WGEAAVDRSARGCGGOTSNDAAAEALNASSKEEALQIIRKIPKYLEFQFHNLSNLT 63
DB 111 FVSGQIDRSARGGQGSANDAYAEALNAGSSEALNLIKKEAPDYILQFHNLSNLT 170
OY 64 F 64
DB 171 F 171

RESULT 12
VAL1_BCTV STANDARD: PRT; 358 AA.
AC P14591;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE AL1 PROTEIN (40.8 KDA PROTEIN).
OS Beet curly top virus (BCTV).
OC Viruses; ssDNA viruses; Geminiviridae; Curtovirus.
OX NCBI_TaxID=10840;
RN [1]
RP SEQUENCE FROM N.A.
RA Stanley J., Markham P.G., Callis R.J., Plummer M.S.;
RT "The nucleotide sequence of an infectious clone of the geminivirus
RT beet curly top virus."
RL EMBO J 5:1761-1767(1986).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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CC -----
DR EMBL; X04144; -. NOT_ANNOTATED_CDS.
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1.1.
DR PRINTS; PR00227; GEMCOATFALL.
DR PRINTS; PR00228; GEMCOATCVLL.
DR ProDom; PD000736; Gemini_AL1.1.
DR ATP-binding.
DR NP_BIND.
DR FT SEQUENCE 358 AA; 40889 MW; 39A45FE3C0B9C333 CRC64;

Query Match
Best Local Similarity 58.2%; Score 210; DB 1; Length 358;
Matches 38; Conservative 16; Mismatches 16; Indels 0; Gaps 0;

OY 1 TLVWGEAAVDRSARGCGGOTSNDAAAEALNASSKEEALQIIRKIPKYLEFQFHNLSNLT 60
DB 110 TIEWGEFQIDRSARGGQOTANDSYAKALNATSLDQALQILKEPKDYVLQHNHNLNA 169
OY 61 DRIFDKTPEP 70
DB 170 QKIFORPPDP 179

RESULT 13
VAL1_TMOV STANDARD: PRT; 361 AA.
AC Q06657;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
```

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DE AL1 PROTEIN.
GN AL1.
OS Tomato mottle virus (isolate Florida) (TMov).
OC Viruses: ssDNA viruses: Geminiviridae; Begomovirus.
OK NCBI_TaxID=36449;
RN [1]
RX MEDLINE=93107858; PubMed=1469361;
RA Abouzaid A.M., Polston J.E., Hiebert E.;
RT "The nucleotide sequence of tomato mottle virus, a new geminivirus
RL isolated from tomatoes in Florida."
J. Gen. Virol. 73:3225-3229(1992).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC -----
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CC -----
DR EMBL: L14460; AAC32414.1; -
DR PIR: JQ1870; JQ1870.
DR InterPro: IPR001191; Gemini_AL1.
DR Pfam: PF00799; Gemini_AL1; 1.
DR PRINTS: PR00227; GEMCOATFALL.
DR PRINTS: PR00228; GEMCOATCVLL.
DR ProDom: PD000736; Gemini_AL1; 1.
RW ATP-binding.
FT NP_BIND 222 229 ATP (BY SIMILARITY).
SQ SEQUENCE 361 AA; 40516 MW; 8138B65CEAC6950 CRC64;

Query Match 58.2%; Score 210; DB 1; Length 361;
Best Local Similarity 54.3%; Pred. No. 3.6e-16;
Matches 38; Conservative 16; Mismatches 16; Indels 0; Gaps 0;

QY 1 TLWGEAAVDSGSRAGGOTSNDAAAFALNASSKEALQIIREKIPKYLQFPHNLNSNL 60
DB 110 TTEMGDFOIDGSRAGGOTSNDAAAFALNASSKEALQIIREKIPKYLQFPHNLNSNL 169
QY 61 DRIPDKTEPP 70
DB 170 ERIFAKAPEP 179

RESULT 14
VAL1_SLICV STANDARD: PRT; 347 AA.
AC P29048;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE AL1 PROTEIN.
OS Squash leaf curl virus.
OC Viruses: ssDNA viruses: Geminiviridae; Begomovirus.
OK NCBI_TaxID=10829;
RN [1]
RX MEDLINE=91082449; PubMed=1984668;
RA Lazarowitz S.G., Lazdins J.B.;
RT "Infectivity and complete nucleotide sequence of the cloned genomic
RT components of a bipartite squash leaf curl geminivirus with a broad
RT host range phenotype."
Virology 180:58-69(1991).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M36183; AAC32410.1; ALT_INT.
DR PIR: C36785; QQCVS1.
DR InterPro: IPR001191; Gemini_AL1.
DR Pfam: PF00799; Gemini_AL1; 1.
DR PRINTS: PR00227; GEMCOATFALL.
DR PRINTS: PR00228; GEMCOATCVLL.
DR ProDom: PD000736; Gemini_AL1; 1.
RW ATP-binding.
FT NP_BIND 218 225 ATP (POTENTIAL).
SQ SEQUENCE 347 AA; 39110 MW; AFDABDDE122110E CRC64;

Query Match 32.4%; Score 117; DB 1; Length 347;
Best Local Similarity 37.9%; Pred. No. 8.3e-06;
Matches 25; Conservative 12; Mismatches 25; Indels 4; Gaps 1;

QY 5 GEAAVDSGSRAGGOTSNDAAAFALNASSKEALQIIREKIPKYLQFPHNLNSNLDRIF 64
DB 116 GQKVSQ-----GSKSNKDDVYHNAMNAGSAGEALDIKAGPKPIYVYHMLANVERLF 171
QY 65 DKTEPP 70
DB 172 QKPEP 177

RESULT 15
LMA3_HUMAN STANDARD: PRT; 1713 AA.
AC Q16787; Q13679; Q13680;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE LAMININ ALPHA-3 CHAIN PRECURSOR (EPILGRIN 170 KDA SUBUNIT) (E170).
GN LMAA3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RX MEDLINE=94357926; PubMed=8077230;
RA Ryan M.C., Tizard R., Vandevanter D.R., Carter W.G.;
RT "Cloning of the Lma3 gene encoding the alpha 3 chain of the adhesive
RT ligand epiligrin. Expression in wound repair."
J. Biol. Chem. 269:22779-22787(1994).
RN [2]
RP SEQUENCE OF 1-1331 FROM N.A. (ISOFORMS A AND B).
RX MEDLINE=96163880; PubMed=8586427;
RA Vidal F., Baudoin C., Miguel C., Galliano M.-F., Christiano A.M.,
RA Uitto J., Ortonne J.-P., Meneguzzi G.;
RT "Cloning of the laminin alpha 3 chain gene (LMA3) and identification
RT of a homozygous deletion in a patient with Herlitz junctional
RT epidermolysis bullosa."
J. Invest. Dermatol. 105:273-280(1995).
CC -1- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR. LAMININ
CC IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF
CC CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING
CC WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.
CC -1- FUNCTION: LAMININ-5 IS THOUGHT TO BE INVOLVED IN (1) CELL ADHESION
CC VIA INTEGRIN ALPHA-3/BETA-1 IN FOCAL ADHESION AND INTEGRIN ALPHA-
CC 6/BETA-4 IN HEMIDESMOSOMES, (2) SIGNAL TRANSDUCTION VIA TYROSINE
CC PHOSPHORYLATION OF PP125-FAK AND P80, (3) DIFFERENTIATION OF
CC KERATINOCYTES.
CC -1- SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE
CC DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND
CC TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE
CC COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.
CC THE ALPHA-3 CHAIN IS A SUBUNIT OF LAMININ-5 (EPILGRIN/KALININ/
CC NICEIN), AND POSSIBLY ALSO A COMPONENT OF LAMININ-6 (K-LAMININ)

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 3, 2002, 15:56:25 ; Search time 131.69 Seconds
(without alignments)
77.751 Million cell updates/sec

Title: US-09-289-346a-8
Perfect score: 361
Sequence: 1 TLWGEAAVDSRGSGCOT.....FOFHNLNSLDRIFDKTPPE 70

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: SP_TREMBL_17:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_plant:*
11: sp_fodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	299	82.8	352	12 09E000	09E000 tomato rugo
2	282	78.1	226	12 009727	009727 leonurus mo
3	282	78.1	226	12 09WHF6	09WHF6 tomato mild
4	280	77.6	361	12 067574	067574 bean golden
5	278	77.0	225	12 09QDB1	09QDB1 cowpea gold
6	278	77.0	314	12 09ELT8	09ELT8 sweet potat
7	278	77.0	364	12 09Q555	09Q555 sweet potat
8	275	76.2	185	12 098693	098693 sida golden
9	267	74.0	149	12 P88975	P88975 macroptilin
10	267	74.0	233	12 09YLA4	09YLA4 macroptilin
11	261	72.3	234	12 039180	039180 potato yell
12	258	71.5	190	12 092089	092089 tobacco lea
13	258	71.5	190	12 092084	092084 tobacco lea
14	257	71.2	190	12 09W827	09W827 tobacco lea
15	257	71.2	208	12 09Z0C4	09Z0C4 tobacco lea
16	255	70.6	208	12 09Z0C0	09Z0C0 tobacco lea
17	255	70.6	208	12 09Z0B8	09Z0B8 tobacco lea
18	253	70.1	208	12 09Z0B6	09Z0B6 tobacco lea
19	252	69.8	203	12 09Z083	09Z083 tobacco lea

20	252	69.8	363	12 073577	073577 cotton leaf
21	247	68.4	360	12 09DX10	09DX10 ageratum ye
22	245	67.9	208	12 09Z0A0	09Z0A0 tobacco lea
23	245	67.9	363	12 072705	072705 cotton leaf
24	245	67.9	363	12 072719	072719 cotton leaf
25	244	67.6	190	12 09Z0B6	09Z0B6 tobacco lea
26	244	67.6	208	12 09Z0C6	09Z0C6 tobacco lea
27	243	67.3	349	12 088888	088888 tomato pseu
28	243	67.3	362	12 056816	056816 chayote mos
29	242	67.0	359	12 09Y2V4	09Y2V4 tomato yell
30	242	67.0	359	12 09Y2V2	09Y2V2 tomato yell
31	242	67.0	359	12 09YUX7	09YUX7 tomato yell
32	242	67.0	359	12 09YU27	09YU27 tomato yell
33	241	66.8	353	12 072692	072692 beet curly
34	241	66.8	354	12 065438	065438 beet curly
35	241	66.8	359	12 088942	088942 tomato yell
36	240	66.5	190	12 09Z0A7	09Z0A7 tobacco lea
37	240	66.5	362	12 091M48	091M48 okra enatio
38	239	66.2	307	12 091EP7	091EP7 cotton leaf
39	239	66.2	361	12 072723	072723 cotton leaf
40	238	65.9	231	12 096620	096620 african tom
41	238	65.9	354	12 091M42	091M42 south afric
42	237	65.7	358	12 065418	065418 beet curly
43	237	65.7	358	12 09JEA2	09JEA2 cassava gem
44	233	64.5	362	12 09YU77	09YU77 althea rose
45	233	64.5	363	12 073494	073494 okra yellow

ALIGNMENTS

RESULT 1
ID 09E000 PRELIMINARY: PRT: 352 AA.
AC 09E000:
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE REPLICATION-ASSOCIATED PROTEIN.
GN AC1.
OS Tomato rugose mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID-134599;
RN [1]
RP SEQUENCE FROM N.A.
RA Fernandes J.T., Fontes E.P.B., Brommonschenkel S.H., Carvalho M.G.,
RZ Zambolim E.M., Zerbini F.M.;
RT "Molecular Cloning and Characterization of Tomato rugose mosaic virus
RT (TRMV), a Begomovirus isolated from Tomatoes at Triangulo Mineiro,
RT Minas Gerais, Brazil.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF291705; AAG15546.1; -
DR InterPro: IPR001191; Gemin1_AL1.
DR Pfam: PF00799; Gemin1_AL1; 1.
DR PRINTS: PR00227; GEMCOATP1.
DR ProDom: PD000736; Gemin1_AL1; 1.
SQ SEQUENCE 352 AA: 40012 MW: 47CD55838E24D613 CRC64:

Query Match Best Local Similarity 82.8%; Score 299; DB 12; Length 352;
Matches 56; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 TLWGEAAVDSRGSGCOTSDAAAEALNASSKEEALQIREKIPKYLFOFHNLNSL 60
DB 11 TLWGEAFAVDSRGSGCOTSDAAAEALNASSKEEALQIREKIPKYLFOFHNLNSL 170
QY 61 DRIFDKTPPE 70
DB 171 DRIFARPEP 180
RESULT 2

DR EMBL; AF188708; AAF06318.1; -
 DR InterPro: IPR001191; Gemini_AL1.
 DR Pfam: PF00799; Gemini_AL1.1.
 DR PRINTS: PR00227; GEMCOATL1.
 DR ProDom: PD000736; Gemini_AL1.1.
 FT NON_TER 225
 SO SEQUENCE 225 AA; 25766 MW; 1089CB6BD8D15B5D CRC64;

Query Match 77.0%; Score 278; DB 12; Length 225;
 Best Local Similarity 77.6%; Pred. No. 2e-22;
 Matches 52; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

OY 4 WGEAAVDCRSARGCGCOTSDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLNSNL 63
 Db 113 WGEFQIDGRSARGCGOQTANDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLNSNLDRI 172

OY 64 FDKTPEP 70
 Db 173 FKKRPEP 179

RESULT 6
 O9ELT8 PRELIMINARY; PRT; 314 AA.
 AC O9ELT8;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE REPLICATION ASSOCIATION PROTEIN.
 GN AC1.
 OS sweet potato leaf curl virus.
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OX NCBI_TaxID=100755;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lotrakul P., Valverde R.A., Clark C.A., Sim J., De La Torre R.;
 RT "Detection of a geminivirus infecting sweet potato in the United
 States."
 RL Plant Dis. 82:1253-1257(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Lotrakul P., Valverde R.A.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF288227; AAG01006.1;
 DR InterPro: IPR001191; Gemini_AL1.
 DR Pfam: PF00799; Gemini_AL1.1.
 DR PRINTS: PR00227; GEMCOATL1.
 DR ProDom: PD000736; Gemini_AL1.1.
 SO SEQUENCE 314 AA; 35153 MW; 6B6220613046943F CRC64;

Query Match 77.0%; Score 278; DB 12; Length 314;
 Best Local Similarity 80.9%; Pred. No. 2.9e-22;
 Matches 55; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

OY 1 TLVWGEAAVDCRSARGCGCOTSDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLNSNL 60
 Db 110 TITWGEFQIDGRSARGCGOQTANDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLNSNL 169

OY 61 DRIFDKTP 68
 Db 170 DRIFSPPP 177

RESULT 7
 O9QS55 PRELIMINARY; PRT; 364 AA.
 AC O9QS55;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE REPLICATION INITIATION PROTEIN AC1.

GN AC1.
 OS sweet potato leaf curl virus.
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OX NCBI_TaxID=100755;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lotrakul P., Valverde R.A., Clark C.A., Sim J., De La Torre R.;
 RT "Detection of a geminivirus infecting sweet potato in the United
 States."
 RL Plant Dis. 82:1253-1257(1998).
 DR EMBL; AF104036; AAD47173.1; -
 DR InterPro: IPR001191; Gemini_AL1.
 DR Pfam: PF00799; Gemini_AL1.1.
 DR PRINTS: PR00227; GEMCOATL1.
 DR ProDom: PD000736; Gemini_AL1.1.
 SO SEQUENCE 364 AA; 40680 MW; 5F79752431A09D6E CRC64;

Query Match 77.0%; Score 278; DB 12; Length 364;
 Best Local Similarity 80.9%; Pred. No. 3.4e-22;
 Matches 55; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

OY 1 TLVWGEAAVDCRSARGCGCOTSDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLNSNL 60
 Db 110 TITWGEFQIDGRSARGCGOQTANDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLNSNL 169

OY 61 DRIFDKTP 68
 Db 170 DRIFSPPP 177

RESULT 8
 O98693 PRELIMINARY; PRT; 185 AA.
 AC O98693;
 DT 01-FEB-1997 (TREMBlrel. 02, Created)
 DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE REP PROTEIN (FRAGMENT).
 GN AC1.
 OS sida golden mosaic virus.
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OX NCBI_TaxID=51034;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-JAMAICA;
 RA Roye M.E., McLaughlin W.A., Nakhia N.K., Maxwell D.P.;
 RL Plant Dis. 81:1251-1258(1997).
 DR EMBL; U67926; AAB97865.1; -
 DR InterPro: IPR001191; Gemini_AL1.
 DR Pfam: PF00799; Gemini_AL1.1.
 DR PRINTS: PR00227; GEMCOATL1.
 DR ProDom: PD000736; Gemini_AL1.1.
 FT NON_TER 1
 FT NON_TER 1
 SO SEQUENCE 185 AA; 20975 MW; 3913850A025A5EE1 CRC64;

Query Match 76.2%; Score 275; DB 12; Length 185;
 Best Local Similarity 71.4%; Pred. No. 3.4e-22;
 Matches 50; Conservative 12; Mismatches 8; Indels 0; Gaps 0;

OY 1 TLVWGEAAVDCRSARGCGCOTSDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLNSNL 60
 Db 89 TIEWGVFQIDGRSARGCGOQTANDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLNSNL 148

OY 61 DRIFDKTP 70
 Db 149 DRIFSKPEP 158

RESULT 9
 P88975

Fri Jan 4 09:39:52 2002

us-09-289-346a-8.rspt

Page 6

Job time: 1122 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 3, 2002, 15:38:51 ; Search time 65.28 Seconds
(without alignments)
24.130 Million cell updates/sec

Title: US-09-289-346A-8
Perfect score: 361
Sequence: 1 TLWGEAAVDSGRSARGCQT.....FQFHNLNSLDRIFDKTPPE 70

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/plodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/plodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/plodata/2/1aa/6A_COMB.pep:*
4: /cgn2_6/plodata/2/1aa/6B_COMB.pep:*
5: /cgn2_6/plodata/2/1aa/PCtus_COMB.pep:*
6: /cgn2_6/plodata/2/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match Length	DB ID	Description
1	216	59.8	353	4	US-08-838-151A-44 Sequence 44, Appl
2	216	59.8	353	4	US-08-838-151A-46 Sequence 46, Appl
3	216	59.8	353	4	US-08-838-151A-49 Sequence 49, Appl
4	216	59.8	353	4	US-08-838-151A-52 Sequence 52, Appl
5	216	59.8	353	4	US-08-838-151A-55 Sequence 55, Appl
6	216	59.8	353	4	US-08-103B-2 Sequence 2, Appl
7	216	59.8	359	4	US-08-103B-4 Sequence 4, Appl
8	216	59.8	359	4	US-08-809-103B-6 Sequence 6, Appl
9	216	59.8	359	4	US-08-809-103B-8 Sequence 8, Appl
10	214	59.3	361	4	US-08-838-151A-2 Sequence 2, Appl
11	214	59.3	361	4	US-08-838-151A-4 Sequence 4, Appl
12	214	59.3	361	4	US-08-838-151A-6 Sequence 6, Appl
13	214	59.3	361	4	US-08-838-151A-8 Sequence 8, Appl
14	212	58.7	357	4	US-08-838-151A-24 Sequence 24, Appl
15	212	58.7	357	4	US-08-838-151A-27 Sequence 27, Appl
16	212	58.7	357	4	US-08-838-151A-30 Sequence 30, Appl
17	204	56.5	357	4	US-08-838-151A-20 Sequence 20, Appl
18	68.5	19.0	1713	3	US-08-600-982-24 Sequence 24, Appl
19	68.5	19.0	1713	3	PCT-US94-10261A-24 Sequence 24, Appl
20	63.5	17.6	2161	1	US-07-745-206A-2 Sequence 2, Appl
21	63.5	17.6	2161	1	US-08-455-543A-49 Sequence 49, Appl
22	63.5	17.6	2161	1	US-08-455-543A-51 Sequence 51, Appl
23	63.5	17.6	2161	2	US-08-223-305C-49 Sequence 49, Appl
24	63.5	17.6	2161	2	US-08-223-305C-51 Sequence 51, Appl
25	63.5	17.6	2161	2	US-08-311-363-2 Sequence 2, Appl
26	60	16.6	446	2	US-08-672-814D-11 Sequence 11, Appl
27	60	16.6	446	4	US-09-333-696-11 Sequence 11, Appl

28	58	16.1	171	2	US-08-609-049A-22 Sequence 22, Appl
29	58	16.1	171	4	US-09-170-996-22 Sequence 22, Appl
30	58	16.1	844	3	US-09-029-267-20 Sequence 20, Appl
31	57.5	15.9	334	6	5290690-11 Patent No. 5290690
32	57.5	15.9	439	1	US-07-637-870-9 Sequence 9, Appl
33	57.5	15.9	439	1	US-07-637-389-6 Sequence 6, Appl
34	57.5	15.9	439	1	US-08-112-703-6 Sequence 6, Appl
35	57	15.8	165	4	US-08-995-369-4 Sequence 4, Appl
36	57	15.8	165	5	PCT-US95-10075-4 Sequence 4, Appl
37	56	15.5	454	3	US-08-446-100-31 Sequence 31, Appl
38	55	15.2	384	4	US-08-928-442-3 Sequence 3, Appl
39	54.5	15.1	103	1	US-08-552-142A-13 Sequence 13, Appl
40	54.5	15.1	497	2	US-08-570-311-2 Sequence 2, Appl
41	54.5	15.1	497	2	US-08-353-485-2 Sequence 2, Appl
42	54.5	15.1	2628	2	US-08-570-311-14 Sequence 14, Appl
43	54	15.0	454	3	US-08-446-100-30 Sequence 30, Appl
44	54	15.0	602	2	US-08-419-652-6 Sequence 6, Appl
45	54	15.0	771	1	US-07-923-976-6 Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-08-838-151A-44
Sequence 44, Application US/08838151A
Patent No. 6291743
GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Lau, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Gemintivirus
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rocky, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SYS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5460
FAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 353 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-838-151A-44
Query Match 59.8% Score 216; DB 4; Length 353;
Best local Similarity 58.6%; Pred. No. 3.9e-20;
Matches 41; Conservative 13; Mismatches 16; Indels 0; Gaps 0;
Oy 1 TLWGEAAVDSGRSARGCQTSNDAAAEALNASSKEEALQIIREKIPERYLFQFHNLNSL 60

Db 110 TTEMGOFVYDGRSARGGQSANDSYAKALNADISIALTLILKEQPKDYVLQHHNRSL 169
QY 61 DRIFDKTPEP 70
Db 170 ERIFVKVPEP 179

RESULT 2

US-08-838-151A-46

Sequence 46, Application US/08838151A

Patent No. 6291743

GENERAL INFORMATION:

APPLICANT: Stout, John T

APPLICANT: Lau, Hang T

APPLICANT: Maxwell, Douglas

APPLICANT: Ahlquist, Paul

APPLICANT: Hanson, Steve

TITLE OF INVENTION: Transgenic Plants Expressing GeminiVirus

TITLE OF INVENTION: Genes

NUMBER OF SEQUENCES: 63

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dressler, Rocky, Milnamow & Katz

STREET: Two Prudential Plaza, Suite 4700

CITY: Chicago

STATE: Illinois

COUNTRY: U.S.A.

ZIP: 60601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/838,151A

FILING DATE:

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Mueller, Lisa V

REGISTRATION NUMBER: 38,978

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-616-5400

TELEFAX: 312-616-5460

INFORMATION FOR SEQ ID NO: 46:

SEQUENCE CHARACTERISTICS:

LENGTH: 353 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-838-151A-46

Query Match 59.8%; Score 216; DB 4; Length 353;

Best Local Similarity 58.6%; Pred. No. 3.9e-20;

Matches 41; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY 1 TLVWGAADVGRSARGGQCTSDNDAAEALNASSKEEALQIIREKIPKYLFOFHNLSNL 60

Db 110 TTEMGOFVYDGRSARGGQSANDSYAKALNADISIALTLILKEQPKDYVLQHHNRSL 169

QY 61 DRIFDKTPEP 70

Db 170 ERIFVKVPEP 179

RESULT 3

US-08-838-151A-49

Sequence 49, Application US/08838151A

Patent No. 6291743

GENERAL INFORMATION:

APPLICANT: Stout, John T

APPLICANT: Lau, Hang T

APPLICANT: Maxwell, Douglas

APPLICANT: Ahlquist, Paul

APPLICANT: Hanson, Steve

TITLE OF INVENTION: Transgenic Plants Expressing GeminiVirus

TITLE OF INVENTION: Genes

NUMBER OF SEQUENCES: 63

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dressler, Rocky, Milnamow & Katz

STREET: Two Prudential Plaza, Suite 4700

CITY: Chicago

STATE: Illinois

COUNTRY: U.S.A.

ZIP: 60601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing GeminiVirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:

ADDRESSEE: Dressler, Rocky, Milnamow & Katz

STREET: Two Prudential Plaza, Suite 4700

CITY: Chicago

STATE: Illinois

COUNTRY: U.S.A.

ZIP: 60601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/838,151A

FILING DATE:

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Mueller, Lisa V

REGISTRATION NUMBER: 38,978

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-616-5400

TELEFAX: 312-616-5460

INFORMATION FOR SEQ ID NO: 49:

SEQUENCE CHARACTERISTICS:

LENGTH: 353 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-838-151A-49

Query Match 59.8%; Score 216; DB 4; Length 353;

Best Local Similarity 58.6%; Pred. No. 3.9e-20;

Matches 41; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY 1 TLVWGAADVGRSARGGQCTSDNDAAEALNASSKEEALQIIREKIPKYLFOFHNLSNL 60

Db 110 TTEMGOFVYDGRSARGGQSANDSYAKALNADISIALTLILKEQPKDYVLQHHNRSL 169

QY 61 DRIFDKTPEP 70

Db 170 ERIFVKVPEP 179

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 353 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-838-151A-52

Query Match 59.8%; Score 216; DB 4; Length 353;
Best Local Similarity 58.6%; Pred. No. 3.9e-20;
Matches 41; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

OY 1 TLWGCAVNDGSRAGCGCSTNDAAAEALNASSKEEALQIREKIPKYLFFQHNLSNL 60
Db 110 TLWGCFQVNDGSRAGCGGQSSANDSYAKALNADSIETALTLKEQPKDYVLOHNNIRSNL 169

OY 61 DRIFDKTPEP 70
Db 170 ERIFVKVPEP 179

RESULT 5

US-08-838-151A-55
Sequence 55, Application US/08838151A
Patent No. 6291743
GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Luu, Haog T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rocky, Milnamov & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 55:

SEQUENCE CHARACTERISTICS:
LENGTH: 353 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-838-151A-55

Query Match 59.8%; Score 216; DB 4; Length 353;
Best Local Similarity 58.6%; Pred. No. 3.9e-20;
Matches 41; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

OY 1 TLWGCAVNDGSRAGCGCSTNDAAAEALNASSKEEALQIREKIPKYLFFQHNLSNL 60
Db 110 TLWGCFQVNDGSRAGCGGQSSANDSYAKALNADSIETALTLKEQPKDYVLOHNNIRSNL 169

OY 61 DRIFDKTPEP 70
Db 170 ERIFVKVPEP 179

RESULT 6

US-08-809-103B-2
Sequence 2, Application US/08809103B
Patent No. 6133505
GENERAL INFORMATION:
APPLICANT: GROENENBORN, Bruno
TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: YOUNG & THOMPSON
STREET: 745 South 23rd Street
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,103B
FILING DATE: 17-MAR-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94,11040
FILING DATE: 15-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR95/01192
FILING DATE: 15-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: PATCH, Andrew J.
REGISTRATION NUMBER: 32,925
REFERENCE/DOCKET NUMBER: US8944L CNR TOM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 521-2297
TELEFAX: (703) 685-0573
TELEX: 248425 EMBON
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-809-103B-2

Query Match 59.8%; Score 216; DB 4; Length 359;
Best Local Similarity 56.5%; Pred. No. 3.9e-20;
Matches 39; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,103B
FILING DATE: 17-MAR-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94.11040
FILING DATE: 15-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR95/01192
FILING DATE: 15-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: PATCH, Andrew J.
REGISTRATION NUMBER: 32,925
REFERENCE/DOCKET NUMBER: US94AL CNR TOM
TELEPHONE: (703) 521-2297
TELEFAX: (703) 685-0573
TELEX: 248425 EMBON
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-809-103B-8

Query Match 59.8%; Score 216; DB 4; Length 359;
Best Local Similarity 56.5%; Pred. No. 3.9e-20;
Matches 39; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

QY 2 LWGEAAVDSRGSGCOTSDNAAEALNASSKEALQIREKIPERYLFOFHNLSNL 61
DB 111 LEMGDFQIDGSRAGGQOTANDAKAINAGSKSOALDIVIKELAPRDVLFHFNHNSL 170

QY 62 RIFDKTREP 70
DB 171 KVFQVPAP 179

RESULT 10
US-08-838-151A-2
Sequence 2, Application US/08838151A
Patent No. 6291743
GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
NUMBER OF INVENTION: 63
CORRESPONDENCE ADDRESSES:
ADDRESS: Dressler, Rockey, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A

FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 361 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-838-151A-2

Query Match 59.3%; Score 214; DB 4; Length 361;
Best Local Similarity 55.7%; Pred. No. 7.2e-20;
Matches 39; Conservative 16; Mismatches 15; Indels 0; Gaps 0;

QY 1 TLWGEAAVDSRGSGCOTSDNAAEALNASSKEALQIREKIPERYLFOFHNLSNL 60
DB 110 TIEMGDFQIDGSRAGGQOSANDSYAKALNASSVOSALAVIREQPKDFVLONHNIRSL 169

QY 61 RIFDKTREP 70
DB 170 ERIFAKREP 179

RESULT 11
US-08-838-151A-4
Sequence 4, Application US/08838151A
Patent No. 6291743

GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
NUMBER OF INVENTION: 63
CORRESPONDENCE ADDRESSES:
ADDRESS: Dressler, Rockey, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 361 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-838-151A-4

Query Match 59.3%; Score 214; DB 4; Length 361;
Best Local Similarity 55.7%; Pred. No. 7.2e-20;
Matches 39; Conservative 16; Mismatches 15; Indels 0; Gaps 0;

OY 1 TLVWGEAAVDDGRSARGGCGTSDNDAAEALNASSKEEALQIIRKIPERYLFOFHNLSNL 60
DB 110 TIEMGDFOIDGRSARGGCGQSANDSYAKALNASSVSALAVLREOPKDFVLONHNIRSNL 169

OY 61 DRIEDKTEPP 70
DB 170 ERIFAKAPPP 179

RESULT 12

US-08-838-151A-6
Sequence 6, Application US/08838151A
Patent No. 6291743

GENERAL INFORMATION:

APPLICANT: Stout, John T

APPLICANT: Lou, Hang T

APPLICANT: Maxwell, Douglas

APPLICANT: Ahlquist, Paul

APPLICANT: Hanson, Steve

TITLE OF INVENTION: Transgenic Plants Expressing Gemlinivirus

NUMBER OF SEQUENCES: 63

CORRESPONDENCE ADDRESSES:

ATTORNEY/AGENT INFORMATION:

NAME: Mueller, Lisa V

REGISTRATION NUMBER: 38,978

REFERENCE/DOCKET NUMBER: SYS3801P0260

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-616-5400

TELEFAX: 312-616-5400

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 361 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-838-151A-6

Query Match 59.3%; Score 214; DB 4; Length 361;
Best Local Similarity 55.7%; Pred. No. 7.2e-20;
Matches 39; Conservative 16; Mismatches 15; Indels 0; Gaps 0;

OY 1 TLVWGEAAVDDGRSARGGCGTSDNDAAEALNASSKEEALQIIRKIPERYLFOFHNLSNL 60
DB 110 TIEMGDFOIDGRSARGGCGQSANDSYAKALNASSVSALAVLREOPKDFVLONHNIRSNL 169

OY 61 DRIEDKTEPP 70
DB 170 ERIFAKAPPP 179

RESULT 13

US-08-838-151A-8
Sequence 8, Application US/08838151A
Patent No. 6291743

GENERAL INFORMATION:

APPLICANT: Stout, John T

APPLICANT: Lou, Hang T

APPLICANT: Maxwell, Douglas

APPLICANT: Ahlquist, Paul

APPLICANT: Hanson, Steve

TITLE OF INVENTION: Transgenic Plants Expressing Gemlinivirus

NUMBER OF SEQUENCES: 63

CORRESPONDENCE ADDRESSES:

ATTORNEY/AGENT INFORMATION:

NAME: Mueller, Lisa V

REGISTRATION NUMBER: 38,978

REFERENCE/DOCKET NUMBER: SYS3801P0260

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-616-5400

TELEFAX: 312-616-5400

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 361 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-838-151A-8

Query Match 59.3%; Score 214; DB 4; Length 361;
Best Local Similarity 55.7%; Pred. No. 7.2e-20;
Matches 39; Conservative 16; Mismatches 15; Indels 0; Gaps 0;

OY 1 TLVWGEAAVDDGRSARGGCGTSDNDAAEALNASSKEEALQIIRKIPERYLFOFHNLSNL 60
DB 110 TIEMGDFOIDGRSARGGCGQSANDSYAKALNASSVSALAVLREOPKDFVLONHNIRSNL 169

OY 61 DRIEDKTEPP 70
DB 170 ERIFAKAPPP 179

RESULT 14

US-08-838-151A-24
Sequence 24, Application US/08838151A
Patent No. 6291743

GENERAL INFORMATION:

APPLICANT: Stout, John T

APPLICANT: Lou, Hang T

APPLICANT: Maxwell, Douglas

APPLICANT: Ahlquist, Paul

APPLICANT: Hanson, Steve

TITLE OF INVENTION: Transgenic Plants Expressing Gemlinivirus

NUMBER OF SEQUENCES: 63

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Dressler, Rockey, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
City: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 357 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-838-151A-24

Query Match 58.7%; Score 212; DB 4; Length 357;
Best Local Similarity 65.6%; Pred. No. 1.3e-19;
Matches 40; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY 4 WGEAAVDRSARGCGQTSNDAAAEALNASKKEALQIREKIPKYLFOFHNLSNLDRI 63
:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 111 FGVSDIDRSARGGQSANDBAYAEALNLSGSKSEALNIKEKAPKDYIIQFINLSNLDRI 170

QY 64 F 64
|
Db 171 F 171

RESULT 15
US-08-838-151A-27
Sequence 27, Application US/08838151A
Patent No. 6291743
GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Lau, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Gemlinivirus
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rockey, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
City: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 357 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-838-151A-27

Query Match 58.7%; Score 212; DB 4; Length 357;
Best Local Similarity 65.6%; Pred. No. 1.3e-19;
Matches 40; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY 4 WGEAAVDRSARGCGQTSNDAAAEALNASKKEALQIREKIPKYLFOFHNLSNLDRI 63
:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 111 FGVSDIDRSARGGQSANDBAYAEALNLSGSKSEALNIKEKAPKDYIIQFINLSNLDRI 170

QY 64 F 64
|
Db 171 F 171

Search completed: January 3, 2002, 15:38:51
Job time: 228 sec

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OM protein - protein search, using sw model

Run on: January 3, 2002, 15:37:38 ; Search time 144.17 Seconds
(without alignments)
35,965 Million cell updates/sec

Title: US-09-289-346a-9

Sequence: 1 TLVWGEFVAGHSARGCCOT.....PQFHLNLSNLDKIPDKTPPP 70

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5.

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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3: /SIDSR/gcgdata/geneseq/geneseq/AA1982.DAT:*

4: /SIDSR/gcgdata/geneseq/geneseq/AA1983.DAT:*

5: /SIDSR/gcgdata/geneseq/geneseq/AA1984.DAT:*

6: /SIDSR/gcgdata/geneseq/geneseq/AA1985.DAT:*

7: /SIDSR/gcgdata/geneseq/geneseq/AA1986.DAT:*

8: /SIDSR/gcgdata/geneseq/geneseq/AA1987.DAT:*

9: /SIDSR/gcgdata/geneseq/geneseq/AA1988.DAT:*

10: /SIDSR/gcgdata/geneseq/geneseq/AA1989.DAT:*

11: /SIDSR/gcgdata/geneseq/geneseq/AA1990.DAT:*

12: /SIDSR/gcgdata/geneseq/geneseq/AA1991.DAT:*

13: /SIDSR/gcgdata/geneseq/geneseq/AA1992.DAT:*

14: /SIDSR/gcgdata/geneseq/geneseq/AA1993.DAT:*

15: /SIDSR/gcgdata/geneseq/geneseq/AA1994.DAT:*

16: /SIDSR/gcgdata/geneseq/geneseq/AA1995.DAT:*

17: /SIDSR/gcgdata/geneseq/geneseq/AA1996.DAT:*

18: /SIDSR/gcgdata/geneseq/geneseq/AA1997.DAT:*

19: /SIDSR/gcgdata/geneseq/geneseq/AA1998.DAT:*

20: /SIDSR/gcgdata/geneseq/geneseq/AA1999.DAT:*

21: /SIDSR/gcgdata/geneseq/geneseq/AA2000.DAT:*

22: /SIDSR/gcgdata/geneseq/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	362	100.0	70	21	AA18685
2	356	98.3	70	21	AA18677
3	356	98.3	356	21	AA18687
4	345	95.3	70	21	AA18688
5	344	95.0	70	21	AA18692
6	342	94.5	70	21	AA18684
7	342	94.5	70	21	AA18690
8	341	94.2	70	21	AA18678
9	341	94.2	70	21	AA18686
10	340	93.9	70	21	AA18689
11	338	93.4	70	21	AA18680

12	338	93.4	70	21	AA18691	Mutant peptide der
13	335	92.5	70	21	AA18681	Mutant peptide der
14	334	92.3	70	21	AA18683	Mutant peptide der
15	332	91.7	70	21	AA18682	Mutant peptide der
16	324	89.5	70	21	AA18679	Mutant peptide der
17	222	61.3	353	18	AAW34338	Bean golden mosaic
18	222	61.3	353	18	AAW34332	Bean golden mosaic
19	222	61.3	353	18	AAW34333	Bean golden mosaic
20	222	61.3	353	18	AAW34334	Bean golden mosaic
21	222	61.3	353	18	AAW34335	Bean golden mosaic
22	222	61.3	359	17	AAW34335	Sardinian tomato y
23	222	61.3	359	17	AAW34335	Sardinian tomato y
24	222	61.3	359	17	AAW34335	Sardinian tomato y
25	220	60.8	353	8	AAW34335	ORF 4 gene product
26	220	60.8	361	18	AAW34335	Tomato mottle viru
27	220	60.8	361	18	AAW34335	Tomato mottle viru
28	220	60.8	361	18	AAW34335	Tomato mottle viru
29	220	60.8	361	18	AAW34335	Tomato mottle viru
30	213.5	59.0	361	8	AAW34335	Product of ORF 4 f
31	208	57.5	362	19	AAW56495	Tobacco leaf curl
32	207	57.2	357	18	AAW34329	Tomato yellow leaf
33	207	57.2	357	18	AAW34330	Tomato yellow leaf
34	207	57.2	357	18	AAW34331	Tomato yellow leaf
35	199	55.0	357	18	AAW34337	Tomato yellow leaf
36	65	18.0	292	21	AAW92317	Geminivirus Rep C1
37	65	18.0	335	21	AAW92318	Mastrevirus Rep in
38	64.5	17.8	299	18	AAW5450	H. pylori ORF 02ae
39	64.5	17.8	512	19	AAW68473	Hiv-1 strain YBF30
40	62.5	17.3	447	21	AAW96659	Human GTPase assoc
41	62.5	17.3	447	21	AAW96659	Human secreted pro
42	62.5	17.3	447	21	AAW66744	Membrane-bound pro
43	62.5	17.3	447	21	AAW50947	Human adult aorta
44	62.5	17.3	447	21	AAW50947	Human gene 26 enco
45	62.5	17.3	447	22	AAW5267	Human PRO1125 (UNQ

ALIGNMENTS

RESULT 1	
AA18685	AA18685 standard; peptide: 70 AA.
XX	
AC	AA18685;
XX	
DT	22-JAN-2001 (first entry)
XX	
DE	Mutant peptide derived from amino acids 110-179 of Rep (Al1) protein.
XX	
KW	Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
KW	Ribosome binding region; resistance; geminivirus infection.
XX	
OS	Synthetic.
OS	Tomato golden mosaic virus.
FT	Key
FT	Misc-difference 10
FT	Location/Qualifiers
XX	
XX	W0200054573-A1.
XX	
PD	21-SEP-2000.
XX	
XX	15-MAR-2000; 2000WO-US06759.
XX	
PR	18-MAR-1999; 99US-0125004.
XX	
PR	09-APR-1999; 99US-0289346.
XX	
PA	(UYNC-) UNIV NORTH CAROLINA STATE.
XX	
PI	Hanley-Bowdoin L, Orozco BM, Kong L;
XX	
DR	WPI: 2000-618851/59.

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XX Transgenic plants with increased resistance to geminivirus infection
PT comprise a nucleic acid construct containing a nucleic acid sequence
PT encoding a mutant AL1 protein with a mutation in the Rb binding region
PS
XX Claim 53; Page 46; 73pp; English.
PS
XX The present sequence represents a mutant peptide, derived from a
CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
CC protein are used to produce transgenic plants. The mutation in AL1 is
CC present in a ribosome binding region, and expression of mutant AL1
CC protein imparts increased resistance to geminivirus infection in the
CC plant. Mutant AL1 proteins are useful for producing plants having
CC increased resistance or reduced sensitivity to a geminivirus such as
CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
CC virus, cotton leaf curl virus or beet curly top virus.
XX
SQ Sequence 70 AA:

Query Match 100.0%; Score 362; DB 21; Length 70;
Best Local Similarity 100.0%; Pred. NO. 5.5e-38;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLVWGEFVAGRSARGCCTSDAAEAALNASKKEALQITREKIPKYLFOFHNLSNL 60
   |||||||
Db 1 tlwgefvgvgrsargcgqtsndaadaaalnasskeaalqitrekipekylfqfhnlnsl 60
   |||||||

QY 61 DRFDKTPPEP 70
   |||||||
Db 61 drfdktkpep 70
   |||||||

RESULT 2
AAB18677 standard; peptide: 70 AA.
ID AAB18677;
AC AAB18677;
XX
XX 22-JAN-2001 (first entry)
DT
XX
XX Peptide fragment from Rep protein of TGMV (amino acids 110-179).
DE
XX
XX Geminivirus: replication protein; Rep protein; AL1; transgenic plant;
KW ribosome binding region; resistance; geminivirus infection.
XX
XX Tomato golden mosaic virus.
OS
XX
XX WO200054573-A1.
PN
XX
XX 21-SEP-2000.
PD
XX
XX 15-MAR-2000; 2000MO-US06759.
PF
XX
XX 18-MAR-1999; 99US-0125004.
PR
XX 09-APR-1999; 99US-0289346.
XX
XX (UYNC-) UNIV NORTH CAROLINA STATE.
PA
XX
XX Hanley-Bowdoin L, Orozco BM, Kong L;
PI
XX
XX WPI: 2000-618851/59;
DR
XX
XX Transgenic plants with increased resistance to geminivirus infection
PT comprise a nucleic acid construct containing a nucleic acid sequence
PT encoding a mutant AL1 protein with a mutation in the Rb binding region
PT
XX

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XX
XX Disclosure; Page 18; 73pp; English.
PS
XX
XX The present sequence is derived from a geminivirus replication (Rep)
CC protein, which is also known as AL1. AL1 binds double-stranded DNA,
CC catalyses cleavage and ligation of single-stranded DNA, and interacts
CC with other viral and host proteins. Mutants of the AL1 protein are used
CC to produce transgenic plants. The mutation in AL1 is present in a
CC ribosome binding region, and expression of mutant AL1 protein imparts
CC increased resistance to geminivirus infection in the plant. Mutant AL1
CC proteins are useful for producing plants having increased resistance or
CC reduced sensitivity to a geminivirus such as tomato golden mosaic virus,
CC tomato mottle virus, tomato yellow leaf curl virus, tomato leaf curl
CC virus, African cassava mosaic virus, Indian cassava mosaic virus, potato
CC yellow mosaic virus, bean golden mosaic virus, bean dwarf mosaic virus,
CC squash leaf curl virus, Texas pepper virus, cotton leaf curl virus or
CC beet curly top virus.
XX
SQ Sequence 70 AA:

Query Match 98.3%; Score 356; DB 21; Length 70;
Best Local Similarity 98.6%; Pred. NO. 3.1e-37;
Matches 69; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TLVWGEFVAGRSARGCCTSDAAEAALNASKKEALQITREKIPKYLFOFHNLSNL 60
   |||||||
Db 1 tlwgefvgvgrsargcgqtsndaadaaalnasskeaalqitrekipekylfqfhnlnsl 60
   |||||||

QY 61 DRFDKTPPEP 70
   |||||||
Db 61 drfdktkpep 70
   |||||||

RESULT 3
AAB18687 standard; peptide: 356 AA.
ID AAB18687;
AC AAB18687;
XX
XX 22-JAN-2001 (first entry)
DT
XX
XX Amino acid sequence of a geminivirus replication protein of TGMV.
DE
XX
XX Geminivirus: replication protein; Rep protein; AL1; transgenic plant;
KW ribosome binding region; resistance; geminivirus infection.
XX
XX Tomato golden mosaic virus.
OS
XX
XX Key Location/Qualifiers
FH MISC-difference 354
FT /note= "unspecified amino acid"
XX
XX WO200054573-A1.
PN
XX
XX 21-SEP-2000.
PD
XX
XX 15-MAR-2000; 2000MO-US06759.
PF
XX
XX 18-MAR-1999; 99US-0125004.
PR
XX 09-APR-1999; 99US-0289346.
XX
XX (UYNC-) UNIV NORTH CAROLINA STATE.
PA
XX
XX Hanley-Bowdoin L, Orozco BM, Kong L;
PI
XX
XX WPI: 2000-618851/59.
DR
XX
XX Transgenic plants with increased resistance to geminivirus infection
PT comprise a nucleic acid construct containing a nucleic acid sequence
PT encoding a mutant AL1 protein with a mutation in the Rb binding region
PT
XX

```


Sequence 356 AA;

QY	1 TLVWGEFVOVARSRKRGCGOTSNDAAAEALNNAKSKEEALQITIREKIPERYLFOFNNLSNL	60
Dd	110 tlvwgefvdvgrsrargcgotsndaaaealnnaakceaalqitirekiperylftfnnlnsl	163
QY	61 DRFDKPPEP 70	
Dd	170 drfdkdppep 179	

ID AAB18688 standard; peptide; 70 AA.

AC AAB18688;

DT 22-JAN-2001 (first entry)

DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.

KW ribosome binding region; resistance; geminivirus infection.

05 synthetic.

FH	Key	Location/Qualifiers
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	FT
/note=	"wild type residue replaced with Ala"

FT	/note= "wild type residue replaced with Ala"
FT	

PN W0200054573-A1.

PD 21-SEP-2000.

PF 15-MAR-2000; 2000WO-US06759.

PR 18-MAR-1999; 99US-0125004.

XX

XX

XX

DR WPI; 2000-618851/59

PT Transgenic plants with increased resistance to geminivirus infection
PT comprise a nucleic acid construct containing a nucleic acid sequence
PT encoding a mutant Al1 protein with a mutation in the Rb-binding region

CC The present sequence represents a mutant peptide, derived from a
CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
CC protein are used to produce transgenic plants. The mutation in AL1 is
CC present in a ribosome binding region, and expression of mutant AL1
CC protein imparts increased resistance to geminivirus infection in the
CC plant. Mutant AL1 proteins are useful for producing plants having
CC increased resistance or reduced sensitivity to a geminivirus such as
CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
CC virus, cotton leaf curl virus or beet curly top virus.

Sequence 70 AA;

Query Match	95.38;	Score 345;	DB 21;	length 70;
Best Local Similarity	95.78;	Pred. No. 7.5e-36;		
Matches 67;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;

Oy 1 TLWGCFQVAGSARGCCQT^{*}SNDAAEALNASSKEAQLTIREKIPERYLFOFHNLSNL 60
 ++++++ | ++++++ | ++++++ | ++++++ | ++++++ | ++++++ | ++++++ | ++++++ |
Db 1 tlvwgefvydrtarsargcaasndaaaealnasskeeaqlirekipekylfqlfnlnsl 60

QY	61	DRIEDKTPPEP	700
Db	61	drifdktppep	700

RESULT 5

ID AAB18692 standard; peptide; 70 AA

AC AAB18692;

DT 22-JAN-2001 (first entry)

DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.

KW ribosome binding region; resistance; geminivirus infection.

OS Synthetic.

XX

FT Misc-difference 66

FT	Misc-difference	69
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XX

XX

XX

XX

PR 09-APR-1999; 99US-0289346.

PA (UYNC-) UNIV NORTH CAROLINA STATE

PI Hanley-Bowdoin L, Orozco BM, Kong L,

DR WPI; 2000-618851/59.

PT Transgenic plants with increased resistance to geminivirus infection

PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region
 PT
 PS Disclosure: Page 50; 73pp; English.

CC The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
 CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
 CC protein are used to produce transgenic plants. The mutation in AL1 is
 CC present in a ribosome binding region, and expression of mutant AL1
 CC protein impacts increased resistance to geminivirus infection in the
 CC plant. Mutant AL1 proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.

XX Sequence 70 AA:

SO Query Match 95.0%; Score 344; DB 21; Length 70;

Best Local Similarity 95.7%; Pred. No. 1e-35; Mismatches 0; Gaps 0;

Matches 67; Conservative 0; Mismatches 3; Indels 0;

OY 1 TLVWGEFQVAGRSARGGCGTSDNDAAEALNMSKEEALQITREKIPERYLFOFHNLSNL 60

Db 1 TLVWGEFQVdgrsarggqtsndaaaealnmskeeaqlirekipekyltqfhnlnsl 60

OY 61 DRFDKPEP 70

Db 61 drltdaapap 70

Db

RESULT 6 AAB18684

ID AAB18684 standard; peptide: 70 AA.

XX AAB18684;

XX 22-JAN-2001 (first entry)

XX DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.

XX DE Geminivirus; replication protein; Rep protein; AL1; transgenic plant;

XX KW ribosome binding region; resistance; geminivirus infection.

XX OS Synthetic.

XX OS Tomato golden mosaic virus.

XX FT Key Location/Qualifiers

XX FT MISC-difference 7 /note= "wild type residue replaced with Ala"

XX FT MISC-difference 8 /note= "wild type residue replaced with Ala"

XX FT WO200054573-A1.

XX PD 21-SEP-2000.

XX PF 15-MAR-2000; 2000WO-US06759.

XX PR 18-MAR-1999; 99US-0125004.

XX PR 09-APR-1999; 99US-0289346.

XX PA (UYNC-) UNIV NORTH CAROLINA STATE.

XX PI Hanley-Bowdoin L, Orozco BM, Kong L;

XX DR WPI; 2000-618851/59;

XX Transgenic plants with increased resistance to geminivirus infection
 PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region
 PT
 PS Claim 52; Page 45; 73pp; English.

CC The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
 CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
 CC protein are used to produce transgenic plants. The mutation in AL1 is
 CC present in a ribosome binding region, and expression of mutant AL1
 CC protein impacts increased resistance to geminivirus infection in the
 CC plant. Mutant AL1 proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.

XX Sequence 70 AA:

SO Query Match 94.5%; Score 342; DB 21; Length 70;

Best Local Similarity 95.7%; Pred. No. 1.8e-35; Mismatches 3; Indels 0; Gaps 0;

Matches 67; Conservative 0; Mismatches 3; Indels 0;

OY 1 TLVWGEFQVAGRSARGGCGTSDNDAAEALNMSKEEALQITREKIPERYLFOFHNLSNL 60

Db 1 TLVWGEFQVdgrsarggqtsndaaaealnmskeeaqlirekipekyltqfhnlnsl 60

OY 61 DRFDKPEP 70

Db 61 drltdkpep 70

Db

RESULT 7 AAB18690

ID AAB18690 standard; peptide: 70 AA.

XX AAB18690;

XX 22-JAN-2001 (first entry)

XX DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.

XX DE Geminivirus; replication protein; Rep protein; AL1; transgenic plant;

XX KW ribosome binding region; resistance; geminivirus infection.

XX OS Synthetic.

XX OS Tomato golden mosaic virus.

XX FT Key Location/Qualifiers

XX FT MISC-difference 27 /note= "wild type residue replaced with Ala"

XX FT MISC-difference 30 /note= "wild type residue replaced with Ala"

XX FT WO200054573-A1.

XX PD 21-SEP-2000.

XX PF 15-MAR-2000; 2000WO-US06759.

XX PR 18-MAR-1999; 99US-0125004.

XX PR 09-APR-1999; 99US-0289346.

XX PA (UYNC-) UNIV NORTH CAROLINA STATE.

XX PI Hanley-Bowdoin L, Orozco BM, Kong L;

XX WPI: 2000-618851/59.
 DR Transgenic plants with increased resistance to geminivirus infection
 XX comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region
 PT -
 XX
 PS Disclosure: Page 49; 73pp; English.
 XX
 CC The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
 CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
 CC protein are used to produce transgenic plants. The mutation in AL1 is
 CC present in a ribosome binding region, and expression of mutant AL1
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant AL1 proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 CC
 SQ Sequence 70 AA:

Query Match 94.5%; Score 342; DB 21; Length 70;
 Best Local Similarity 95.7%; Pred. No. 1.8e-35;
 Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TLVWGEFOVAGRSARGCGCOTSDNDAAEALNASSKEEALQITREKIPEKYLFPFHINSL 60
 Db 1 tlwgeifqvdgrsargcgctsdnaaaalasskeeaqlitrekipekylfqfhnlnsl 60
 QY 61 DRIFDKTPEP 70
 Db 61 drifdktppep 70

RESULT 8
 AAB18678
 ID AAB18678 standard; peptide: 70 AA.
 AC AAB18678;
 XX
 DT 22-JAN-2001 (first entry)
 XX
 DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
 KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
 XX ribosome binding region; resistance; geminivirus infection.
 OS Synthetic.
 XX Tomato golden mosaic virus.
 XX
 FH Key Location/Qualifiers
 FT MISC-difference 12 /note= "wild type residue replaced with Ala"
 FT MISC-difference 13 /note= "wild type residue replaced with Ala"
 FT MISC-difference 15 /note= "wild type residue replaced with Ala"
 FT
 XX WO200054573-A1.
 XX
 PD 21-SEP-2000.
 XX
 PF 15-MAR-2000; 2000WO-US06759.
 XX
 PR 18-MAR-1999; 99US-0125004.
 PR 09-APR-1999; 99US-0289346.
 XX

XX (UNNC-) UNIV NORTH CAROLINA STATE.
 PA Hanley-Bowdoin L, Orozco BM, Kong L;
 XX WPI: 2000-618851/59.
 DR Transgenic plants with increased resistance to geminivirus infection
 XX comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region
 PT -
 XX
 PS Claim 53; Page 42-43; 73pp; English.
 XX
 CC The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
 CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
 CC protein are used to produce transgenic plants. The mutation in AL1 is
 CC present in a ribosome binding region, and expression of mutant AL1
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant AL1 proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 CC
 SQ Sequence 70 AA:

Query Match 94.2%; Score 341; DB 21; Length 70;
 Best Local Similarity 94.3%; Pred. No. 2.4e-35;
 Matches 66; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TLVWGEFOVAGRSARGCGCOTSDNDAAEALNASSKEEALQITREKIPEKYLFPFHINSL 60
 Db 1 tlwgeifqvdgaaagcgctsdnaaaalasskeeaqlitrekipekylfqfhnlnsl 60
 QY 61 DRIFDKTPEP 70
 Db 61 drifdktppep 70

RESULT 9
 AAB18686
 ID AAB18686 standard; peptide: 70 AA.
 AC AAB18686;
 XX
 DT 22-JAN-2001 (first entry)
 XX
 DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
 KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
 XX ribosome binding region; resistance; geminivirus infection.
 OS Synthetic.
 XX Tomato golden mosaic virus.
 XX
 FH Key Location/Qualifiers
 FT MISC-difference 24 /note= "wild type residue replaced with Leu"
 FT MISC-difference 25 /note= "wild type residue replaced with Leu"
 FT MISC-difference 26 /note= "wild type residue replaced with Leu"
 FT
 XX WO200054573-A1.
 XX
 PD 21-SEP-2000.
 XX
 PF 15-MAR-2000; 2000WO-US06759.
 XX
 PR 18-MAR-1999; 99US-0125004.
 PR 09-APR-1999; 99US-0289346.
 XX

PF 15-MAR-2000; 2000WO-US06759.
XX
XX 18-MAR-1999; 99US-0125004.
PR 09-APR-1999; 99US-0289346.
XX
XX (UYNC-) UNIV NORTH CAROLINA STATE.
PA
XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX
XX WPI: 2000-618851/59.
DR
XX Transgenic plants with increased resistance to geminivirus infection
PT comprise a nucleic acid construct containing a nucleic acid sequence
PT encoding a mutant AL1 protein with a mutation in the Rb binding region
PT
XX
XX
PS Clatm 53; Page 46; 73pp; English.
XX
XX The present sequence represents a mutant peptide, derived from a
CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
CC protein are used to produce transgenic plants. The mutation in AL1 is
CC present in a ribosome binding region, and expression of mutant AL1
CC protein imparts increased resistance to geminivirus infection in the
CC plant. Mutant AL1 proteins are useful for producing plants having
CC increased resistance or reduced sensitivity to a geminivirus such as
CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
CC virus, cotton leaf curl virus or beet curly top virus.
XX
XX Sequence 70 AA;
SQ

Query Match 94.2%; Score 341; DB 21; Length 70;
Best Local Similarity 94.3%; Pred. No. 2.4e-35;
Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 TLVWGEFQVAGSARGCGQTSNDAAAEALNMSKKEALQITREKIPERYLFGFHNLSNL 60
Db 1 TLVWGEFQVdgsarqgqtsndlllealnasskeaalqllrekipekylfgfhnlnsl 60
OY 61 DRIPDKTEP 70
Db 61 drifdktp 70

RESULT 10

AAB18689
ID AAB18689 standard; peptide: 70 AA.

AC AAB18689;

DT 22-JAN-2001 (first entry)

DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.

XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
KW ribosome binding region; resistance; geminivirus infection.

XX Synthetic.

OS Tomato golden mosaic virus.

XX Key Location/Qualifiers

FT Misc-difference 22 /note= "wild type residue replaced with Ala"

FT Misc-difference 23 /note= "wild type residue replaced with Ala"

XX W0200054573-A1.

XX

PD 21-SEP-2000.
XX
XX 15-MAR-2000; 2000WO-US06759.
PR 18-MAR-1999; 99US-0125004.
PR 09-APR-1999; 99US-0289346.
XX
XX (UYNC-) UNIV NORTH CAROLINA STATE.
PA
XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX
XX WPI: 2000-618851/59.
DR
XX Transgenic plants with increased resistance to geminivirus infection
PT comprise a nucleic acid construct containing a nucleic acid sequence
PT encoding a mutant AL1 protein with a mutation in the Rb binding region
PT
XX
XX
PS Disclosure: Page 48-49; 73pp; English.
XX
XX The present sequence represents a mutant peptide, derived from a
CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
CC protein are used to produce transgenic plants. The mutation in AL1 is
CC present in a ribosome binding region, and expression of mutant AL1
CC protein imparts increased resistance to geminivirus infection in the
CC plant. Mutant AL1 proteins are useful for producing plants having
CC increased resistance or reduced sensitivity to a geminivirus such as
CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
CC virus, cotton leaf curl virus or beet curly top virus.
XX
XX Sequence 70 AA;
SQ

Query Match 93.9%; Score 340; DB 21; Length 70;
Best Local Similarity 95.7%; Pred. No. 3.2e-35;
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 TLVWGEFQVAGSARGCGQTSNDAAAEALNMSKKEALQITREKIPERYLFGFHNLSNL 60
Db 1 TLVWGEFQVdgsarqgqtsaaaaalnasskeaalqllrekipekylfgfhnlnsl 60
OY 61 DRIPDKTEP 70
Db 61 drifdktp 70

RESULT 11

AAB18680
ID AAB18680 standard; peptide: 70 AA.

AC AAB18680;

DT 22-JAN-2001 (first entry)

DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.

XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
KW ribosome binding region; resistance; geminivirus infection.

XX Synthetic.

OS Tomato golden mosaic virus.

XX Key Location/Qualifiers

FT Misc-difference 42 /note= "wild type residue replaced with Ala"

FT Misc-difference 43 /note= "wild type residue replaced with Ala"

XX W0200054573-A1.

XX

```

FT      /note= "wild type residue replaced with Ala"
XX
XX      WO200054573-A1.
PN
PD      21-SEP-2000.
XX
XX      15-MAR-2000; 2000WO-US06759.
PF
PR      18-MAR-1999; 99US-0125004.
PR      09-APR-1999; 99US-0289346.
XX
XX      (UYNC-) UNIV NORTH CAROLINA STATE.
XX
XX      Hanley-Bowdoin L, Orozco BM, Kong L;
XX      WPI; 2000-618851/59.
XX
XX      Transgenic plants with increased resistance to geminivirus infection
PT      comprise a nucleic acid construct containing a nucleic acid sequence
PT      encoding a mutant AL1 protein with a mutation in the Rb binding region
PT
PS      Claim 52, Page 43-44; 73pp; English.
XX
XX      The present sequence represents a mutant peptide, derived from a
XX      geminivirus replication (Rep) protein, also known as AL1. AL1 binds
XX      double-stranded DNA, catalyses cleavage and ligation of single-stranded
XX      DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX      protein are used to produce transgenic plants. The mutation in AL1 is
XX      present in a ribosome binding region, and expression of mutant AL1
XX      protein imparts increased resistance to geminivirus infection in the
XX      plant. Mutant AL1 proteins are useful for producing plants having an
XX      increased resistance or reduced sensitivity to a geminivirus such as
XX      tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX      virus, tomato leaf curl virus, African cassava mosaic virus, Indian
XX      cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX      virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX      virus, cotton leaf curl virus or beet curly top virus.
XX
XX      Sequence 70 AA:
SQ
Query Match      93.4%; Score 338; DB 21; Length 70;
Best Local Similarity 94.3%; Pred. No. 5.6e-35;
Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 TLVWGEFQVAGRSARGCGQTSDNDAAEALNMSKKEALQIIREKIPKYLQFPHNLNSL 60
DB      1 TLVWGEFQVdgrsargcgqtstndaaaealnsskkeealqiiarekyltqfhnlnsl 60

QY      61 DRIFDKTPEP 70
DB      61 drifdktp 70

RESULT 12
AAB18691
ID      AAB18691 standard; peptide: 70 AA.
XX
XX      AAB18691;
AC
XX      22-JAN-2001 (first entry)
DT
XX
XX      Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
DE
XX      Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
KW      ribosome binding region; resistance; geminivirus infection.
XX
XX      Synthetic.
OS      Tomato golden mosaic virus.
XX
XX      Key Location/Qualifiers
FH      Misc-difference 34
FT

```

```

FT      /note= "wild type residue replaced with Ala"
FT      Misc-difference 35
FT      /note= "wild type residue replaced with Ala"
FT      Misc-difference 36
FT      /note= "wild type residue replaced with Ala"
XX
XX      WO200054573-A1.
XX
XX      21-SEP-2000.
XX
XX      15-MAR-2000; 2000WO-US06759.
XX
XX      18-MAR-1999; 99US-0125004.
XX      09-APR-1999; 99US-0289346.
XX
XX      (UYNC-) UNIV NORTH CAROLINA STATE.
XX
XX      Hanley-Bowdoin L, Orozco BM, Kong L;
XX      WPI; 2000-618851/59.
XX
XX      Transgenic plants with increased resistance to geminivirus infection
PT      comprise a nucleic acid construct containing a nucleic acid sequence
PT      encoding a mutant AL1 protein with a mutation in the Rb binding region
PT
PS      Disclosure; Page 49; 73pp; English.
XX
XX      The present sequence represents a mutant peptide, derived from a
XX      geminivirus replication (Rep) protein, also known as AL1. AL1 binds
XX      double-stranded DNA, catalyses cleavage and ligation of single-stranded
XX      DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX      protein are used to produce transgenic plants. The mutation in AL1 is
XX      present in a ribosome binding region, and expression of mutant AL1
XX      protein imparts increased resistance to geminivirus infection in the
XX      plant. Mutant AL1 proteins are useful for producing plants having an
XX      increased resistance or reduced sensitivity to a geminivirus such as
XX      tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX      virus, tomato leaf curl virus, African cassava mosaic virus, Indian
XX      cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX      virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX      virus, cotton leaf curl virus or beet curly top virus.
XX
XX      Sequence 70 AA:
SQ
Query Match      93.4%; Score 338; DB 21; Length 70;
Best Local Similarity 94.3%; Pred. No. 5.6e-35;
Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 TLVWGEFQVAGRSARGCGQTSDNDAAEALNMSKKEALQIIREKIPKYLQFPHNLNSL 60
DB      1 TLVWGEFQVdgrsargcgqtstndaaaealnsskkeealqiiarekyltqfhnlnsl 60

QY      61 DRIFDKTPEP 70
DB      61 drifdktp 70

RESULT 13
AAB18681
ID      AAB18681 standard; peptide: 70 AA.
XX
XX      AAB18681;
AC
XX      22-JAN-2001 (first entry)
DT
XX
XX      Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
DE
XX      Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
KW      ribosome binding region; resistance; geminivirus infection.
XX
XX      Synthetic.
OS

```

```

KW Geminivirus; replication protein; Rep protein; ALI; transgenic plant;
KM Ribosome binding region; resistance; geminivirus infection.
XX Synthetic.
OS Tomato golden mosaic virus.
XX
XX Key Location/Qualifiers
FT Misc-difference 59 /note= "wild type residue replaced with Ala"
FT FT Misc-difference 61 /note= "wild type residue replaced with Ala"
FT FT Misc-difference 62 /note= "wild type residue replaced with Ala"
FT FT Misc-difference 62 /note= "wild type residue replaced with Ala"
XX
XX WO200054573-A1.
XX PN
XX PD 21-SEP-2000.
XX XX
XX PF 15-MAR-2000; 2000MO-US06759.
XX PR 18-MAR-1999; 99US-0125004.
PR PR 09-APR-1999; 99US-0289346.
XX XX
XX PA (UYNC-) UNIV NORTH CAROLINA STATE.
XX PI Hanley-Bowdoin L, Orozco BM, Kong L;
XX DR WPI; 2000-618851/59.
XX PT Transgenic plants with increased resistance to geminivirus infection
PT comprise a nucleic acid construct containing a nucleic acid sequence
PT encoding a mutant ALI protein with a mutation in the Rb binding region
PT -
XX PS Claim 53; Page 45; 73pp; English.
XX CC The present sequence represents a mutant peptide, derived from a
CC geminivirus replication (Rep) protein, also known as ALI. ALI binds
CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
CC DNA, and interacts with other viral and host proteins. Mutants of the ALI
CC protein are used to produce transgenic plants. The mutation in ALI is
CC present in a ribosome binding region, and expression of mutant ALI
CC protein imparts increased resistance to geminivirus infection in the
CC plant. Mutant ALI proteins are useful for producing plants having
CC increased resistance or reduced sensitivity to a geminivirus such as
CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
CC virus, cotton leaf curl virus or beet curly top virus.
XX SQ Sequence 70 AA.
XX
XX Query Match 92.3%; Score 334; DB 21; Length 70;
Best Local Similarity 94.3%; Pred.No.1.8e-34;
Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 1 TLVWGEFOVAGRSANGCGCOTSDNDAAEKLNASSKKREALQIIIREKIPEKYTLQFHNLSNL 60
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
db 1 TlVwGeFoVaGrSangcGCoTsdNdAaeKlnAsskReAlqIIRekIpEkytlQfHnLsnL 60
OY 61 DRIFDKPDP 70
| | | | | | | |
db 61 aaifdkpdp 70
RESULT 15
AAAB18682 standard; peptide: 70 AA.
AC AAB18682;
XX
```

Job time: 155 sec

DT 22-JAN-2001 (first entry)

XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.

DE

XX Geminiivirus; replication protein; Rep protein; AL1; transgenic plant;

KW ribosome binding region; resistance; geminivirus infection.

XX

OS Synthetic.

XX Tomato golden mosaic virus.

XX

XX Key Location/Qualifiers

PH Misc-difference 52 /note= "wild type residue replaced with Ala"

FT Misc-difference 54 /note= "wild type residue replaced with Ala"

FT Misc-difference 55 /note= "wild type residue replaced with Ala"

FT

XX WO200054573-A1.

XX

XX 21-SEP-2000.

PD

XX 15-MAR-2000; 2000MO-US06759.

PF

XX 18-MAR-1999; 99US-0125004.

PR 09-APR-1999; 99US-0289346.

XX

PA (UYNC-) UNIV NORTH CAROLINA STATE.

XX

XX Hanley-Bowdoin L, Orozco BM, Kong L;

PI

XX WPI; 2000-618851/59.

DR

XX

XX Transgenic plants with increased resistance to geminivirus infection

PT comprise a nucleic acid construct containing a nucleic acid sequence

PT encoding a mutant AL1 protein with a mutation in the Rb binding region

PT

XX

PS Claim 53; Page 44-45; 73pp; English.

XX

CC The present sequence represents a mutant peptide, derived from a

CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds

CC double-stranded DNA, catalyses cleavage and ligation of single-stranded

CC DNA, and interacts with other viral and host proteins. Mutants of the AL1

CC protein are used to produce transgenic plants. The mutation in AL1 is

CC present in a ribosome binding region, and expression of mutant AL1

CC protein imparts increased resistance to geminivirus infection in the

CC plant. Mutant AL1 proteins are useful for producing plants having

CC increased resistance or reduced sensitivity to a geminivirus such as

CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl

CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian

CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic

CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper

CC virus, cotton leaf curl virus or beet curly top virus.

XX

SQ Sequence 70 AA:

Query Match 91.7%; Score 332; DB 21; Length 70;

Best Local Similarity 94.3%; Pred. No. 3.2e-34;

Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TLVWGEFQVAGRSARGCGCOTSNDAAEALNASSKEEALQITREKIPKYLQFHINLSNL 60

DB 1 TLVWGEFQVAGRSARGCGCOTSNDAAEALNASSKEEALQITREKIPKYLQFHINLSNL 60

QY 61 DRIPDKTPEP 70

DB 61 DRIPDKTPEP 70

Fri Jan 4 09:40:03 2002

us-09-289-346a-9.rag

Page 10

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 3, 2002, 15:40:11 ; Search time 72.79 Seconds

(without alignments)
73.255 Million cell updates/sec

Title: US-09-289-346a-9

Perfect score: 362

Sequence: 1 TLVWGEFQVAGRSARGCGCT.....FOFHNLSNLDKIFDKTPEP 70

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	356	98.3	352	1	QOCVLI
2	256	70.7	361	1	QOCVPT
3	243	67.1	358	1	S07594
4	236	65.2	362	1	QJ1887
5	229	63.3	359	2	S39211
6	225	62.2	349	2	J02300
7	225	62.2	349	2	S31875
8	222	61.3	359	2	S22593
9	219	60.5	351	2	J02327
10	219	60.5	355	1	QOCVLI
11	216	59.7	358	1	J01870
12	216	59.7	359	2	S39235
13	216	59.7	385	2	S28360
14	209	57.7	360	2	S59885
15	207	57.2	357	1	QOCVLI
16	142	39.2	131	2	S45059
17	125	34.5	347	1	QOCVLI
18	68	18.8	587	2	JC1419
19	67	18.5	840	2	T36175
20	64.5	17.8	299	2	B71967
21	62.5	17.3	447	2	T12544
22	62	17.1	295	2	D42452
23	61.5	17.0	201	2	A81380
24	61.5	17.0	481	2	A70091
25	61	16.9	1502	1	RGBYH1
26	60.5	16.7	1713	2	A55347
27	60.5	16.7	2137	2	T05244
28	60	16.6	160	2	G82060
29	60	16.6	447	2	S52437

30	60	16.6	988	2	F86316	protein T10022.13
31	59	16.3	397	2	B71078	probable NADH oxid
32	59	16.3	416	2	A82892	hypothetical prote
33	59	16.3	862	2	H82182	conserved hypothet
34	59	16.3	1287	2	S55954	viral mRNA transla
35	59	16.3	1341	2	JG0166	lamdRI protein - L
36	58.5	16.2	180	2	D84082	hypothetical prote
37	58.5	16.2	230	2	S46332	homeotic protein G
38	58.5	16.2	297	1	MANRV	nonstructural prot
39	58.5	16.2	299	2	G64541	cell binding facto
40	58.5	16.2	589	2	D64125	hypothetical prote
41	58.5	16.2	1044	2	T43800	protein kinase bub
42	58.5	16.2	1265	2	T47626	structural mainen
43	58	16.2	1245	2	S76632	hypothetical prote
44	58	16.0	256	2	S37926	hypothetical prote
45	58	16.0	488	2	B84197	anthranilate synth

ALIGNMENTS

```
RESULT 1
QOCVLI
A1: protein - tomato golden mosaic virus
C: Species: tomato golden mosaic virus
A: Note: host Nicotiana sp. (tobacco)
C: Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 08-Apr-1994
C: Accession: A04170
R: Hamilton, W.D.O.; Stein, V.E.; Coutts, R.H.A.; Buck, K.W.
EMBO J. 3, 2197-2205, 1984
A: Title: Complete nucleotide sequence of the infectious cloned DNA components of toma
A: Reference number: A04163
A: Accession: A04170
A: Molecule type: DNA
A: Residues: 1-352 <HAM>
C: Comment: The genome consists of two circular, single-stranded DNA components, DNA A
C: Genetics:
A: Map position: segment A
C: Superfamily: tomato golden mosaic virus A1: protein

Query Match 98.3% Score 356; DB 1; Length 352;
Best Local Similarity 98.6% Pred. No. 2,1e-32;
Matches 69; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVAGRSARGCGCTSDAAAEALNASSKEALQITREKIPKYLQFHNLSNL 60
Db 111 TLVWGEFQVAGRSARGCGCTSDAAAEALNASSKEALQITREKIPKYLQFHNLSNL 170

Qy 61 DRIFDKTPEP 70
Db 171 DRIFDKTPEP 180

RESULT 2
QOCVPT
A1: protein - potato yellow mosaic virus (isolate Venezuela)
C: Species: potato yellow mosaic virus
C: Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Jun-2000
C: Accession: J00364
R: Coutts, R.H.A.; Coffin, R.S.; Roberts, E.J.F.; Hamilton, W.D.O.
J. Gen. Virol. 72, 1515-1520, 1991
A: Title: The nucleotide sequence of the infectious cloned DNA components of potato ye
A: Reference number: J00362; MUID: 91311403
A: Accession: J00364
A: Status: translation not shown
A: Molecule type: DNA
A: Residues: 1-361 <COU>
A: Cross-references: GB:D00940; NID:g222458; PIDN:BAA00782.1; PID:g222459
C: Genetics:
A: Map position: segment A
C: Superfamily: tomato golden mosaic virus A1: protein
```

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 3, 2002, 15:57:17 ; Search time 43.68 Seconds

(Without alignments)
58.758 Million cell updates/sec

Title: US-09-289-346a-9

Perfect score: 362
Sequence: 1 TLWGEFQVAGRSARGGCT.....PQFHNLSMIDRFKTPPEP 70

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SWISSPROT_39:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	356	98.3	352	1 VAL1_TGMV	P03567 tomato gold
2	256	70.7	361	1 VAL1_PMYV	P27258 potato yell
3	243	67.1	358	1 VAL1_CLVK	P14982 cassava lat
4	243	67.1	358	1 VAL1_CIVN	P14972 cassava lat
5	236	65.2	362	1 VAL1_TYCA	P36279 tomato yell
6	229	63.3	359	1 VAL1_TYCU	P38609 tomato yell
7	225	62.2	349	1 VAL1_PHV	P06923 pepper huas
8	222	61.3	359	1 VAL1_TYLCM	P27260 tomato yell
9	220	60.8	353	1 VAL1_BGMV	P05175 bean golden
10	219	60.5	355	1 VAL1_ABMVW	P21947 abutilon mo
11	216	59.7	358	1 VAL1_BGV	P14991 beet curly
12	216	59.7	361	1 VAL1_TMOV	P06657 tomato moct
13	207	57.2	357	1 VAL1_TYLCV	P27259 tomato yell
14	125	34.5	347	1 VAL1_SLCV	P29048 squash leaf
15	64.5	17.8	299	1 Y175_HELPJ	O94977 helicobacte
16	62.5	17.3	447	1 TBL2_HUMAN	O94943 homo sapien
17	62	17.1	295	1 VAL1_TYDVA	P1617 tobacco yel
18	61	16.9	1483	1 CYP1_YEAST	P12351 saccharomyc
19	60.5	16.7	1713	1 LMA3_HUMAN	Q16787 homo sapien
20	60	16.6	447	1 CDSA_DROME	P56079 d phosphati
21	59	16.3	1287	1 SK12_YEAST	P35207 saccharomyc
22	58.5	16.2	297	1 RRP5_RABVP	P06747 rabies viru
23	58.5	16.2	299	1 Y175_HELPY	P56112 helicobacte
24	58.5	16.2	367	1 LHX4_MOUSE	P53776 mus musculu
25	58.5	16.2	589	1 YE67_HAELN	P45221 haemophilus
26	58.5	16.2	1044	1 BUB1_SCHPO	O94751 schizosacch
27	58	16.0	207	1 IL6_MARMO	O35736 marmota mon
28	58	16.0	256	1 YKJ9_YEAST	P34247 saccharomyc
29	58	16.0	617	1 YACH_ECOLI	P36682 escheichia
30	58	16.0	874	1 SLAP_BACLI	P49052 bacillus li
31	57.5	15.9	136	1 Y452_CAEEL	O62250 caenorhabd
32	57	15.7	355	1 CRTB_RHOSH	P54905 rhodobacter
33	57	15.7	492	1 MOT3_MOUSE	O35308 mus musculu

34	57	15.7	492	1 MOT3_RAT	O70461 rattus norv
35	56.5	15.6	428	1 GBAL_CANAL	P28868 candida alb
36	56.5	15.6	470	1 RSHA_RHME	O92372 rhizobium m
37	56.5	15.6	511	1 HOTH_VIRCH	O9K94 vibrio chol
38	56	15.5	332	1 IPAD_SHIEL	P18013 shigella fl
39	56	15.5	336	1 Y625_METJA	O58042 methanococc
40	56	15.5	432	1 PROA_DEIRA	O9719 delinococcus
41	56	15.5	513	1 HEMO_CHICK	P18080 gallus gall
42	56	15.5	601	1 CYSJ_BUCAL	P57503 buchnera ap
43	56	15.5	795	1 LON_AQUAE	O66505 aquilex aeo
44	56	15.5	799	1 AFSK_STRCO	P54741 streptomyce
45	56	15.5	807	1 AFSK_STRGR	P54742 streptomyce

ALIGNMENTS

RESULT 1	VAL1_TGMV	STANDARD:	PRT: 352 AA.
AC	P03567		
DT	21-JUL-1986 (Rel. 01, Created)		
DT	21-JUL-1986 (Rel. 01, Last sequence update)		
DT	01-JUN-1994 (Rel. 29, Last annotation update)		
DE	AL1 PROTEIN.		
GN	AC1.		
OS	Tomato golden mosaic virus (TGMV).		
OC	Viruses; ssDNA viruses; Geminiviridae; Begomovirus.		
OX	NCBI_TaxID=10831;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Hamilton W.D.O., Stein V.E., Courts R.H.A., Buck K.W.;		
RT	*Complete nucleotide sequence of the infectious cloned DNA components		
RT	of tomato golden mosaic virus: potential coding regions and regulatory		
RT	sequences.*		
RL	EMBO J. 3:2197-2205(1984).		
CC	-1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.		
CC	-----		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -		
CC	the European Bioinformatics Institute. There are no restrictions on its		
CC	use by non-profit institutions as long as its content is in no way		
CC	modified and this statement is not removed. Usage by and for commercial		
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/		
CC	or send an email to license@sib-sib.ch).		
CC	-----		
DR	EMBL; K02029; -; NOT_ANNOTATED_CDS.		
DR	PIR; A04170; QOCVLI.		
DR	InterPro; IPR001191; Geminl_AL1.		
DR	Pfam; PF00799; Geminl_AL1; 1.		
DR	PRINTS; PR00227; GEMCOATL1.		
DR	PRINTS; PR00228; GEMCOATL1.		
DR	Prodom; PD000736; Geminl_AL1; 1.		
KW	Atp-binding.		
FT	NP_BIND 223		
FT	NP_BIND 230		
FT	SEQUENCE 352 AA: 40332 MW: C33C938E9644B44A CRC64:		
Query Match	98.3%; Score 356; DB 1; Length 352;		
Best Local Similarity	98.6%; Pred. No. 3.6e-32;		
Matches	69; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
OY	1 TLWGEFQVAGRSARGGCTSDAAAEALNMSKKEALQITREKIPERYLPQFHNLSNL 60		
DB	111 TLWGEFQVAGRSARGGCTSDAAAEALNMSKKEALQITREKIPERYLPQFHNLSNL 170		
OY	61 DRIFKTPPEP 70		
DB	171 DRIFKTPPEP 180		
RESULT 2	VAL1_PMYV		

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ID VAL1_PYMV STANDARD; PRT; 361 AA.
AC P27258;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE AL1 PROTEIN.
OS Potaro yellow mosaic virus (isolate Venezuela).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10828;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91311403; PubMed=1856690;
RA Coutts R.H.A., Coffin R.S., Roberts E.J.F., Hamilton W.D.O.;
RT "The nucleotide sequence of the infectious cloned DNA components of
RU potaro yellow mosaic virus."
RL J. Gen. Virol. 72:1515-1520(1991).
CC -i- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC -----
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CC -----
DR EMBL: D00940; BAA00782.1; -.
DR PIR: J00364; OCCPT.
DR InterPro: IPR001191; Gemin1_AL1.
DR Pfam: PF00799; Gemin1_AL1.
DR PRINTS: PR00227; GEMCOATAL1.
DR PRINTS: PR00228; GEMCOATCLVL.
DR ProDom: PD000736; Gemin1_AL1; 1.
KW ATP-binding.
FT NP_BIND 222 229 ATP (POTENTIAL).
SQ SEQUENCE 361 AA; 40850 MW; 5627A3BF1264383 CRC64;

Query Match 70.7%; Score 256; DB 1; Length 361;
Best Local Similarity 69.6%; Pred. No. 4.3e-21;
Matches 48; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

OY 1 TLWGEFQVAGSARGGCGTSDNAAEALNASSKEALQIREKIPEXYLFQFHNLSNL 60
DB 110 TLWGEFQIDGSRGCGQTVDAAEALNLSGTEAKMIKEKLPKFLFYHNLSCUL 169
OY 61 DRIFDKTEP 69
DB 170 DRIFDKAPE 178

RESULT 3
VAL1_CLVK STANDARD; PRT; 358 AA.
AC P14982;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 PROTEIN (40.4 KDA PROTEIN).
GN AC1.
OS Cassava latent virus (strain West Kenyan 844).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10818;
RN [1]
RP SEQUENCE FROM N.A.
RA Stanley J., Gay M.R.;
RT "Nucleotide sequence of cassava latent virus DNA."
RL Nature 301:260-262(1983).
CC -i- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC -----
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CC -----
DR EMBL: J02057; -. NOT_ANNOTATED_CDS.
DR InterPro: IPR001191; Gemin1_AL1.
DR Pfam: PF00799; Gemin1_AL1; 1.
DR PRINTS: PR00227; GEMCOATAL1.
DR PRINTS: PR00228; GEMCOATCLVL.
DR ProDom: PD000736; Gemin1_AL1; 1.
KW ATP-binding.
FT NP_BIND 220 227 ATP (POTENTIAL).
SQ SEQUENCE 358 AA; 40346 MW; ED173B753ED2D69 CRC64;

Query Match 67.1%; Score 243; DB 1; Length 358;
Best Local Similarity 62.9%; Pred. No. 1.2e-19;
Matches 44; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

OY 1 TLWGEFQVAGSARGGCGTSDNAAEALNASSKEALQIREKIPEXYLFQFHNLSNL 60
DB 109 TLWGEFQIDGSRGCGQSDANDAYAKALNSGSEALNVRELVPKQFVLQFHNLSNL 168
OY 61 DRIFDKTEP 70
DB 169 DRIFDKPEAP 178

RESULT 4
VAL1_CLVN STANDARD; PRT; 358 AA.
AC P14972;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 PROTEIN (40.4 KDA PROTEIN).
GN AC1.
OS Cassava latent virus (strain Nigerian).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10819;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90174930; PubMed=2308831;
RA Morris B., Coates L., Lowe S., Richardson K., Eddy P.;
RT "Nucleotide sequence of the infectious cloned DNA components of
RL African cassava mosaic virus (Nigerian strain).";
CC -i- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC -----
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CC -----
DR EMBL: X17095; CAA34953.1; -.
DR PIR: S07594; S07594.
DR InterPro: IPR001191; Gemin1_AL1.
DR Pfam: PF00799; Gemin1_AL1; 1.
DR PRINTS: PR00227; GEMCOATAL1.
DR PRINTS: PR00228; GEMCOATCLVL.
DR ProDom: PD000736; Gemin1_AL1; 1.
KW ATP-binding.
FT NP_BIND 220 227 ATP (POTENTIAL).
SQ SEQUENCE 358 AA; 40435 MW; 1DB16B0CB2D5E2C CRC64;

Query Match 67.1%; Score 243; DB 1; Length 358;
Best Local Similarity 62.9%; Pred. No. 1.2e-19;
Matches 44; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

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Db 171 KVFQVPPAP 179

RL Virology 178:461-468(1990).

RL Virology 178:461-468(1990).

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CC -----
DR EMBL: X15983; NOT_ANNOTATED_CDS.
DR PIR: A36214; OOCVW1.
DR InterPro: IPR001191; Gemini_AL1.
DR Pfam: PF00799; Gemini_AL1.1.
DR PRINTS: PR00227; GEMCOATFALL.
DR ProDom: PD000736; Gemini_AL1.1.
DR ATP-binding.
KW NP-BIND
FT SEQUENCE 355 AA: 40257 MW: 16A2CA8A63251E95 CRC64;

Query Match 60.5%; Score 219; DB 1; Length 355;
Best Local Similarity 58.6%; Pred. No. 5.2e-17;
Matches 41; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

Oy 1 TLWGEPVAGRSARGGCGTSDAAAEALNASSKEALQIIRKIPKYLQFHNLSNL 60
Db 110 TAEWGFQIDGRSARGGQGTANDSYAKALNAGDVOSALNLIKPEPKDYVLOHNHLSNL 169

Oy 61 DRFDKTPPEP 70
Db 170 ERIFAKAPEP 179

RESULT 11
VAL1_BCTV STANDARD: PRT: 358 AA.
AC P14991;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE AL1 PROTEIN (40.8 KDA PROTEIN).
OS Beet curly top virus (BCTV).
OC Viruses; ssDNA viruses; Geminiviridae; Curtovirus.
OX NCBI_TaxID=10840;
RN [1]
RP SEQUENCE FROM N.A.
RA Stanley J., Martham P.G., Callis R.J., Pinner M.S.;
RT "The nucleotide sequence of an infectious clone of the geminivirus
RT beet curly top virus."
RL EMBL J. 511761-1767(1986).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC -----
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CC -----
DR EMBL: X04144; NOT_ANNOTATED_CDS.
DR InterPro: IPR001191; Gemini_AL1.
DR Pfam: PF00799; Gemini_AL1.1.
DR PRINTS: PR00227; GEMCOATFALL.
DR ProDom: PD000736; Gemini_AL1.1.
DR ATP-binding.
KW NP-BIND
FT SEQUENCE 358 AA: 40889 MW: 39A45FE3C0B9C333 CRC64;

Query Match 59.7%; Score 216; DB 1; Length 358;

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Best Local Similarity 55.7%; Pred. No. 1.1e-16;
Matches 39; Conservative 16; Mismatches 15; Indels 0; Gaps 0;

Oy 1 TLWGEPVAGRSARGGCGTSDAAAEALNASSKEALQIIRKIPKYLQFHNLSNL 60
Db 110 TIEWEFDQIDGRSARGGQGTANDSYAKALNAGVSALVIREEPKDFVLOHNHLSNL 169

Oy 61 DRFDKTPPEP 70
Db 170 OKIFORPPDP 179

RESULT 12
VAL1_TM0V STANDARD: PRT: 361 AA.
AC Q06657;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 PROTEIN.
GN AL1.
OS Tomato mottle virus (isolate Florida) (TM0V).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=36449;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93107858; PubMed=1469361;
RA Abouzid A.M., Polston J.E., Hiebert E.;
RT "The nucleotide sequence of tomato mottle virus, a new geminivirus
RT isolated from tomatoes in Florida."
RL J. Gen. Virol. 73:3225-3229(1992).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC -----
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CC -----
DR EMBL: L14460; AAC32414.1; -.
DR PIR: J01870; J01870.
DR InterPro: IPR001191; Gemini_AL1.
DR Pfam: PF00799; Gemini_AL1.1.
DR PRINTS: PR00227; GEMCOATFALL.
DR ProDom: PD000736; Gemini_AL1.1.
DR ATP-binding.
KW NP-BIND
FT SEQUENCE 361 AA: 40516 MW: 8138B65CEBAC6950 CRC64;

Query Match 59.7%; Score 216; DB 1; Length 361;
Best Local Similarity 55.7%; Pred. No. 1.1e-16;
Matches 39; Conservative 16; Mismatches 15; Indels 0; Gaps 0;

Oy 1 TLWGEPVAGRSARGGCGTSDAAAEALNASSKEALQIIRKIPKYLQFHNLSNL 60
Db 110 TIEWEFDQIDGRSARGGQGTANDSYAKALNAGVSALVIREEPKDFVLOHNHLSNL 169

Oy 61 DRFDKTPPEP 70
Db 170 ERIFAKAPEP 179

RESULT 13
VAL1_TYLCV STANDARD: PRT: 357 AA.
AC P27259;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)

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DE AL1 PROTEIN (C1 PROTEIN).
GN C1.
OS Tomato yellow leaf curl virus (TYLCV).
CC Viruses: ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10832;
RN
  (1)
  SEQUENCE FROM N.A.
RX MEDLINE=92024070; PubMed=1926771;
RA Navot N., Pichersky E., Zeidan M., Zamir D., Czosnek H.;
RT "Tomato yellow leaf curl virus: a whitefly-transmitted geminivirus
  with a single genomic component.";
RL Virology 185:151-161(1991).
CC - SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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-----
DR EMBL: X15656; CAN368.1; -
DR PIR: D40779; Q0CVL1.
DR InterPro: IPR001191; Geminl_AL1.
DR Pfam: PF00799; Geminl_AL1; 1.
DR PRINTS: PR00227; GEMCOATALL.
DR PRINTS: PR00228; GEMCOATCLVL.
DR ProDom: PD000736; Geminl_AL1; 1.
KM ATP-binding.
FT NP_BIND 219 226 ATP (POTENTIAL).
SQ SEQUENCE 357 AA; 40678 MW; 939AB68E1AB3B2A7 CRC64;

Query Match 57.2%; Score 207; DB 1; Length 357;
Best Local Similarity 65.6%; Pred. No. 1.1e-15;
Matches 40; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

OY 4 GEFQVAGRSARCCGCTSDNAAAEALNASSKEEALQIREKIPKYLPOFHNLSNLDRI 63
DB 111 FGVSLDGRSARCCGCOSSANDAYAEALNASSKEEALNILEKRAKPYIILQFHLNSNLDRI 170
OY 64 F 64
DB 171 F 171

RESULT 14
VAL1_SLVCV STANDARD; PRT; 347 AA.
AC P29048;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE AL1 PROTEIN.
OS Squash leaf curl virus.
CC Viruses: ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10829;
RN
  (1)
  SEQUENCE FROM N.A.
RX MEDLINE=91082449; PubMed=1984668;
RA Lazarowitz S.G., Jazdzins I.B.;
RT "Infectivity and complete nucleotide sequence of the cloned genomic
  components of a bipartite squash leaf curl geminivirus with a broad
  host range phenotype.";
RL Virology 180:58-69(1991).
CC - SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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-----
DR EMBL: M38183; AAC32410.1; ALT_INIT.
DR PIR: C36785; Q0CVS1.
DR InterPro: IPR001191; Geminl_AL1.
DR Pfam: PF00799; Geminl_AL1; 1.
DR PRINTS: PR00227; GEMCOATALL.
DR PRINTS: PR00228; GEMCOATCLVL.
DR ProDom: PD000736; Geminl_AL1; 1.
KM ATP-binding.
FT NP_BIND 218 225 ATP (POTENTIAL).
SQ SEQUENCE 347 AA; 39110 MW; AFDABDDDEL22110E CRC64;

Query Match 34.5%; Score 125; DB 1; Length 347;
Best Local Similarity 37.9%; Pred. No. 1.3e-06;
Matches 25; Conservative 15; Mismatches 22; Indels 4; Gaps 1;

OY 5 GEFQVAGRSARCCGCTSDNAAAEALNASSKEEALQIREKIPKYLPOFHNLSNLDRI 64
DB 116 GQYKXSG-----GSKSNKRDVYHNNAVNASGAEALDIIRAGDPKPTIVYHNLAVERLF 171
OY 65 DKTPEP 70
DB 172 QKPEP 177

RESULT 15
Y175_HELPJ STANDARD; PRT; 299 AA.
AC O92M07;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HYPOTHETICAL PROTEIN JHP0161 PRECURSOR.
GN JHP0161.
OS Helicobacter pylori J99 (Campylobacter pylori J99).
CC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
CC Helicobacter.
OX NCBI_TaxID=85963;
RN
  (1)
  SEQUENCE FROM N.A.
RX MEDLINE=99120557; PubMed=9923682;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carnel G.,
RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
RA Gibson R., Werberg D., Mills S.D., Jiang Q., Taylor D.E., Voyis G.F.,
RA Trust T.J.;
RT "Genomic sequence comparison of two unrelated isolates of the human
  gastric pathogen Helicobacter pylori.";
RL Nature 397:176-180(1999).
CC - SIMILARITY: BELONGS TO THE PPRC/PARVULIN FAMILY OF ROTAMASES.
-----
CC STRONG, TO C.JEJUNT CBF2.
-----
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-----
DR EMBL: AE001454; AAD05744.1; -
DR HSSP: Q13526; IPTN.
DR InterPro: IPR000297; Rotamase.
DR Pfam: PF00639; Rotamase; 1.
DR PROSITE: PS01096; PPRC; PPIASE; 1; 1.
KW Hypothetical protein; Isomerase; Rotamase; signal; Complete proteome.
FT SIGNAL 1 21
FT CHAIN 22 299 HYPOTHETICAL PROTEIN JHP0161.
FT DOMAIN 154 253 PPRC-LIKE.
SQ SEQUENCE 299 AA; 34040 MW; 9C037B1CD1110143 CRC64;

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Query Match 17.88; Score 64.5; DB 1; Length 299;
 Best Local Similarity 28.18; Pred. No. 5.4;
 Matches 18; Conservative 14; Mismatches 11; Indels 21; Gaps 2;

QY 22 NDAAAEALNMS-----SKEPALQIREKIEPEKYLFOFHNLSNDR 62
 |:| | | | | : |::| : : : | | | | : | | | |
 Db 93 NEAKAEKLNQTPPEFKAMEAVKKOALVEFWAKKQAEVKKIQIPEKEMQDFY--NANKDQ 150
 QY 63 IFDR 66
 : | |
 Db 151 LFWK 154

Search completed: January 3, 2002, 15:57:18
 Job time: 1104 sec

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Fri Jan 4 09:40:17 2002

us-09-289-346a-9.rspst

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 3, 2002, 15:56:26 ; Search time 131.69 Seconds
(without alignments)
77.751 Million cell updates/sec

Title: US-09-289-346a-9
Perfect score: 362
Sequence: 1 TLWGEFQVAGRSARGGCOT.....RFPHNLNSLDRIFDKTPPEP 70

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues
Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL.17:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_todent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	305	84.3	352	12	Q9E000
2	288	79.6	226	12	O09727
3	288	79.6	226	12	O9WHF6
4	286	79.0	361	12	O67574
5	284	78.5	225	12	O9QDB1
6	284	78.5	314	12	O9ELT8
7	281	77.6	185	12	O9Q555
8	273	75.4	149	12	O98693
9	273	75.4	223	12	O9YL44
10	267	73.8	234	12	O39180
11	267	73.8	190	12	O92089
12	264	72.9	190	12	O92084
13	263	72.7	190	12	O9W827
14	263	72.7	208	12	O920C4
15	263	72.1	208	12	O920C0
16	261	72.1	208	12	O920B8
17	259	71.5	208	12	O920B6
18	258	71.5	203	12	O92083
19					

20	258	71.3	363	12	073577	073577 cotton leaf
21	253	69.9	360	12	Q9DX10	Q9DX10 ageratum ye
22	251	69.3	208	12	Q920A0	Q920A0 tobacco lea
23	251	69.3	363	12	072705	072705 cotton leaf
24	251	69.3	363	12	072719	072719 cotton leaf
25	250	69.1	190	12	Q92086	Q92086 tobacco lea
26	250	69.1	208	12	Q920C6	Q920C6 tobacco lea
27	249	68.8	349	12	Q88888	Q88888 tomato psu
28	248	68.5	352	12	056816	056816 chayote mos
29	248	68.5	359	12	Q9Y2V4	Q9Y2V4 tomato yell
30	248	68.5	359	12	Q9Y2V2	Q9Y2V2 tomato yell
31	248	68.5	359	12	Q9Y2V7	Q9Y2V7 tomato yell
32	248	68.5	359	12	Q9Y127	Q9Y127 tomato yell
33	247	68.2	353	12	072692	072692 beet curly
34	247	68.2	354	12	065438	065438 beet curly
35	247	68.2	359	12	Q88942	Q88942 tobacco yell
36	246	68.0	190	12	Q920A7	Q920A7 tobacco lea
37	246	68.0	362	12	Q91N48	Q91N48 okra enatio
38	245	67.7	307	12	Q91E87	Q91E87 cotton leaf
39	245	67.7	361	12	072723	072723 cotton leaf
40	244	67.4	231	12	Q96620	Q96620 african tom
41	244	67.4	354	12	Q91N42	Q91N42 south afric
42	243	67.1	358	12	065418	065418 beet curly
43	243	67.1	358	12	Q91EA2	Q91EA2 cassava gem
44	239	66.0	362	12	Q9Y2T7	Q9Y2T7 althea rose
45	239	66.0	363	12	073494	073494 okra yellow

ALIGNMENTS

RESULT 1
ID Q9E000 PRELIMINARY; PRT: 352 AA.
AC Q9E000;
DP 01-MAR-2001 (TREMBLrel.16, Created)
DT 01-MAR-2001 (TREMBLrel.16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel.17, Last annotation update)
DE REPLICATION-ASSOCIATED PROTEIN.
GN AC1.
OS Tomato rugose mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=134599;
RN [1]
RP SEQUENCE FROM N.A.
RA Fernandes J.J., Fontes E.P.B., Brommonschenkel S.H., Carvalho M.G.,
RA Zambolim E.M., Zerbini F.M.;
RT "Molecular Cloning and Characterization of Tomato rugose mosaic virus
(TRMV), a Begomovirus Isolated from Tomatoes at Triangulo Mineiro,
RT Minas Gerais, Brazil." to the EMBL/GenBank/DBJ databases.
RL Submitted (JUL-2000)
DR EMBL; AF291705; AAG1546.1;
DR InterPro: IPR001191; Gemin_A1.
DR Pfam: PF00799; Gemin_A1; 1.
DR PRINTS: PR00227; GEMCOATFALL.
DR ProDom: PD000736; Gemin_A1; 1.
SQ SEQUENCE 352 AA; 40012 MW; 47CD55838E24D613 CRC64;

Query Match 84.3%; Score 305; DB 12; Length 352;
Best local Similarity 81.4%; Pred. No. 8.4e-26;
Matches 57; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 1 TLWGEFQVAGRSARGGCOTSDAAEALINASSKEBALDIIEKPIPEKTLFPHNLNSL 60
I:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 111 TLWGEFQIDGSRARGCOTANDAAEALINAPSKDIALDIIEKPIPEKTLFPHNLNSL 170
QY 61 DRIFDKTPPEP 70
|||:|:|
Db 171 DRIFDKTPPEP 180

RESULT 2

009727
ID 009727 PRELIMINARY; PRT; 226 AA.
AC 009727;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE REP PROTEIN (FRAGMENT).
GN REP.
OS Leovirus mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=58177;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LEMV-BRAZIL.1;
RA Faria J.C., Maxwell D.P.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: U92532; AAB51157.1; -;
DR InterPro: IPR001191; Geminl_AL1.
DR Pfam: PF00799; Geminl_AL1.1.
DR PRINTS: PR00227; GEMCOATL1.
DR Prodom: PD000736; Geminl_AL1.1.
FT NON_TER 226
SQ SEQUENCE 226 AA; 25617 MW; 73CDB6E766083FC5 CRC64;

Query Match 79.6%; Score 288; DB 12; Length 226;
Best Local Similarity 80.0%; Pred. No. 3.9e-24;
Matches 56; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 TLVNGEFOVAGRSARGCGQTSNDAAAEALNASSKEEALQIIRKPEKYLFOFHNLNSNL 60
111 TLVNGEFOVAGRSARGCGQTSNDAAAEALNASSKEEALQIIRKPEKYLFOFHNLNSNL 170
Db 61 DRIEDKTPPE 70
171 DRIEFAKAPPE 180

RESULT 3
Q9WHF6 PRELIMINARY; PRT; 226 AA.
AC Q9WHF6;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE REPLICATION-ASSOCIATED PROTEIN (FRAGMENT).
GN tomato mild mottle geminivirus.
OC Viruses; ssDNA viruses; Geminiviridae; Unclassified Geminiviridae.
OX NCBI_TaxID=92943;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HN96-H5KW;
RA Nakhlia M.K., Mejia L., Ramirez P., Karkashian J.P., Doyle M.M.,
RA Maxwell D.P.;
RT "Molecular characterization and DNA-based detection methods for
vegetable-infecting geminiviruses in Central America."
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF131071; AAD53471.1; -;
DR InterPro: IPR001191; Geminl_AL1.
DR Pfam: PF00799; Geminl_AL1.1.
DR PRINTS: PR00227; GEMCOATL1.
DR Prodom: PD000736; Geminl_AL1.1.
FT NON_TER 226
SQ SEQUENCE 226 AA; 25941 MW; 2EAA116712871A23 CRC64;

Query Match 79.6%; Score 288; DB 12; Length 226;
Best Local Similarity 75.7%; Pred. No. 3.9e-24;
Matches 53; Conservative 12; Mismatches 5; Indels 0; Gaps 0;
QY 1 TLVNGEFOVAGRSARGCGQTSNDAAAEALNASSKEEALQIIRKPEKYLFOFHNLNSNL 60
111 TLVNGEFOVAGRSARGCGQTSNDAAAEALNASSKEEALQIIRKPEKYLFOFHNLNSNL 170

Db 111 TLVNGEFOIDGRSARGGOQTANDAAAEALNASSKEEAMRIKELPKRFLFOYHNLNSNL 170
QY 61 DRIEDKTPPE 70
171 DRIEFAKAPPE 180

RESULT 4
Q67574 PRELIMINARY; PRT; 361 AA.
AC Q67574;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE PUTATIVE REPLICATIVE PROTEIN.
GN AL1.
OS Bean golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10839;
RN [1]
RP SEQUENCE FROM N.A.
RA Gilbertson R.L., Faria J.C., Hanson S.F., Morales F.J., Ahlquist P.G.,
RA Maxwell D.P., Russell D.R.;
RL Phytopathology 81:980-985(1991).
RN [2]
RP SEQUENCE FROM N.A.
RA Gilbertson R.L., Hidayat S.H., Martinez R.T., Leong S.A., Faria J.C.,
RA Morales F.J., Maxwell D.P.;
RL Plant Dis. 75:336-342(1991).
RN [3]
RP SEQUENCE FROM N.A.
RA Gilbertson R.L., Faria J.C., Ahlquist P.G., Maxwell D.P.;
RL Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.
DR EMBL: M88686; AAA46312.1; -;
DR InterPro: IPR001191; Geminl_AL1.
DR Pfam: PF00799; Geminl_AL1.1.
DR PRINTS: PR00227; GEMCOATL1.
DR Prodom: PD000736; Geminl_AL1.1.
SQ SEQUENCE 361 AA; 41041 MW; 0094C7ACAF06B788 CRC64;

Query Match 79.0%; Score 286; DB 12; Length 361;
Best Local Similarity 79.1%; Pred. No. 1.1e-23;
Matches 53; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

QY 4 WGEFOVAGRSARGCGQTSNDAAAEALNASSKEEALQIIRKPEKYLFOFHNLNSNL 63
113 WGEFOVAGRSARGCGQTSNDAAAEALNASSKEEAMRIKELPKRFLFOYHNLNSNL 172
Db 64 FDKTPPE 70
173 FTRAPPE 179

RESULT 5
Q9QDB1 PRELIMINARY; PRT; 225 AA.
AC Q9QDB1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE REPLICATION ASSOCIATED PROTEIN (FRAGMENT).
GN REP.
OS Cowpea golden mosaic geminivirus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=69263;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CGWY-BR;
RA Faria J.C.;
RT "Partial nucleotide sequence of cowpea golden mosaic geminivirus from
Brazil."
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF188708; AAF06318.1; -
 DR InterPro: IPR001191; Gemini_AL1.
 DR Pfam: PF00799; Gemini_AL1.
 DR PRINTS: PR00227; GEMCOATL1.
 DR ProDom: PD000736; Gemini_AL1.
 FT NON_TER 225
 SQ SEQUENCE 225 AA; 25766 MW; 1089CB8D8D15B5D CRC64;

Query Match 78.5%; Score 284; DB 12; Length 225;
 Best Local Similarity 79.1%; Pred. No. 1.1e-23;
 Matches 53; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 4 WGEFQVAGRSARGCGCOTSDNDAAEALNASSKEEALQIIRKIPKYLQFPHNLNSNL 63
 Db 113 WGHQIDGRSARGGQGTANDAAEALNASSKEEALQIIRKIPKYLQFPHNLNSNL 172

QY 64 DRIKTPP 70
 Db 173 FKRPPEP 179

RESULT 6
 Q9ELT8 PRELIMINARY; PRT: 314 AA.
 ID Q9ELT8
 AC Q9ELT8;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE REPLICATION ASSOCIATION PROTEIN.
 GN ACI.
 OS sweet potato leaf curl virus.
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OX NCBI_TaxID=100755;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lotrakul P., Valverde R.A., Clark C.A., Slim J., De la Torre R.;
 RT "Detection of a geminivirus infecting sweet potato in the United
 States."
 RL Plant Dis. 82:1253-1257(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Lotrakul P., Valverde R.A.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF288227; AAC61006.1;
 DR InterPro: IPR001191; Gemini_AL1.
 DR Pfam: PF00799; Gemini_AL1.
 DR PRINTS: PR00227; GEMCOATL1.
 DR ProDom: PD000736; Gemini_AL1.
 SQ SEQUENCE 314 AA; 35153 MW; 6B6220613046943F CRC64;

Query Match 78.5%; Score 284; DB 12; Length 314;
 Best Local Similarity 82.4%; Pred. No. 1.6e-23;
 Matches 56; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 TLVWGEFQVAGRSARGCGCOTSDNDAAEALNASSKEEALQIIRKIPKYLQFPHNLNSNL 60
 Db 110 TIEWGFQVDSARGGQGTANDAAEALNASSKEEALQIIRKIPKYLQFPHNLNSNL 169

QY 61 DRIKTPP 68
 Db 170 DRIKTPP 177

RESULT 7
 ID Q9GS55 PRELIMINARY; PRT: 364 AA.
 AC Q9GS55;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE REPLICATION INITIATION PROTEIN ACI.

GN ACI.
 OS sweet potato leaf curl virus.
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OX NCBI_TaxID=100755;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lotrakul P., Valverde R.A., Clark C.A., Slim J., De la Torre R.;
 RT "Detection of a geminivirus infecting sweet potato in the United
 States."
 RL Plant Dis. 82:1253-1257(1998).
 DR EMBL: AF104036; AAD47173.1;
 DR InterPro: IPR001191; Gemini_AL1.
 DR Pfam: PF00799; Gemini_AL1.
 DR PRINTS: PR00227; GEMCOATL1.
 DR ProDom: PD000736; Gemini_AL1.
 SQ SEQUENCE 364 AA; 40680 MW; 5F79752431A09D6E CRC64;

Query Match 78.5%; Score 284; DB 12; Length 364;
 Best Local Similarity 82.4%; Pred. No. 1.8e-23;
 Matches 56; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 TLVWGEFQVAGRSARGCGCOTSDNDAAEALNASSKEEALQIIRKIPKYLQFPHNLNSNL 60
 Db 110 TIEWGFQVDSARGGQGTANDAAEALNASSKEEALQIIRKIPKYLQFPHNLNSNL 169

QY 61 DRIKTPP 68
 Db 170 DRIKTPP 177

RESULT 8
 Q98693 PRELIMINARY; PRT: 185 AA.
 ID Q98693
 AC Q98693;
 DT 01-FEB-1997 (TREMBlrel. 02, Created)
 DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE REP PROTEIN (FRAGMENT).
 GN ACI.
 OS sida golden mosaic virus.
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OX NCBI_TaxID=51034;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=JAMAICA;
 RA Roye M.E., McLaughlin W.A., Nakha N.K., Maxwell D.P.;
 RL Plant Dis. 81:1251-1258(1997).
 DR EMBL: U67926; AAB97865.1;
 DR InterPro: IPR001191; Gemini_AL1.
 DR Pfam: PF00799; Gemini_AL1.
 DR PRINTS: PR00227; GEMCOATL1.
 DR ProDom: PD000736; Gemini_AL1.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 185 AA; 20975 MW; 3913850A025A5EE1 CRC64;

Query Match 77.6%; Score 281; DB 12; Length 185;
 Best Local Similarity 72.9%; Pred. No. 1.8e-23;
 Matches 51; Conservative 12; Mismatches 7; Indels 0; Gaps 0;

QY 1 TLVWGEFQVAGRSARGCGCOTSDNDAAEALNASSKEEALQIIRKIPKYLQFPHNLNSNL 60
 Db 89 TIEWGFQVDSARGGQGTANDAAEALNASSKEEALQIIRKIPKYLQFPHNLNSNL 148

QY 61 DRIKTPP 70
 Db 149 DRIKTPP 158

RESULT 9
 P88975

ID P88975 PRELIMINARY; PRT: 149 AA.
 AC P88975;
 DT 01-MAY-1997 (TReMBLrel. 03, Created)
 DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
 DE REPLICATION-ASSOCIATED PROTEIN (FRAGMENT).
 GN ACL.
 OS Macroptilium golden mosaic geminivirus.
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OX NCBI_TaxID=51676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-JAMAICAN;
 RA Roye M.E.;
 RL Thesis (1996), Biochemistry, University of the West Indies, Jamaica.
 DR EMBL; U75278; AAB36919.1; -;
 DR InterPro; IPR01191; Gemini_AL1.
 DR Pfam; PF00799; Gemini_AL1.1.
 DR PRINTS; PR00227; GEMCOATALL.
 DR Prodom; PD000736; Gemini_AL1.1.
 FT NON_TER 1 1
 FT SEQUENCE 149 AA; 16785 MW; E4CF5EED4C9CD508 CRC64;

Query Match
 Best Local Similarity 75.4%; Score 273; DB 12; Length 149;
 Matches 50; Conservative 12; Mismatches 8; Indels 0; Gaps 0;

QY 1 TLVNGEFOVAGRSARGGCGTSDNDAAEALNASKKEALQITREKIPKYLEFOFHNLSNL 60
 Db 52 TIEMGVFOIDGRSARGGCGTSDNDAAEALNASKKEALQITREKIPKYLEFOFHNLSNL 111
 QY 61 DRIFDKTPEP 70
 Db 112 DRIFDKTPEP 121

RESULT 10
 O9YL44 PRELIMINARY; PRT: 233 AA.
 AC O9YL44;
 DT 01-MAY-1999 (TReMBLrel. 10, Created)
 DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
 DE REPLICATION ASSOCIATED PROTEIN (FRAGMENT).
 GN REP.
 OS Macroptilium golden mosaic geminivirus.
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OX NCBI_TaxID=51676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-JAMAICA STRAIN 1;
 RA Roye M.E.;
 RT "Genetic diversity and phylogeny of whitefly-transmitted geminiviruses from Jamaica."
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-JAMAICA STRAIN 1;
 RA Roye M.E., McLaughlin W.A., Maxwell D.P.;
 RT "Molecular characterization of two distinct geminiviruses infecting M. lathyroides from Jamaica."
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF098940; AAD17850.1; -;
 DR InterPro; IPR001191; Gemini_AL1.
 DR Pfam; PF00799; Gemini_AL1.1.
 DR PRINTS; PR00227; GEMCOATALL.
 DR Prodom; PD000736; Gemini_AL1.1.
 FT NON_TER 233 233
 FT SEQUENCE 233 AA; 26555 MW; AAA90AFAD2166A02 CRC64;

Query Match
 Best Local Similarity 75.4%; Score 273; DB 12; Length 233;
 Matches 50; Conservative 12; Mismatches 8; Indels 0; Gaps 0;

QY 1 TLVNGEFOVAGRSARGGCGTSDNDAAEALNASKKEALQITREKIPKYLEFOFHNLSNL 60
 Db 110 TIEMGVFOIDGRSARGGCGTSDNDAAEALNASKKEALQITREKIPKYLEFOFHNLSNL 169
 QY 61 DRIFDKTPEP 70
 Db 170 DRIFDKTPEP 179

RESULT 11
 O39180 PRELIMINARY; PRT: 234 AA.
 AC O39180;
 DT 01-JAN-1998 (TReMBLrel. 05, Created)
 DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
 DE REPLICATION-ASSOCIATED PROTEIN (FRAGMENT).
 GN Potato yellow mosaic virus.
 OS Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OX NCBI_TaxID=10827;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-TOMATO STRAIN;
 RA Guzman P., Arredondo C.R., Emmatty D., Portillo R.J., Gilbertson R.L.;
 RL Plant Dis. 81:312-312(1997).
 DR EMBL; AF026553; AAB82605.1; -;
 DR InterPro; IPR001191; Gemini_AL1.
 DR Pfam; PF00799; Gemini_AL1.1.
 DR PRINTS; PR00227; GEMCOATALL.
 DR Prodom; PD000736; Gemini_AL1.1.
 FT NON_TER 234 234
 FT SEQUENCE 234 AA; 26486 MW; 9EDBF0697105CD19 CRC64;

Query Match
 Best Local Similarity 73.8%; Score 267; DB 12; Length 234;
 Matches 49; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

QY 1 TLVNGEFOVAGRSARGGCGTSDNDAAEALNASKKEALQITREKIPKYLEFOFHNLSNL 60
 Db 110 TIEMGVFOIDGRSARGGCGTSDNDAAEALNASKKEALQITREKIPKYLEFOFHNLSNL 169
 QY 61 DRIFDKTPEP 70
 Db 170 DRIFDKTPEP 179

RESULT 12
 O9Z089 PRELIMINARY; PRT: 190 AA.
 AC O9Z089;
 DT 01-MAY-1999 (TReMBLrel. 10, Created)
 DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
 DE C1 AND C4 GENES, CLONE YOKOHAMA3-1, PARTIAL AND COMPLETE CDS (FRAGMENT).
 GN C1.
 OS tobacco leaf curl virus.
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OX NCBI_TaxID=67762;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-YOKOHAMA3;
 RA Ooi K., Ohshita S., Ishii I., Yahara T.;
 RT "Molecular phylogeny of geminivirus infecting wild plants in Japan."
 RL J. Plant Res. 110:247-257(1997).
 DR EMBL; AB001315; BAA34033.1; -;
 DR InterPro; IPR001191; Gemini_AL1.
 DR Pfam; PF00799; Gemini_AL1.1.

DR PRINTS; PRO0227; GEMCOATALL.
DR PRODOM; PD000736; Gemini_AL1. 1.
FT NON_TER 1 190
FT NON_TER 190
SQ SEQUENCE 190 AA; 21432 MW; AAC093D1D1610FAD CRC64;

Query Match 72.9%; Score 264; DB 12; Length 190;
Best Local Similarity 61.2%; Pred. No. 1,4e-21;
Matches 52; Conservative 8; Mismatches 9; Indels 16; Gaps 1;

OY 1 TLVWGEFVAGRSARGCGCOTSDNDAAEALNASSKEEALQIIREKIPEKYLFOFHNLNSNL 60
DB 85 TLEWGTFOVDGSRARGCGCONANDACAEALNASSKAELALIREKLPKDFLFOYHNLNSNL 144

OY 61 DRI-----FDKTPPE 69
DB 145 DRIFAPPLEVFCPFSSFDQVPE 169

RESULT 13

OY2084 PRELIMINARY; PRT; 190 AA.
AC 092084;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE C1 AND C4 GENES, CLONE YOKOHAMA5-2, PARTIAL AND COMPLETE CDS (FRAGMENT).
DE C1.
GN tobacco leaf curl virus.
OS Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OC NCBI_TaxID=67762;
OX [1]
RN SEQUENCE FROM N.A.
RC STRAIN=YOKOHAMA5;
RA Ooi K., Ohshita S., Ishii I., Yahara T.;
RT "Molecular phylogeny of geminivirus infecting wild plants in Japan.";
RL J. Plant Res. 110:247-257(1997).
DR EMBL; AB001318; BAA34039.1;
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1.1.
DR PRINTS; PR00227; GEMCOATALL.
DR PRODOM; PD000736; Gemini_AL1. 1.
FT NON_TER 1 190
FT NON_TER 190
SQ SEQUENCE 190 AA; 21444 MW; AAC1C2943E3F01AD CRC64;

Query Match 72.9%; Score 264; DB 12; Length 190;
Best Local Similarity 61.2%; Pred. No. 1,4e-21;
Matches 52; Conservative 8; Mismatches 9; Indels 16; Gaps 1;

OY 1 TLVWGEFVAGRSARGCGCOTSDNDAAEALNASSKEEALQIIREKIPEKYLFOFHNLNSNL 60
DB 85 TLEWGTFOVDGSRARGCGCONANDACAEALNASSKAELALIREKLPKDFLFOYHNLNSNL 144

OY 61 DRI-----FDKTPPE 69
DB 145 DRIFAPPLEVFCPFSSFDQVPE 169

RESULT 14

OY2827 PRELIMINARY; PRT; 190 AA.
AC 092827;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE C1 PROTEIN (FRAGMENT).
DE C1.
GN tobacco leaf curl virus.
OS Viruses; ssDNA viruses; Geminiviridae; Begomovirus.

OX NCBI_TaxID=67762;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GORAL;
RA Ooi K., Ohshita S., Ishii I., Yahara T.;
RT "Molecular phylogeny of geminivirus infecting wild plants in Japan.";
RL J. Plant Res. 110:247-257(1997).
DR EMBL; AB001303; BAA34010.1;
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1.1.
DR PRINTS; PR00227; GEMCOATALL.
DR PRODOM; PD000736; Gemini_AL1. 1.
FT NON_TER 1 190
FT NON_TER 190
SQ SEQUENCE 190 AA; 21444 MW; 93C3742A8BDB7EB CRC64;

Query Match 72.7%; Score 263; DB 12; Length 190;
Best Local Similarity 61.2%; Pred. No. 1,8e-21;
Matches 52; Conservative 8; Mismatches 9; Indels 16; Gaps 1;

OY 1 TLVWGEFVAGRSARGCGCOTSDNDAAEALNASSKEEALQIIREKIPEKYLFOFHNLNSNL 60
DB 85 TLEWGTFOVDGSRARGCGCONANDACAEALNASSKAELALIREKLPKDFLFOYHNLNSNL 144

OY 61 DRI-----FDKTPPE 69
DB 145 DRIFAPPLEVFCPFSSFDQVPE 169

RESULT 15

OY20C4 PRELIMINARY; PRT; 208 AA.
AC 0920C4;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE C1 AND C4 GENES, CLONE ABURA3-1, PARTIAL AND COMPLETE CDS (FRAGMENT).
DE C1.
GN tobacco leaf curl virus.
OS Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OC NCBI_TaxID=67762;
OX [1]
RN SEQUENCE FROM N.A.
RC STRAIN=ABURA3;
RA Ooi K., Ohshita S., Ishii I., Yahara T.;
RT "Molecular phylogeny of geminivirus infecting wild plants in Japan.";
RL J. Plant Res. 110:247-257(1997).
DR EMBL; AB001294; BAA33992.1;
DR InterPro; IPR001191; Gemini_AL1.
DR Pfam; PF00799; Gemini_AL1.1.
DR PRINTS; PR00227; GEMCOATALL.
DR PRODOM; PD000736; Gemini_AL1. 1.
FT NON_TER 1 208
FT NON_TER 208
SQ SEQUENCE 208 AA; 23526 MW; 249CC31D8729C72D CRC64;

Query Match 72.7%; Score 263; DB 12; Length 208;
Best Local Similarity 61.2%; Pred. No. 2e-21;
Matches 52; Conservative 8; Mismatches 9; Indels 16; Gaps 1;

OY 1 TLVWGEFVAGRSARGCGCOTSDNDAAEALNASSKEEALQIIREKIPEKYLFOFHNLNSNL 60
DB 102 TLEWGTFOVDGSRARGCGCONANDACAEALNASSKAELALIREKLPKDFLFOYHNLNSNL 161

OY 61 DRI-----FDKTPPE 69
DB 162 DRIFAPPLEVFCPFSSFDQVPE 186

Search completed: January 3, 2002, 15:56:26

Fri Jan 4 09:40:17 2002

Job time: 1122 sec

us-09-289-346a-9.ispt

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 3, 2002, 15:38:51 ; Search time 65.28 Seconds
(without alignments)
24.130 Million cell updates/sec

Title: US-09-289-346a-9
Perfect score: 362
Sequence: 1 TLWGEFVAGRSARGCQT.....FOFHNLNSLDRFPDKTPEP 70

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/plodata/2/1aa/5B-COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	222	61.3	353	4	US-08-838-151A-44 Sequence 44, Appl
2	222	61.3	353	4	US-08-838-151A-46 Sequence 46, Appl
3	222	61.3	353	4	US-08-838-151A-49 Sequence 49, Appl
4	222	61.3	353	4	US-08-838-151A-52 Sequence 52, Appl
5	222	61.3	353	4	US-08-838-151A-55 Sequence 55, Appl
6	222	61.3	353	4	US-08-809-103B-2 Sequence 2, Appl
7	222	61.3	353	4	US-08-809-103B-4 Sequence 4, Appl
8	222	61.3	353	4	US-08-809-103B-6 Sequence 6, Appl
9	222	61.3	353	4	US-08-809-103B-8 Sequence 8, Appl
10	222	60.8	361	4	US-08-838-151A-2 Sequence 2, Appl
11	220	60.8	361	4	US-08-838-151A-4 Sequence 4, Appl
12	220	60.8	361	4	US-08-838-151A-6 Sequence 6, Appl
13	220	60.8	361	4	US-08-838-151A-8 Sequence 8, Appl
14	207	57.2	357	4	US-08-838-151A-24 Sequence 24, Appl
15	207	57.2	357	4	US-08-838-151A-27 Sequence 27, Appl
16	207	57.2	357	4	US-08-838-151A-30 Sequence 30, Appl
17	199	55.0	357	4	US-08-838-151A-20 Sequence 20, Appl
18	60.5	16.7	1713	3	US-08-600-982-24 Sequence 24, Appl
19	60.5	16.7	1713	5	PCT-US94-10261A-24 Sequence 24, Appl
20	60	16.6	446	2	US-09-333-696-11 Sequence 11, Appl
21	60	16.6	446	3	US-09-333-696-11 Sequence 11, Appl
22	58	16.0	844	3	US-09-029-267-20 Sequence 20, Appl
23	56	15.5	454	3	US-08-446-100-31 Sequence 31, Appl
24	56	15.5	602	2	US-08-419-652-6 Sequence 6, Appl
25	56	15.5	771	1	US-07-923-976-6 Patent No. 5422248
26	56	15.5	783	6	US-07-923-976-6 Patent No. 5422248
27	56	15.5	836	1	US-07-923-976-4 Sequence 4, Appl

28	56	15.5	863	1	US-07-923-976-8 Sequence 8, Appl
29	56	15.5	2161	1	US-07-745-206A-2 Sequence 2, Appl
30	56	15.5	2161	1	US-08-455-543A-49 Sequence 49, Appl
31	56	15.5	2161	1	US-08-455-543A-51 Sequence 51, Appl
32	56	15.5	2161	2	US-08-223-305C-49 Sequence 49, Appl
33	56	15.5	2161	2	US-08-223-305C-51 Sequence 2, Appl
34	56	15.5	2161	4	US-08-311-363-2 Sequence 3, Appl
35	55	15.2	384	2	US-08-928-442-3 Sequence 3, Appl
36	54	14.9	454	3	US-08-446-100-30 Sequence 30, Appl
37	53.5	14.8	81	4	US-08-995-159-6 Sequence 6, Appl
38	53.5	14.8	91	4	US-09-042-785A-27 Sequence 27, Appl
39	53.5	14.8	312	1	US-08-414-625-2 Sequence 2, Appl
40	53	14.6	258	4	US-09-251-645-5 Sequence 5, Appl
41	53	14.6	266	2	US-07-857-224B-40 Sequence 40, Appl
42	53	14.6	454	3	US-08-446-100-26 Sequence 26, Appl
43	53	14.6	454	3	US-08-446-100-27 Sequence 27, Appl
44	53	14.6	454	3	US-08-446-100-28 Sequence 28, Appl
45	53	14.6	454	3	US-08-446-100-29 Sequence 29, Appl

ALIGNMENTS

RESULT 1
US-08-838-151A-44
: Sequence 44, Application US/08838151A
: Patent No. 6291743
: GENERAL INFORMATION:
: APPLICANT: Stout, John T
: APPLICANT: Luu, Hang T
: APPLICANT: Maxwell, Douglas
: APPLICANT: Ahlquist, Paul
: APPLICANT: Hanson, Steve
: TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
: TITLE OF INVENTION: Genes
: NUMBER OF SEQUENCES: 63
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Dressler, Rocky, Milnamov & Katz
: STREET: Two Prudential Plaza, Suite 4700
: CITY: Chicago
: STATE: Illinois
: COUNTRY: U.S.A.
: ZIP: 60601
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/838, 151A
: FILING DATE:
: CLASSIFICATION: 800
: ATTORNEY/AGENT INFORMATION:
: NAME: Mueller, Lisa V
: REGISTRATION NUMBER: 38,978
: REFERENCE/DOCKET NUMBER: SVS3801P0260
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312-616-5400
: TELEFAX: 312-616-5460
: INFORMATION FOR SEQ ID NO: 44:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 353 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-838-151A-44
Query Match 61.3%, Score 222, DB 4, Length 353;
Best Local Similarity 60.0%, Pred. No. 9e-21;
Matches 42; Conservative 13; Mismatches 15; Gaps 0;
OY 1 TLWGEFVAGRSARGCQTSNDAAEALNASKREALQIIREKIPRYLFOFHNLNSNL 60

Db 110 TTEMGQFVVDGSRAGCGQGSANDSYAKALNMDISALTIILKEBPKRYVLOHHNRSL 169
QY 61 DRIEDKPEP 70
Db 170 ERIFVKVPEP 179

RESULT 2

US-08-838-151A-46
Sequence 46, Application US/08838151A
Patent No. 6291743
GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rocky, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 353 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-838-151A-46

Query Match 61.3%, Score 222, DB 4, Length 353;
Best Local Similarity 60.0%, Pred. No. 9e-21;
Matches 42; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 TLVWGEFVAVARSARGCGQTSNDAAAEALNASSKEALQITREKIPKYLQFHNLSNL 60
Db 110 TTEMGQFVVDGSRAGCGQGSANDSYAKALNMDISALTIILKEBPKRYVLOHHNRSL 169
QY 61 DRIEDKPEP 70
Db 170 ERIFVKVPEP 179

RESULT 3

US-08-838-151A-49
Sequence 49, Application US/08838151A
Patent No. 6291743
GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Luu, Hang T

APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rocky, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 353 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-838-151A-49

Query Match 61.3%, Score 222, DB 4, Length 353;
Best Local Similarity 60.0%, Pred. No. 9e-21;
Matches 42; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 TLVWGEFVAVARSARGCGQTSNDAAAEALNASSKEALQITREKIPKYLQFHNLSNL 60
Db 110 TTEMGQFVVDGSRAGCGQGSANDSYAKALNMDISALTIILKEBPKRYVLOHHNRSL 169
QY 61 DRIEDKPEP 70
Db 170 ERIFVKVPEP 179

RESULT 4

US-08-838-151A-52
Sequence 52, Application US/08838151A
Patent No. 6291743
GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rocky, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,103B
FILING DATE: 17-MAR-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94.11040
FILING DATE: 15-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR95/01192
FILING DATE: 15-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: PATCH, Andrew J.
REGISTRATION NUMBER: 32,925
REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 521-2297
TELEFAX: (703) 685-0573
TELEX: 248425 EMBRON
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-809-103B-8

Query Match 61.3%; Score 222; DB 4; Length 359;
Best Local Similarity 58.0%; Pred. No. 9.2e-21;
Matches 40; Conservative 11; Mismatches 18; Indels 0; Gaps 0;
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DB 111 LEMGTQDGRSARGGQOTANDYAKAINAGSKSOLVDYIKELAPRDYLAHNNHSND 170
OY 62 RIFDKTPEP 70
DB 171 KVFQVPAP 179
RESULT 10
US-08-838-151A-2
Sequence 2, Application US/08838151A
Patent No. 6291743
GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Lau, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rockey, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A

FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 361 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-838-151A-2

Query Match 60.8%; Score 220; DB 4; Length 361;
Best Local Similarity 57.1%; Pred. No. 1.7e-20;
Matches 40; Conservative 16; Mismatches 14; Indels 0; Gaps 0;
OY 1 TLWGEFVAGRSARGCOTSDNDAAEALNASSKEALQIIRKIPERYLFQPHNLSND 60
DB 110 TLEMGDFQDGRSARGGQSDANDYAKALNASSVGSALAVLEEQPKDPVLAQNNHNRSL 169
OY 61 DRIFDKTPEP 70
DB 170 ERIFAKAPEP 179

RESULT 11
US-08-838-151A-4
Sequence 4, Application US/08838151A
Patent No. 6291743
GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Lau, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rockey, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 361 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

ADDRESS: Dressler, Rocky, Milamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 357 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-838-151A-24

Query Match	57.28	Score	207	DB	4	Length	357
Best Local Similarity	65.68	Pred. No.	7.9e-19				
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						Gaps	0

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Db	111 FGVSGIDPGRSARGGQGSANDPAAAEALNAASSFEALNLTKEKAPRDYILQFHNLSNDRI 176

RESULT 15
 US-08-838-151A-27
 : Sequence 27, Application US/08838151A
 : Patent No. 6281743
 : GENERAL INFORMATION:
 : APPLICANT: Stout, John T
 : APPLICANT: Liu, Haog T
 : APPLICANT: Maxwell, Douglas
 : APPLICANT: Ahlquist, Paul
 : APPLICANT: Hanson, Steve
 : TITLE OF INVENTION: Transgenic Plants Expressing GeminiViruses
 : NUMBER OF SEQUENCES: 63
 : CORRESPONDENCE ADDRESSES:
 : ADDRESSEE: Dressler, Rocky, Milnamow & Katz
 : STREET: Two Prudential Plaza, Suite 4700
 : CITY: Chicago
 : STATE: Illinois
 : COUNTRY: U.S.A.
 : ZIP: 60601
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/838,151A
 : FILING DATE:
 : CLASSIFICATION: 800

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:      ATTORNEY/AGENT INFORMATION:
:      NAME:  Mueller, Lisa V
:      REGISTRATION NUMBER:  38,978
:      REFERENCE/DOCKET NUMBER:  SYS3801P0260
:      TELECOMMUNICATION INFORMATION:
:      TELEPHONE:  312-616-5400
:      TELEFAX:  312-616-5460
:      INFORMATION FOR SEQ ID NO:  27:
:      SEQUENCE CHARACTERISTICS:
:      LENGTH:  357 amino acids
:      TYPE:  amino acid
:      TOPOLOGY:  linear
:      MOLECULE TYPE:  protein
:      US-08-838-151A-27

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Query Match	57.28;	Score 207;	DB 4;	Length 357;
Best Local Similarity	65.68;	Pred. No. 7.9e-19;		
Matches 40;	Conservative 10;	Mismatches 11;	Indels 0;	Gaps 0;

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Db      111 FGVSGIDGRSARGCGGGSANDAYAEALNCGSRSEALNIIKERAPROYIILQPHINLSNDRI 170
QY      64 F 64
Db      171 F 171

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Job time: 228 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 3, 2002, 15:37:38 : Search time 144.17 Seconds
(without alignments)
35.965 Million cell updates/sec

Title: US-09-289-346A-10

Perfect score: 364
Sequence: 1 TLWNGEPQVDFRSARGGCGT.....FGFHNLNSNDRLEFKTPEP 70

Scoring table:

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Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Listing first 45 summaries

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21: /SID88/gcgdata/geneSeq/geneSeq/AA2000.DAT:*
22: /SID88/gcgdata/geneSeq/geneSeq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	364	100.0	70	21	AA18686
2	349	98.9	70	21	AA18677
3	349	95.9	356	21	AA18687
4	341	93.7	70	21	AA18685
5	338	92.9	70	21	AA18688
6	337	92.6	70	21	AA18692
7	335	92.0	70	21	AA18684
8	335	92.0	70	21	AA18690
9	334	91.8	70	21	AA18678
10	333	91.5	70	21	AA18689
11	331	90.9	70	21	AA18680

Result No.	Score	Query Match	Length	DB ID	Description
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13	328	90.1	70	21	AA18681
14	327	89.8	70	21	AA18683
15	325	89.3	70	21	AA18682
16	317	87.1	70	21	AA18679
17	323	86.3	353	18	AAW34338
18	323	86.3	353	18	AAW34332
19	323	86.3	353	18	AAW34333
20	323	86.3	353	18	AAW34334
21	323	86.3	353	18	AAW34335
22	321	86.7	353	8	AAW70407
23	321	86.7	359	17	AAW88870
24	321	86.7	359	17	AAW88871
25	321	86.7	359	17	AAW88872
26	321	86.7	361	18	AAW34336
27	321	86.7	361	18	AAW34324
28	321	86.7	361	18	AAW34325
29	321	86.7	361	18	AAW34326
30	321	86.7	361	18	AAW34327
31	321	86.7	361	18	AAW34328
32	321	86.7	361	18	AAW34329
33	321	86.7	361	18	AAW34330
34	321	86.7	361	18	AAW34331
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36	321	86.7	361	18	AAW34333
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38	321	86.7	361	18	AAW34335
39	321	86.7	361	18	AAW34336
40	321	86.7	361	18	AAW34337
41	321	86.7	361	18	AAW34338
42	321	86.7	361	18	AAW34339
43	321	86.7	361	18	AAW34340
44	321	86.7	361	18	AAW34341
45	321	86.7	361	18	AAW34342

ALIGNMENTS

RESULT 1
AA18686 standard; peptide: 70 AA.
AC AA18686;
DT 22-JAN-2001 (first entry)
DE Mutant peptide derived from amino acids 110-179 of Rep (All) protein.
XX Geminivirus: replication protein; Rep protein; All: transgenic plant;
KW Ribosome binding region; resistance; geminivirus infection.
XX Synthetic.
OS Tomato golden mosaic virus.
XX Key location/Qualifiers
FT Misc-difference 24 /note= "wild type residue replaced with Leu"
FT Misc-difference 25 /note= "wild type residue replaced with Leu"
FT Misc-difference 26 /note= "wild type residue replaced with Leu"
FT WO200054573-A1.
PN 21-SEP-2000.
PD 15-MAR-2000; 2000WO-US06759.
PF 18-MAR-1999; 9905-0125004.
PR 09-APR-1999; 9905-0289346.
XX (UYNC-) UNIV NORTH CAROLINA STATE.

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XX  Hanley-Bowdoin L., Orozco BM, Kong L.;
PI  WPI; 2000-618851/59.
XX
XX  Transgenic plants with increased resistance to geminivirus infection
PT  comprise a nucleic acid construct containing a nucleic acid sequence
PT  encoding a mutant AL1 protein with a mutation in the Rb binding region
PT
PS  Claim 53; Page 46; 73pp; English.
XX
XX  The present sequence represents a mutant peptide, derived from a
CC  geminivirus replication (Rep) protein, also known as AL1. AL1 binds
CC  double-stranded DNA, catalyzes cleavage and ligation of single-stranded
CC  DNA, and interacts with other viral and host proteins. Mutants of the AL1
CC  protein are used to produce transgenic plants. The mutation in AL1 is
CC  present in a ribosome binding region, and expression of mutant AL1
CC  protein imparts increased resistance to geminivirus infection in the
CC  plant. Mutant AL1 proteins are useful for producing plants having
CC  increased resistance or reduced sensitivity to a geminivirus such as
CC  tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
CC  virus, tomato leaf curl virus, African cassava mosaic virus, Indian
CC  cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
CC  virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
CC  virus, cotton leaf curl virus or beet curly top virus.
XX
SO  Sequence 70 AA:

Query Match          100.0%; Score 364; DB 21; Length 70;
Best Local Similarity 100.0%; Pred. No. 7.8e-39;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 TLVWGEFQVNGRSARGCGCOTSNLDLEALNASSKEEALQIRREKIPKYLFOFHNLNSNL 60
    |||||||
DB  1 tlwgefgydgsarsargcgctsndlaaenasskeaalqirrekipkyllfgfhlnsnl 60

QY  61 DRIFDKTPEP 70
    |||||||
DB  61 drifdktppep 70

RESULT 2
AAB18677
ID  AAB18677 standard; peptide; 70 AA.
XX
XX  AAB18677;
AC  XX
XX  22-JAN-2001 (first entry)
DT  XX
XX  Peptide fragment from Rep protein of TGMV (amino acids 110-179).
DE  XX
XX  Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
KW  ribosome binding region; resistance; geminivirus infection.
XX
XX  Tomato golden mosaic virus.
OS  XX
XX  WO200054573-A1.
PN  XX
XX  21-SEP-2000.
PD  XX
XX  15-MAR-2000; 2000WO-US06759.
PF  XX
XX  18-MAR-1999; 99US-0125004.
PR  09-APR-1999; 99US-0289346.
XX
XX  (UYNC-) UNIV NORTH CAROLINA STATE.
PA  Hanley-Bowdoin L., Orozco BM, Kong L.;
PI  WPI; 2000-618851/59.
XX
XX

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PT  Transgenic plants with increased resistance to geminivirus infection
PT  comprise a nucleic acid construct containing a nucleic acid sequence
PT  encoding a mutant AL1 protein with a mutation in the Rb binding region
PT
PS  Disclosure; Page 18; 73pp; English.
XX
XX  The present sequence is derived from a geminivirus replication (Rep)
CC  protein, which is also known as AL1. AL1 binds double-stranded DNA,
CC  catalyzes cleavage and ligation of single-stranded DNA, and interacts
CC  with other viral and host proteins. Mutants of the AL1 protein are used
CC  to produce transgenic plants. The mutation in AL1 is present in a
CC  ribosome binding region, and expression of mutant AL1 protein imparts
CC  increased resistance to geminivirus infection in the plant. Mutant AL1
CC  proteins are useful for producing plants having increased resistance or
CC  reduced sensitivity to a geminivirus such as tomato golden mosaic virus,
CC  tomato mottle virus, tomato yellow leaf curl virus, tomato leaf curl
CC  virus, African cassava mosaic virus, Indian cassava mosaic virus, potato
CC  yellow mosaic virus, bean golden mosaic virus, bean dwarf mosaic virus,
CC  squash leaf curl virus, Texas pepper virus, cotton leaf curl virus or
CC  beet curly top virus.
XX
SO  Sequence 70 AA:

Query Match          95.9%; Score 349; DB 21; Length 70;
Best Local Similarity 95.7%; Pred. No. 6.3e-37;
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  1 TLVWGEFQVNGRSARGCGCOTSNLDLEALNASSKEEALQIRREKIPKYLFOFHNLNSNL 60
    |||||||
DB  1 tlwgefgydgsarsargcgctsndaaenasskeaalqirrekipkyllfgfhlnsnl 60

QY  61 DRIFDKTPEP 70
    |||||||
DB  61 drifdktppep 70

RESULT 3
AAB18687
ID  AAB18687 standard; peptide; 356 AA.
XX
XX  AAB18687;
AC  XX
XX  22-JAN-2001 (first entry)
DT  XX
XX  Amino acid sequence of a geminivirus replication protein of TGMV.
DE  XX
XX  Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
KW  ribosome binding region; resistance; geminivirus infection.
XX
XX  Tomato golden mosaic virus.
OS  XX
XX  Key Location/Qualifiers
FH  Misc-difference 354
FT  /note="unspecified amino acid"
XX
XX  WO200054573-A1.
PN  XX
XX  21-SEP-2000.
PD  XX
XX  15-MAR-2000; 2000WO-US06759.
PF  XX
XX  18-MAR-1999; 99US-0125004.
PR  09-APR-1999; 99US-0289346.
XX
XX  (UYNC-) UNIV NORTH CAROLINA STATE.
PA  Hanley-Bowdoin L., Orozco BM, Kong L.;
PI  WPI; 2000-618851/59.
XX
XX  Transgenic plants with increased resistance to geminivirus infection
PT

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PT comprise a nucleic acid construct containing a nucleic acid sequence
PT encoding a mutant AL1 protein with a mutation in the Rb binding region

PS Disclosure: Page 47-48; 73pp; English.

CC The present sequence represents a geminivirus replication (Rep)
CC protein, which is also known as AL1. AL1 binds double-stranded DNA,
CC catalyzes cleavage and ligation of single-stranded DNA, and interacts
CC with other viral and host proteins. Mutants of the AL1 protein are used
CC to produce transgenic plants. The mutation in AL1 is present in a
CC ribosome binding region, and expression of mutant AL1 protein imparts
CC increased resistance to geminivirus infection in the plant. Mutant AL1
CC proteins are useful for producing plants having increased resistance or
CC reduced sensitivity to a geminivirus such as tomato golden mosaic virus,
CC tomatillo mottle virus, tomato yellow leaf curl virus, tomato leaf curl
CC virus, African cassava mosaic virus, Indian cassava mosaic virus, potato
CC yellow mosaic virus, bean golden mosaic virus, bean dwarf mosaic virus,
CC squash leaf curl virus, Texas pepper virus, cotton leaf curl virus or
CC beet curly top virus.

SO Sequence 356 AA;

Query Match 95.9%; Score 349; DB 21; Length 356;
Best Local Similarity 95.7%; Pred. No. 4.9e-36;
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 TLWGEFOYDGNRAGCGCQTSNDLLLEALNASSKEEALQIRREKIPKYLFGHNINSNL 60
|||||

DB 110 TLWGEFGYDGRSARGCGQTSNDAAEAALNASSKEEALQIRREKIPKYLFGHNINSNL 169
|||||

OY 61 DRIFDKTPPEP 70
|||||

DB 170 DRIFDKTPPEP 179

RESULT 4

AAB18685
ID AAB18685 standard; peptide; 70 AA.

AC AAB18685;

DT 22-JAN-2001 (first entry)

DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.

XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;

KW ribosome binding region; resistance; geminivirus infection.

OS Synthetic.

OS Tomato golden mosaic virus.

FT Key Location/Qualifiers

FT Misc-difference 10 /note= "wild type residue replaced with Ala"

PN WO200054573-A1.

PD 21-SEP-2000.

PF 15-MAR-2000; 2000MO-US06759.

PR 18-MAR-1999; 99US-0125004.

PR 09-APR-1999; 99US-0289346.

PA (UYNC-) UNIV NORTH CAROLINA STATE.

PI Hanley-Bowdoin L, Orozco BM, Kong L;

DR WPI; 2000-618851/59.

PT Transgenic plants with increased resistance to geminivirus infection

PT comprise a nucleic acid construct containing a nucleic acid sequence
PT encoding a mutant AL1 protein with a mutation in the Rb binding region

PS Claim 53; Page 46; 73pp; English.

CC The present sequence represents a mutant peptide, derived from a
CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
CC protein are used to produce transgenic plants. The mutation in AL1 is
CC present in a ribosome binding region, and expression of mutant AL1
CC protein imparts increased resistance to geminivirus infection in the
CC plant. Mutant AL1 proteins are useful for producing plants having
CC increased resistance or reduced sensitivity to a geminivirus such as
CC tomato golden mosaic virus, tomatillo mottle virus, tomato yellow leaf curl
CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
CC virus, cotton leaf curl virus or beet curly top virus.

SO Sequence 70 AA;

Query Match 93.7%; Score 341; DB 21; Length 70;
Best Local Similarity 94.3%; Pred. No. 6.5e-36;
Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 TLWGEFOYDGNRAGCGCQTSNDLLLEALNASSKEEALQIRREKIPKYLFGHNINSNL 60
|||||

DB 1 TLWGEFGYDGRSARGCGQTSNDAAEAALNASSKEEALQIRREKIPKYLFGHNINSNL 60
|||||

OY 61 DRIFDKTPPEP 70
|||||

DB 61 DRIFDKTPPEP 70

RESULT 5

AAB18688
ID AAB18688 standard; peptide; 70 AA.

AC AAB18688;

DT 22-JAN-2001 (first entry)

DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.

XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;

KW ribosome binding region; resistance; geminivirus infection.

OS Synthetic.

OS Tomato golden mosaic virus.

FT Key Location/Qualifiers

FT Misc-difference 19 /note= "wild type residue replaced with Ala"

FT Misc-difference 20 /note= "wild type residue replaced with Ala"

PN WO200054573-A1.

PD 21-SEP-2000.

PF 15-MAR-2000; 2000MO-US06759.

PR 18-MAR-1999; 99US-0125004.

PR 09-APR-1999; 99US-0289346.

PA (UYNC-) UNIV NORTH CAROLINA STATE.

PI Hanley-Bowdoin L, Orozco BM, Kong L;

DR WPI; 2000-618851/59.

XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX WPI: 2000-618851/59.
XX
XX Transgenic plants with increased resistance to geminivirus infection
XX comprise a nucleic acid construct containing a nucleic acid sequence
XX encoding a mutant AL1 protein with a mutation in the Rb binding region
XX
XX
XX Claim 52: Page 45; 73pp; English.
XX
XX The present sequence represents a mutant peptide, derived from a
XX geminivirus replication (rep) protein, also known as AL1. AL1 binds
XX double-stranded DNA, catalyses cleavage and ligation of single-stranded
XX DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX protein are used to produce transgenic plants. The mutation in AL1 is
XX present in a ribosome binding region, and expression of mutant AL1
XX protein imparts increased resistance to geminivirus infection in the
XX plant. Mutant AL1 proteins are useful for producing plants having
XX increased resistance or reduced sensitivity to a geminivirus such as
XX tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX virus, tomato leaf curl virus, African cassava mosaic virus, Indian
XX cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX virus, cotton leaf curl virus or beet curly top virus.
XX
XX Sequence 70 AA:
SQ
Query Match 92.0%; Score 335; DB 21; Length 70;
Best Local Similarity 92.9%; Pred. No. 3.8e-35;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 TLVWGEFQVNDGSRAGGCGTSDLLLEALNASSKEALQIIREKIPERYLGFPHNLNSL 60
Db 1 tlvwgeavdvgrsargygcqtndaaaalnasskeaalqilirekipekylfghnlmsl 60
QY 61 DRIFFKTPPEP 70
Db 61 drifdktppep 70
RESULT 8
AAB18690
ID AAB18690 standard; peptide: 70 AA.
XX
XX AAB18690;
XX
XX 22-JAN-2001 (first entry)
XX
XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX
XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX
XX Synthetic.
XX
XX Tomato golden mosaic virus.
XX
XX Key Location/Qualifiers
XX FT Misc-difference 27
XX FT Misc-difference 30 /note= "wild type residue replaced with Ala"
XX FT Misc-difference 30 /note= "wild type residue replaced with Ala"
XX
XX WO200054573-A1.
XX
XX 21-SEP-2000.
XX
XX 15-MAR-2000; 2000WO-US06759.
XX
XX 18-MAR-1999; 99US-0125004.
XX
XX 09-APR-1999; 99US-0289346.
XX

XX (UYNC-) UNIV NORTH CAROLINA STATE.
XX
XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX WPI: 2000-618851/59.
XX
XX Transgenic plants with increased resistance to geminivirus infection
XX comprise a nucleic acid construct containing a nucleic acid sequence
XX encoding a mutant AL1 protein with a mutation in the Rb binding region
XX
XX
XX Disclosure: Page 49; 73pp; English.
XX
XX The present sequence represents a mutant peptide, derived from a
XX geminivirus replication (rep) protein, also known as AL1. AL1 binds
XX double-stranded DNA, catalyses cleavage and ligation of single-stranded
XX DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX protein are used to produce transgenic plants. The mutation in AL1 is
XX present in a ribosome binding region, and expression of mutant AL1
XX protein imparts increased resistance to geminivirus infection in the
XX plant. Mutant AL1 proteins are useful for producing plants having
XX increased resistance or reduced sensitivity to a geminivirus such as
XX tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX virus, tomato leaf curl virus, African cassava mosaic virus, Indian
XX cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX virus, cotton leaf curl virus or beet curly top virus.
XX
XX Sequence 70 AA:
SQ
Query Match 92.0%; Score 335; DB 21; Length 70;
Best Local Similarity 92.9%; Pred. No. 3.8e-35;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 TLVWGEFQVNDGSRAGGCGTSDLLLEALNASSKEALQIIREKIPERYLGFPHNLNSL 60
Db 1 tlvwgeavdvgrsargygcqtndaaaalnasskeaalqilirekipekylfghnlmsl 60
QY 61 DRIFFKTPPEP 70
Db 61 drifdktppep 70
RESULT 9
AAB18678
ID AAB18678 standard; peptide: 70 AA.
XX
XX AAB18678;
XX
XX 22-JAN-2001 (first entry)
XX
XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX
XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX
XX Synthetic.
XX
XX Tomato golden mosaic virus.
XX
XX Key Location/Qualifiers
XX FT Misc-difference 12
XX FT Misc-difference 13
XX FT Misc-difference 15 /note= "wild type residue replaced with Ala"
XX FT Misc-difference 15 /note= "wild type residue replaced with Ala"
XX
XX WO200054573-A1.
XX
XX 21-SEP-2000.
XX

PF 15-MAR-2000; 2000MO-US06759.
XX
PR 18-MAR-1999; 99US-0125004.
PR 09-APR-1999; 99US-0289346.
XX
PA (UYNC-) UNIV NORTH CAROLINA STATE.
XX
PI Hanley-Bowdoin L, Orozco BM, Kong L;
XX
DR WPI; 2000-618851/59.
XX
PI Transgenic plants with increased resistance to geminivirus infection
PT comprise a nucleic acid construct containing a nucleic acid sequence
PT encoding a mutant AL1 protein with a mutation in the Rb binding region
PT
XX
PS Claim 53; Page 42-43; 73pp; English.
XX
CC The present sequence represents a mutant peptide, derived from a
CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
CC protein are used to produce transgenic plants. The mutation in AL1 is
CC present in a ribosome binding region, and expression of mutant AL1
CC protein imparts increased resistance to geminivirus infection in the
CC plant. Mutant AL1 proteins are useful for producing plants having
CC increased resistance or reduced sensitivity to a geminivirus such as
CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
CC virus, cotton leaf curl virus or beet curly top virus.
XX
SQ Sequence 70 AA:

Query Match 91.8%; Score 334; DB 21; Length 70;
Best Local Similarity 91.4%; Pred. No. 5e-35;
Matches 64; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 TLWGEFQVDSRGSCGCTSDNLLLEALNASSKEBALQIREKIPKYLFGFHNLSNL 60
Db 1 TLWGEFQVDSRGSCGCTSDNLLLEALNASSKEBALQIREKIPKYLFGFHNLSNL 60

OY 61 DRIFDKTPEP 70
Db 61 drifdktp 70

RESULT 10
AAB18689
ID AAB18689 standard; peptide; 70 AA.
XX
AC AAB18689;
XX
DT 22-JAN-2001 (first entry)
XX
DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX
KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX
OS Synthetic.
OS Tomato golden mosaic virus.
XX
FH Key Location/Qualifiers
FT Misc-difference 22 /note= "wild type residue replaced with Ala"
FT Misc-difference 23 /note= "wild type residue replaced with Ala"
FT
XX
PN WO200054573-A1.
XX

PD 21-SEP-2000.
XX
PF 15-MAR-2000; 2000MO-US06759.
XX
PR 18-MAR-1999; 99US-0125004.
PR 09-APR-1999; 99US-0289346.
XX
PA (UYNC-) UNIV NORTH CAROLINA STATE.
XX
PI Hanley-Bowdoin L, Orozco BM, Kong L;
XX
DR WPI; 2000-618851/59.
XX
PI Transgenic plants with increased resistance to geminivirus infection
PT comprise a nucleic acid construct containing a nucleic acid sequence
PT encoding a mutant AL1 protein with a mutation in the Rb binding region
PT
XX
PS Disclosure; Page 48-49; 73pp; English.
XX
CC The present sequence represents a mutant peptide, derived from a
CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
CC protein are used to produce transgenic plants. The mutation in AL1 is
CC present in a ribosome binding region, and expression of mutant AL1
CC protein imparts increased resistance to geminivirus infection in the
CC plant. Mutant AL1 proteins are useful for producing plants having
CC increased resistance or reduced sensitivity to a geminivirus such as
CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
CC virus, cotton leaf curl virus or beet curly top virus.
XX
SQ Sequence 70 AA:

Query Match 91.5%; Score 333; DB 21; Length 70;
Best Local Similarity 92.9%; Pred. No. 6.8e-35;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 TLWGEFQVDSRGSCGCTSDNLLLEALNASSKEBALQIREKIPKYLFGFHNLSNL 60
Db 1 TLWGEFQVDSRGSCGCTSDNLLLEALNASSKEBALQIREKIPKYLFGFHNLSNL 60

OY 61 DRIFDKTPEP 70
Db 61 drifdktp 70

RESULT 11
AAB18680
ID AAB18680 standard; peptide; 70 AA.
XX
AC AAB18680;
XX
DT 22-JAN-2001 (first entry)
XX
DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX
KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX
OS Synthetic.
OS Tomato golden mosaic virus.
XX
FH Key Location/Qualifiers
FT Misc-difference 42 /note= "wild type residue replaced with Ala"
FT Misc-difference 43 /note= "wild type residue replaced with Ala"
FT
XX
PN WO200054573-A1.
XX

FT /note= "wild type residue replaced with Ala"
 XX WO200054573-A1.
 PN 21-SEP-2000.
 XX 15-MAR-2000; 2000WO-US06759.
 PF 18-MAR-1999; 99US-0125004.
 PR 09-APR-1999; 99US-0289346.
 XX (UYNC-) UNIV NORTH CAROLINA STATE.
 PA Hanley-Bowdoin L, Orozco BM, Kong L;
 XX WPI: 2000-618851/59.
 DR Transgenic plants with increased resistance to geminivirus infection
 XX comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region
 PT -
 XX Clalm 52; Page 43-44; 73pp; English.
 PS The present sequence represents a mutant peptide, derived from a
 XX geminivirus replication (Rep) protein, also known as AL1. AL1 binds
 CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
 CC protein are used to produce transgenic plants. The mutation in AL1 is
 CC present in a ribosome binding region, and expression of mutant AL1
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant AL1 proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 XX Sequence 70 AA:
 SQ
 Query Match 90.9%; Score 331; DB 21; Length 70;
 Best Local Similarity 91.4%; Pred. No. 1.2e-34;
 Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1 TLVWGFQVYDGRSARGCGQTSNDLLLEALNASSKEBALQIREKIPKYLQFPHNLSNL 60
 DB 1 TLVWGFQVYDGRSARGCGQTSNDLLLEALNASSKEBALQIREKIPKYLQFPHNLSNL 60
 QY 61 DRIFDKTPEP 70
 DB 61 DRIFDKTPEP 70
 RESULT 12
 AAB18691
 ID AAB18691 standard; peptide: 70 AA.
 XX AAB18691;
 AC 22-JAN-2001 (first entry)
 DT 22-JAN-2001 (first entry)
 XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
 DE Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
 KW ribosome binding region; resistance; geminivirus infection.
 XX Synthetic.
 OS Tomato golden mosaic virus.
 XX Key Location/Qualifiers
 FT Misc-difference 34

FT /note= "wild type residue replaced with Ala"
 FT Misc-difference 35
 FT FT /note= "wild type residue replaced with Ala"
 FT Misc-difference 36
 FT /note= "wild type residue replaced with Ala"
 XX WO200054573-A1.
 PN 21-SEP-2000.
 XX 15-MAR-2000; 2000WO-US06759.
 PF 18-MAR-1999; 99US-0125004.
 PR 09-APR-1999; 99US-0289346.
 XX (UYNC-) UNIV NORTH CAROLINA STATE.
 PA Hanley-Bowdoin L, Orozco BM, Kong L;
 XX WPI: 2000-618851/59.
 DR Transgenic plants with increased resistance to geminivirus infection
 XX comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region
 PT -
 XX Disclosure: Page 49; 73pp; English.
 PS The present sequence represents a mutant peptide, derived from a
 XX geminivirus replication (Rep) protein, also known as AL1. AL1 binds
 CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
 CC protein are used to produce transgenic plants. The mutation in AL1 is
 CC present in a ribosome binding region, and expression of mutant AL1
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant AL1 proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 XX Sequence 70 AA:
 SQ
 Query Match 90.9%; Score 331; DB 21; Length 70;
 Best Local Similarity 91.4%; Pred. No. 1.2e-34;
 Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1 TLVWGFQVYDGRSARGCGQTSNDLLLEALNASSKEBALQIREKIPKYLQFPHNLSNL 60
 DB 1 TLVWGFQVYDGRSARGCGQTSNDLLLEALNASSKEBALQIREKIPKYLQFPHNLSNL 60
 QY 61 DRIFDKTPEP 70
 DB 61 DRIFDKTPEP 70
 RESULT 13
 AAB18681
 ID AAB18681 standard; peptide: 70 AA.
 XX AAB18681;
 AC 22-JAN-2001 (first entry)
 DT 22-JAN-2001 (first entry)
 XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
 DE Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
 KW ribosome binding region; resistance; geminivirus infection.
 XX Synthetic.
 OS

```
OS Tomato golden mosaic virus.
XX
FH Key Location/Qualifiers
FT MISC-difference 47 /note= "wild type residue replaced with Ala"
FT MISC-difference 48 /note= "wild type residue replaced with Ala"
FT MISC-difference 49 /note= "wild type residue replaced with Ala"
FT MISC-difference 49 /note= "wild type residue replaced with Ala"
XX
PN MO200054573-A1.
XX
PD 21-SEP-2000.
XX
PF 15-MAR-2000; 2000WO-US06759.
XX
PR 18-MAR-1999; 99US-0125004.
PR 09-APR-1999; 99US-0289346.
XX
PA (UYNC-) UNIV NORTH CAROLINA STATE.
XX
PI Hanley-Bowdoin L, Orozco BM, Kong L;
XX
DR WPI; 2000-618851/59.
XX
PT Transgenic plants with increased resistance to geminivirus infection
PT comprise a nucleic acid construct containing a nucleic acid sequence
PT encoding a mutant AL1 protein with a mutation in the Rb binding region
PT
XX
PS Claim 52; Page 44; 73pp; English.
XX
CC The present sequence represents a mutant peptide, derived from a
CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
CC protein are used to produce transgenic plants. The mutation in AL1 is
CC present in a ribosome binding region, and expression of mutant AL1
CC protein imparts increased resistance to geminivirus infection in the
CC plant. Mutant AL1 proteins are useful for producing plants having
CC increased resistance or reduced sensitivity to a geminivirus such as
CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
CC virus, cotton leaf curl virus or beet curly top virus.
XX
SQ Sequence 70 AA;
XX
XX
Query Match 90.1%; Score 328; DB 21; Length 70;
Best Local Similarity 91.4%; Pred. No. 2.9e-34;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
XX
QY 1 TLVWGEFQVYDGNRARGCGCOTSDNLLLEALNASSKEBALQIIREKIPKYLFPFHNLNSNL 60
Db 1 tlwgefgvdygrsargcgctsndaaaealnasskeaalqirekipekylfghnl 60
XX
QY 61 DRIFDKTPEP 70
Db 61 drifdktp 70
XX
RESULT 14
AAB18683
ID AAB18683 standard; peptide: 70 AA.
XX
AC AAB18683;
XX
DT 22-JAN-2001 (first entry)
XX
DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX
```

```
KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
KM ribosome binding region; resistance; geminivirus infection.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT MISC-difference 59 /note= "wild type residue replaced with Ala"
FT MISC-difference 61 /note= "wild type residue replaced with Ala"
FT MISC-difference 61 /note= "wild type residue replaced with Ala"
FT MISC-difference 62 /note= "wild type residue replaced with Ala"
XX
PN MO200054573-A1.
XX
PD 21-SEP-2000.
XX
PF 15-MAR-2000; 2000WO-US06759.
XX
PR 18-MAR-1999; 99US-0125004.
PR 09-APR-1999; 99US-0289346.
XX
PA (UYNC-) UNIV NORTH CAROLINA STATE.
XX
PI Hanley-Bowdoin L, Orozco BM, Kong L;
XX
DR WPI; 2000-618851/59.
XX
PT Transgenic plants with increased resistance to geminivirus infection
PT comprise a nucleic acid construct containing a nucleic acid sequence
PT encoding a mutant AL1 protein with a mutation in the Rb binding region
PT
XX
PS Claim 53; Page 45; 73pp; English.
XX
CC The present sequence represents a mutant peptide, derived from a
CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
CC protein are used to produce transgenic plants. The mutation in AL1 is
CC present in a ribosome binding region, and expression of mutant AL1
CC protein imparts increased resistance to geminivirus infection in the
CC plant. Mutant AL1 proteins are useful for producing plants having
CC increased resistance or reduced sensitivity to a geminivirus such as
CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
CC virus, cotton leaf curl virus or beet curly top virus.
XX
SQ Sequence 70 AA;
XX
XX
Query Match 89.8%; Score 327; DB 21; Length 70;
Best Local Similarity 91.4%; Pred. No. 3.9e-34;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
XX
QY 1 TLVWGEFQVYDGNRARGCGCOTSDNLLLEALNASSKEBALQIIREKIPKYLFPFHNLNSNL 60
Db 1 tlwgefgvdygrsargcgctsndaaaealnasskeaalqirekipekylfghnl 60
XX
QY 61 DRIFDKTPEP 70
Db 61 aalifdktp 70
XX
RESULT 15
AAB18682
ID AAB18682 standard; peptide: 70 AA.
XX
AC AAB18682;
XX
```

Job time: 155 sec

```

DT 22-JAN-2001 (first entry)
XX
DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX
KW Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX
OS Synthetic.
XX Tomato golden mosaic virus.
XX
FH Key Location/Qualifiers
FT Misc-difference 52 /note= "wild type residue replaced with Ala"
FT Misc-difference 54 /note= "wild type residue replaced with Ala"
FT Misc-difference 55 /note= "wild type residue replaced with Ala"
XX
XX WO200054573-A1.
XX
XX 21-SEP-2000.
XX
XX 15-MAR-2000; 2000WO-US06759.
XX
XX 18-MAR-1999; 99US-0125004.
XX 09-APR-1999; 99US-0289346.
XX
XX (UWNC-) UNIV NORTH CAROLINA STATE.
XX
XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX
XX WPI: 2000-618851/59.
XX
XX Transgenic plants with increased resistance to geminivirus infection
XX comprise a nucleic acid construct containing a nucleic acid sequence
XX encoding a mutant AL1 protein with a mutation in the Rb binding region
XX
XX
XX Claim 53; Page 44-45; 73pp; English.
XX
XX The present sequence represents a mutant peptide, derived from a
XX geminivirus replication (Rep) protein, also known as AL1. AL1 binds
XX double-stranded DNA, catalyses cleavage and ligation of single-stranded
XX DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX protein are used to produce transgenic plants. The mutation in AL1 is
XX present in a ribosome binding region, and expression of mutant AL1
XX protein imparts increased resistance to geminivirus infection in the
XX plant. Mutant AL1 proteins are useful for producing plants having
XX increased resistance or reduced sensitivity to a geminivirus such as
XX tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX virus, tomato leaf curl virus, African cassava mosaic virus, Indian
XX cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX virus, cotton leaf curl virus or beet curly top virus.
XX
XX
XX Sequence 70 AA:

```

```

Query Match      89.3%; Score 325; DB 21; Length 70;
Best local Similarity 91.4%; Pred. No. 7e-34;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSRGSGCOTSDLLLEALNASSKEEALQIIIRKRIPEKYLQFPHNLSNL 60
   |||
Db 1 tlvwgefydvdsrsgcotsndlllealnasskeecalgiirekipekylfafalnsl 60
   |||

QY 61 DRIFDKTPEP 70
   |||
Db 61 drifdktppep 70
   |||

```


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OM protein - protein search, using sw model

Run on: January 3, 2002, 15:40:12 ; Search time 72.79 seconds

(without alignments)
73.255 Million cell updates/sec

Title: US-09-289-346A-10

Perfect score: 364
Sequence: 1 TLVWGEFQVDGRSARGGCQT.....FGPHNLSNLDRIPTKPEP 70

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	349	95.9	352	1 OQCVC1	AL1 protein - toma
2	249	68.4	361	1 OQCVC1	AL1 protein - toma
3	242	66.5	358	1 S07594	hypothetical prote
4	235	64.6	362	1 JQ1887	AL1 protein - toma
5	228	62.6	349	2 JQ2300	replicase - pepper
6	228	62.6	349	2 S31875	AL1 protein - pepp
7	228	62.6	359	2 S39211	gene C1 protein -
8	221	60.7	359	2 S22593	hypothetical prote
9	220	60.4	355	1 OQCVC1	AV1 protein - abut
10	218	59.9	351	2 JQ2327	AL1 protein - toma
11	217	59.6	358	1 JQ1870	AL1 protein - toma
12	217	59.6	385	2 S28360	AL1 protein - toma
13	215	59.1	359	2 S39235	gene C1 protein -
14	208	57.1	360	2 S59885	replication-associ
15	206	56.6	357	1 OQCVC1	AL1 protein - toma
16	138	37.9	131	2 S4059	AC1 protein (clone
17	125	34.3	347	1 OQCVC1	AL1 protein - toma
18	64	17.6	587	1 JQ1419	FC gamma (19g) rec
19	63.5	17.4	1229	2 T48959	kinesin-like prote
20	63	17.3	343	2 S6136	probable enzyme yj
21	63	17.3	343	2 S55595	hypothetical prote
22	62	17.0	295	2 D42452	CI protein - tobac
23	62	17.0	329	2 D85956	hypothetical prote
24	62	17.0	416	2 A82892	hypothetical prote
25	61.5	16.9	333	2 B42476	hypothetical prote
26	61.5	16.9	481	2 A70091	probable phosphos
27	61.5	16.9	1279	2 E64709	type IIS restricti
28	61	16.8	555	2 C45868	glycerol-3-phospha
29	61	16.8	771	2 B38252	granulocyte colony

30	61	16.8	783	2 JH0329	granulocyte colony
31	61	16.8	863	2 C38252	granulocyte colony
32	60.5	16.6	447	2 T12544	hypothetical prote
33	60.5	16.6	1792	2 T13939	myosin V - fruit f
34	60	16.5	247	2 H86844	glutamine ABC tran
35	60	16.5	470	2 T46814	gamma-aminobutyrat
36	60	16.5	799	2 T48889	serine/threonine p
37	60	16.5	1117	2 T14891	telomerase (EC 2.7
38	60	16.5	1265	2 T02131	hypothetical prote
39	59.5	16.3	79	1 A58656	adipokinetic hormo
40	59.5	16.3	210	2 T05021	hypothetical prote
41	59.5	16.3	388	2 C69196	hypothetical prote
42	59.5	16.3	545	2 E85212	hypothetical prote
43	59.5	16.3	546	2 A69484	hypothetical prote
44	59	16.2	215	2 G85710	unknown protein en
45	59	16.2	373	2 A71690	hypothetical prote

ALIGNMENTS

```

RESULT 1
OQCVC1
AL1 protein - tomato golden mosaic virus
C:Species: tomato golden mosaic virus
A:Note: host Nicotiana sp. (tobacco)
C:Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 08-Apr-1994
C:Accession: A04170
R:Hamilton, W.D.O.; Stein, V.E.; Coutts, R.H.A.; Buck, K.W.
EMBO J. 3, 2197-2205, 1984
A:Title: Complete nucleotide sequence of the infectious cloned DNA components of toma
A:Reference number: A04163
A:Accession: A04170
A:Molecule type: DNA
A:Residues: 1-352 <HAW>
C:Comment: The genome consists of two circular, single-stranded DNA components, DNA A
C:Genetics:
A:Map position: segment A
C:Superfamily: tomato golden mosaic virus, AL1 protein

Query Match          95.9%; Score 349; DB 1; Length 352;
Best Local Similarity 95.7%; Pred. No. 2e-31; Indels 0; Gaps 0;
Matches 67; Conservative 0; Mismatches 3;

QY 1 TLVWGEFQVDGRSARGGCQTSNDLLEALNASSKEBALQIREKIPKYLFGPHNLSNL 60
    |||||||
DB 111 TLVWGEFQVDGRSARGGCQTSNDAAEALNASSKEBALQIREKIPKYLFGPHNLSNL 170
QY 61 DRIFDKTPEP 70
    |||||||
DB 171 DRIFDKTPEP 180

RESULT 2
OQCVC1
AL1 protein - potato yellow mosaic virus (isolate Venezuela)
C:Species: potato yellow mosaic virus
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Jun-2000
C:Accession: J00364
R:Coutts, R.H.A.; Coffin, R.S.; Roberts, E.J.F.; Hamilton, W.D.O.
J. Gen. Virol. 72, 1515-1520, 1991
A:Title: The nucleotide sequence of the infectious cloned DNA components of potato ye
A:Reference number: J00362; MUID: 91311403
A:Accession: J00364
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-361 <COU>
A:Cross-references: GB:D00940; MID:g222458; PIDN:BA00782.1; PID:g222459
C:Genetics:
A:Map position: segment A
C:Superfamily: tomato golden mosaic virus, AL1 protein

```

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OM protein - protein search, using sw model

Run on: January 3, 2002, 15:57:18 ; Search time 43.68 Seconds

(without alignments)
58.758 Million cell updates/sec

Title: US-09-289-346A-10

Perfect score: 364
Sequence: 1 TLWGEFQVYDGRSARGGCGT.....FQHNLSNDRIFDKTPRP 70

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 3664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Prod. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	349	95.9	352	1 VAL1_TGMV	P03567 tomato gold
2	249	66.4	361	1 VAL1_PYMV	P27558 tomato yell
3	242	66.5	358	1 VAL1_CLVK	P14982 cassava lat
4	242	66.5	358	1 VAL1_CLVN	P14972 cassava lat
5	235	64.6	362	1 VAL1_TYLC	P36279 tomato yell
6	228	62.6	349	1 VAL1_PHV	Q06823 pepper hus
7	228	62.6	359	1 VAL1_TYLCU	P38609 tomato yell
8	221	60.7	353	1 VAL1_BGMV	P05175 bean golden
9	221	60.7	359	1 VAL1_TYLCM	P27260 tomato yell
10	220	60.4	355	1 VAL1_ABMV	P21947 abutilon mo
11	217	59.6	358	1 VAL1_BCTV	P14991 beet curly
12	217	59.6	361	1 VAL1_TMOV	Q06657 tomato molt
13	206	56.6	357	1 VAL1_TYLCV	P27259 tomato yell
14	125	34.3	347	1 VAL1_SLV	P29048 squash leaf
15	63	17.3	342	1 RSMC_ECOLI	P39406 escherichia
16	62	17.0	295	1 VAL1_TYDVA	P31617 tobacco yell
17	62	17.0	387	1 YAPF_RHISN	P55615 rhizobium s
18	61	16.8	555	1 GLPD_BACSU	P18158 bacillus su
19	61	16.8	836	1 GCSR_HUMAN	Q09062 homo sapien
20	60.5	16.6	447	1 TBL2_HUMAN	Q09493 homo sapien
21	60	16.5	470	1 RBSA_RHIME	Q02372 rhizobium m
22	60	16.5	509	1 CA43_DROME	Q09857 drosophila
23	60	16.5	799	1 AFSK_STRCO	P54741 streptomyc
24	60	16.5	807	1 AFSK_STRGR	P54742 streptomyc
25	60	16.3	1117	1 TERT_TETTH	O77448 tetrahymena
26	59.5	16.3	79	1 AKHD_DROME	P17945 drosophila
27	58.5	16.1	323	1 VAL1_PASVY	Q00338 pauticum str
28	58.5	16.1	397	1 METL_RAT	P13444 rattus norv
29	58.5	16.1	1610	1 CCAD_MESAU	Q09244 mesocricetu
30	58.5	16.1	2161	1 CCAD_HUMAN	Q01668 homo sapien
31	58.5	16.1	2203	1 CCAD_RAT	P27732 rattus norv
32	58	15.9	256	1 YKJ9_YEAST	P34247 saccharomyc
33	58	15.9	354	1 CARA_METUA	Q58425 methanococc

ALIGNMENTS

34	58	15.9	543	1	NFL_HUMAN	P07196 homo sapien
35	58	15.9	1287	1	SK12_YEAST	P35207 saccharomyc
36	57	15.7	784	1	LON_RICER	Q92d92 rickettsia
37	57	15.7	970	1	DA81_YEAST	P21657 saccharomyc
38	57	15.7	1517	1	RPOC_CAMDE	Q9p130 campylobact
39	56.5	15.5	266	1	ETFB_MYCLE	Q33095 mycobacteri
40	56.5	15.5	266	1	ETFB_MYCTU	O53276 mycobacteri
41	56.5	15.5	395	1	METL_HUMAN	Q00266 homo sapien
42	56.5	15.5	1026	1	MY1B_DROME	Q23979 drosophila
43	56.5	15.5	1042	1	TY1B_METUA	Q60295 methanococc
44	56	15.4	247	1	YCP4_YEAST	P25349 saccharomyc
45	56	15.4	299	1	Y175_HELPY	P56112 helicobacte

RESULT 1	VAL1_TGMV	STANDARD:	PRT:	352 AA.
ID	VAL1_TGMV			
AC	P03567:			
DT	21-JUL-1986 (Rel. 01, Created)			
DR	21-JUL-1986 (Rel. 01, Last sequence update)			
DI	01-JUN-1994 (Rel. 29, Last annotation update)			
DE	ALI PROTEIN.			
GN	ACL.			
OS	Tomato golden mosaic virus (TGMV).			
OC	Viruses; ssDNA viruses; Geminiviridae; Begomovirus.			
OX	NCBI_TaxID=10831;			
RM	[1]			
RP	SEQUENCE FROM N.A.			
RA	Hamilton W.D.O., Stein V.E., Coutts R.H.A., Buck K.W.;			
RT	*Complete nucleotide sequence of the infectious cloned DNA components			
RT	of tomato golden mosaic virus: potential coding regions and regulatory			
RT	sequences.*;			
RL	EMBO J. 3:2197-2205(1984).			
CC	-1 SIMILARITY: BELONGS TO GEMINIVIRUSES ALL PROTEIN FAMILY.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@sib-sib.ch).			
CC	-----			
CC	EMBL: R02029; -; NOT_ANNOTATED_CDS.			
CC	PIR: A04170; OOCVLI.			
CC	Interpro: IPR001191; Geminl_ALI.			
CC	DR Pfam: PF00799; Geminl_ALI; 1.			
CC	DR PRINTS: PR00227; GEMCOATL1.			
CC	DR PRINTS: PR00228; GEMCOATL1.			
CC	DR Prodom: PD000736; Geminl_ALI; 1.			
CC	ATP-binding. 223			
CC	FT NP_BIND 223			
CC	SEQUENCE 352 AA; 40332 MW; C33C938E9644B4A4 CRC64;			

Query Match	95.9%;	Score 349;	DB 1;	Length 352;
Best local Similarity	95.7%;	Pred. No. 1.5e-31;		
Matches 67;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;

OY	1	TLWGEFQVYDGRSARGGCGTNDLLEALNASSKEALDIIRKIPKTLFQHNLSNL 60
DB	111	TLWGEFQVYDGRSARGGCGTSDAAEALNASSKEALDIIRKIPKTLFQHNLSNL 170

OY	61	DRIFDKTPRP 70
DB	171	DRIFDKTPRP 180

RESULT 2	VAL1_PYMV
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```

ID VAL1_P1WV STANDARD; PRT; 361 AA.
AC P27258;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE AL1 PROTEIN.
OS Potato yellow mosaic virus (isolate Venezuela).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
ON NCBI_TaxID=10828;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91311403; PubMed=1856690;
RA Coutts R.H.A., Coffin R.S., Roberts E.J.F., Hamilton W.D.O.;
RT "The nucleotide sequence of the infectious cloned DNA components of
RT potato yellow mosaic virus."
RL J. Gen. Virol. 72:1515-1520(1991).
CC -1 SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; D00940; BAA00782.1; -.
CC DR PIR; J0364; QOCVPT.
CC DR InterPro; IPR001191; Gemin1_AL1.
CC DR Pfam; PF00799; Gemin1_AL1.
CC DR PRINTS; PR00227; GEMCOATL1.
CC DR PRINTS; PR00228; GEMCOATL1.
CC DR ProDom; PD000736; Gemin1_AL1; 1.
CC ATP-Binding. 222
CC KW NP_BIND. 229
CC FT SEQUENCE 361 AA; 40850 MW; 5627A3BF1264583 CRC64;
SQ

```

Query Match 68.4%; Score 249; DB 1; Length 361;
 Best Local Similarity 66.7%; Pred. No. 2e-20;
 Matches 46; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

```

QY 1 TLWGEFQVDSRGSGCGTSDLLLEALNASSKEEALQIRKIPKYLFOFHNSNL 60
   1: |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 110 TIEWGTFQIDGRSARGGQGVNDAAEALNSGTREKAMKTIKREKFLFYHNSCNL 169
   1: |||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 DRFDKTPP 69
   1: |||||:|||||:|||||:|||||:|||||:|||||:
DB 170 DRIFMAPE 178

```

RESULT 3
 VAL1_CLVX STANDARD; PRT; 358 AA.
 AC P14982;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE AL1 PROTEIN (40.4 KDA PROTEIN).
 GN AC1.
 OS Cassava latent virus (strain West Kenya 844).
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 ON NCBI_TaxID=10818;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Stanley J., Gay M.R.;
 RT "Nucleotide sequence of cassava latent virus DNA."
 RL Nature 301:260-262(1983).
 CC -1 SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
 CC -----
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 CC -----
 CC EMBL; X17095; CAA34953.1; -.
 CC DR PIR; S07594; S07594.
 CC DR InterPro; IPR001191; Gemin1_AL1.
 CC DR Pfam; PF00799; Gemin1_AL1.
 CC DR PRINTS; PR00227; GEMCOATL1.
 CC DR PRINTS; PR00228; GEMCOATL1.
 CC DR ProDom; PD000736; Gemin1_AL1; 1.
 CC ATP-Binding. 220
 CC KW NP_BIND. 227
 CC FT SEQUENCE 358 AA; 40435 MW; 1DB16B0CB2D5E2C CRC64;
 SQ

```

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CC -----
CC EMBL; J02057; -. NOT_ANNOTATED_CDS.
CC DR InterPro; IPR001191; Gemin1_AL1.
CC DR Pfam; PF00799; Gemin1_AL1; 1.
CC DR PRINTS; PR00227; GEMCOATL1.
CC DR PRINTS; PR00228; GEMCOATL1.
CC DR ProDom; PD000736; Gemin1_AL1; 1.
CC ATP-Binding. 220
CC KW NP_BIND. 227
CC FT SEQUENCE 358 AA; 40346 MW; ED173F753EE93D069 CRC64;
SQ

```

Query Match 66.5%; Score 242; DB 1; Length 358;
 Best Local Similarity 61.4%; Pred. No. 1.2e-19;
 Matches 43; Conservative 13; Mismatches 14; Indels 0; Gaps 0;

```

QY 1 TLWGEFQVDSRGSGCGTSDLLLEALNASSKEEALQIRKIPKYLFOFHNSNL 60
   1: |||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 109 TIEWGTFQIDGRSARGGQGSANDAYAKALNSGSKSALNVIKELVYKDFVLQPHNSNL 168
   1: |||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 DRFDKTPP 70
   1: |||||:|||||:|||||:|||||:|||||:|||||:
DB 169 DRIFQEPAP 178

```

RESULT 4
 VAL1_CLVX STANDARD; PRT; 358 AA.
 AC P14972;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE AL1 PROTEIN (40.4 KDA PROTEIN).
 GN AC1.
 OS Cassava latent virus (strain Nigerian).
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 ON NCBI_TaxID=10819;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90174930; PubMed=2308831;
 RA Morris B., Coates L., Lowe S., Richardson K., Eddy P.;
 RT "Nucleotide sequence of the infectious cloned DNA components of
 RT African cassava mosaic virus (Nigerian strain)."
 RL Nucleic Acids Res. 18:197-198(1990).
 CC -1 SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
 CC -----
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 CC -----
 CC EMBL; X17095; CAA34953.1; -.
 CC DR PIR; S07594; S07594.
 CC DR InterPro; IPR001191; Gemin1_AL1.
 CC DR Pfam; PF00799; Gemin1_AL1.
 CC DR PRINTS; PR00227; GEMCOATL1.
 CC DR PRINTS; PR00228; GEMCOATL1.
 CC DR ProDom; PD000736; Gemin1_AL1; 1.
 CC ATP-Binding. 220
 CC KW NP_BIND. 227
 CC FT SEQUENCE 358 AA; 40435 MW; 1DB16B0CB2D5E2C CRC64;
 SQ

Query Match 66.5%; Score 242; DB 1; Length 358;
 Best Local Similarity 61.4%; Pred. No. 1.2e-19;
 Matches 43; Conservative 13; Mismatches 14; Indels 0; Gaps 0;

```

OY 1 TLWGEFQVDGSRAGCGCOTSDNLLLEALNASSKEBALQIREKIPEKYLQFPHNLSNL 60
DB 109 TLWGEFQVDGSRAGCGCOTSDNLLLEALNASSKEBALQIREKIPEKYLQFPHNLSNL 168
OY 61 DRIPDKTPEP 70
DB 169 DRIPDKTPEP 178

RESULT 5
VAL1_TYLCA STANDARD; PRT; 362 AA.
AC P36279;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE AL1 PROTEIN (C1 PROTEIN).
GN C1.
OS Tomato yellow leaf curl virus (strain Australia) (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=36447;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93139778; PubMed=8423446;
RA Dry I.B., Ridgen J.E., Krake L.R., Mullineaux P.M., Rezaian M.A.;
RT "Nucleotide sequence and genome organization of tomato leaf curl
geminiavirus."
RL J. Gen. Virol. 74:147-151(1993).
CC -1 SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
DR InterPro: IPR001191; Gemini_AL1.
DR Pfam: PF00799; Gemini_AL1.
DR PRINTS: PR00227; GEMCOATLVL.
DR PRODOM: PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP_BIND 221 228 ATP (POTENTIAL).
SQ SEQUENCE 362 AA; 41197 MW; 343E7184B4704098 CRC64;

Query Match 64.6%; Score 235; DB 1; Length 362;
Best Local Similarity 54.1%; Pred. No. 7.2e-19;
Matches 46; Conservative 9; Mismatches 14; Indels 16; Gaps 1;

OY 1 TLWGEFQVDGSRAGCGCOTSDNLLLEALNASSKEBALQIREKIPEKYLQFPHNLSNL 60
DB 110 TLWGEFQVDGSRAGCGCOTSDNLLLEALNASSKEBALQIREKIPEKYLQFPHNLSNL 169
OY 61 DRIPDKTPEP 69
DB 170 DRIPDKTPEP 194

RESULT 6
VAL1_PHVU STANDARD; PRT; 349 AA.
AC 006923;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 PROTEIN.
GN AL1.
OS Pepper huasteco virus (PHV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=28349;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94015007; PubMed=8409944;
RA Torres-Pacheco I., Garzon-Tiznado J.A., Herrera-Estrella L.,
RA Rivera-Bustamante R.F.;
RT "Complete nucleotide sequence of pepper huasteco virus: analysis and
comparison with bipartite geminiviruses."

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RL J. Gen. Virol. 74:2225-2231(1993).
CC -1 SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC -----
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CC -----
DR EMBL: X70418; CAA49856.1;
DR PIR: S31875; S31875.
DR PIR: J02300; J02300.
DR InterPro: IPR001191; Gemini_AL1.
DR Pfam: PF00799; Gemini_AL1.
DR PRINTS: PR00227; GEMCOATLVL.
DR PRODOM: PD000736; Gemini_AL1; 1.
KW ATP-binding.
FT NP_BIND 221 228 ATP (BY SIMILARITY).
SQ SEQUENCE 349 AA; 39722 MW; D5F4E76CD56370F4 CRC64;

Query Match 62.6%; Score 228; DB 1; Length 349;
Best Local Similarity 60.0%; Pred. No. 4.2e-18;
Matches 42; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

OY 1 TLWGEFQVDGSRAGCGCOTSDNLLLEALNASSKEBALQIREKIPEKYLQFPHNLSNL 60
DB 110 TLWGEFQVDGSRAGCGCOTSDNLLLEALNASSKEBALQIREKIPEKYLQFPHNLSNL 169
OY 61 DRIPDKTPEP 70
DB 170 DRIPDKTPEP 179

RESULT 7
VAL1_TYLCA STANDARD; PRT; 359 AA.
AC P38609;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE AL1 PROTEIN (C1 PROTEIN).
GN C1.
OS Tomato yellow leaf curl virus (strain Murcia) (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=37139;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94256836; PubMed=8198442;
RA Norris E., Hidalgo E., Accotto G., Moriones E.;
RT "High similarity among the tomato yellow leaf curl virus isolates
RT from the west Mediterranean basin: the nucleotide sequence of an
RL Arch. Virol. 135:165-170(1994).
CC -1 SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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CC -----
DR EMBL: Z25751; CAA81026.1;
DR PIR: S39211; S39211.
DR InterPro: IPR001191; Gemini_AL1.
DR Pfam: PF00799; Gemini_AL1.
DR PRINTS: PR00227; GEMCOATLVL.

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DR Prodrom; PD000736; Gemini_AL1: 1.
 KW ATP-binding. 221 228 ATP (POTENTIAL).
 SQ SEQUENCE 359 AA; 41065 MW; 2D170A51EF80A3EC CRC64;

Query Match 62.6%; Score 228; DB 1; Length 359;
 Best local Similarity 59.4%; Pred. No. 4.3e-18;
 Matches 41; Conservative 9; Mismatches 19; Indels 0; Gaps 0;

QY 2 LVWGEFQVQGRSARGGCGTSDNLLLEALNASSKEPALQIIRKIPKYLFOFHNLNSND 61
 DB 111 LEMGTQIDGRSARGGCGTANDAYAKAINAGSKSQAADVKEKLPADYVLHFNHNSND 170
 QY 62 RIFDKTPEP 70
 DB 171 RYQVPPAP 179

RESULT 8

VAL1_BGMV STANDARD; PRT; 353 AA.
 AC P05175;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE AL1 PROTEIN (40.2 KDA PROTEIN).
 GN ACL.
 OS Bean golden mosaic virus.
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OX NCBI_TaxID=10839;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Howarth A.J., Caton J., Bossert M., Goodman R.M.;
 RT "Nucleotide sequence of bean golden mosaic virus and a model for gene
 regulation in geminiviruses."
 RL Proc. Natl. Acad. Sci. U.S.A. 82:3572-3576(1985).
 CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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 CC
 CC EMBL: M10070; AAA6318.1;
 DR InterPro: IPR001191; Gemini_AL1.
 DR Pfam: PF00799; Gemini_AL1; 1.
 DR PRINTS: PR00227; GEMCOATFALL.
 DR PRINTS: PR00228; GEMCOATCLVLL.
 DR PRODROM: PD000736; Gemini_AL1; 1.
 KW ATP-binding. 229
 FT NP_BIND
 SQ SEQUENCE 353 AA; 40190 MW; 80FA779DF6029A34 CRC64;

Query Match 60.7%; Score 221; DB 1; Length 353;
 Best local Similarity 60.0%; Pred. No. 2.5e-17;
 Matches 42; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

QY 1 TLVWGEFQVQGRSARGGCGTSDNLLLEALNASSKEPALQIIRKIPKYLFOFHNLNSND 60
 DB 110 TIMMGCPQVQGRSARGGCGSANDSYAKALNADIESALVTILKEQPKDYVLQNHNRNSND 169
 QY 61 RIFDKTPEP 70
 DB 170 ERIFFKVPPEP 179

RESULT 9

VAL1_TYLCM

ID VAL1_TYLCM STANDARD; PRT; 359 AA.
 AC P27260;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE AL1 PROTEIN (CI PROTEIN).
 GN C1.
 OS Tomato yellow leaf curl virus (strain Marmande) (TYLCV).
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OX NCBI_TaxID=10833;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92107660; PubMed=1840676;
 RA Kheyr-Pour A., Bendahmane M., Matzeit V., Accotto G.P., Crespi S.,
 RA Gronenborn B.;
 RT "Tomato yellow leaf curl virus from Sardinia is a
 RT whitefly-transmitted monopartite geminivirus."
 RL Nucleic Acids Res. 19:6763-6769(1991).
 CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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 CC
 CC EMBL: X61153; CAA43466.1;
 DR PIR: S22593; S22593.
 DR InterPro: IPR001191; Gemini_AL1.
 DR Pfam: PF00799; Gemini_AL1; 1.
 DR PRINTS: PR00227; GEMCOATFALL.
 DR PRINTS: PR00228; GEMCOATCLVLL.
 DR PRODROM: PD000736; Gemini_AL1; 1.
 KW ATP-binding. 220
 FT NP_BIND
 SQ SEQUENCE 359 AA; 40733 MW; 9717BA407C93EFA7 CRC64;

Query Match 60.7%; Score 221; DB 1; Length 359;
 Best local Similarity 56.5%; Pred. No. 2.6e-17;
 Matches 39; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

QY 2 LVWGEFQVQGRSARGGCGTSDNLLLEALNASSKEPALQIIRKIPKYLFOFHNLNSND 61
 DB 111 LEMGTQIDGRSARGGCGTANDAYAKAINAGSKSQAADVKEKLPADYVLHFNHNSND 170
 QY 62 RIFDKTPEP 70
 DB 171 KVFQVPPAP 179

RESULT 10

VAL1_ABMV STANDARD; PRT; 355 AA.
 AC P21947;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE AL1 PROTEIN.
 GN ACL.
 OS Abutilon mosaic virus (isolate West India).
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OX NCBI_TaxID=10816;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91020984; PubMed=2219703;
 RA Frischmuth T., Zimmat G., Jeske H.;
 RT "The nucleotide sequence of abutilon mosaic virus reveals prokaryotic
 RT as well as eukaryotic features."
 RL Virology 178:461-468(1990).
 CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.

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 CC -----
 DR EMBL: X15983; -, NOT_ANNOTATED_CDS.
 DR PIR: A36214; OQCVW1.
 DR InterPro: IPR001191; Gemini_AL1.
 DR Pfam: PF00799; Gemini_AL1; 1.
 DR PRINTS: PR00227; GEMCOATCIVL.
 DR PRINTS: PR00228; GEMCOATCIVL.
 DR Prodom: PD000736; Gemini_AL1; 1.
 DR ATP-binding. 221
 KW NP_BIND
 FT SEQUENCE 355 AA; 40257 MW; 16A2CA8A63251E95 CRC64;

Query Match 60.4%; Score 220; DB 1; Length 355;
 Best Local Similarity 58.6%; Pred. No. 3.3e-17;
 Matches 41; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

QY 1 TLWGEFQVDSARGGCGTSDNLLLEALNASSKEBALQIREKIPKYLFGFHNLNSML 60
 DB 110 TLWGEFQVDSARGGCGTSDNLLLEALNASSKEBALQIREKIPKYLFGFHNLNSML 169
 QY 61 DRIFPKTEPP 70
 DB 170 ERIFAKAPEP 179

RESULT 11
 VAL1_BCTV STANDARD; PRT; 358 AA.
 AC P14991;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 01-AUG-1992 (Rel. 23, Last annotation update)
 DE AL1 PROTEIN (40.8 KDA PROTEIN).
 OS Beet curly top virus (BCTV).
 OC Viruses: ssDNA viruses; Geminiviridae; Curtovirus.
 OX NCBI_TaxID=10840;
 RX NCBII_TaxID=10840;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Stanley J., Markham P.G., Callis R.J., Pinner M.S.;
 RT "The nucleotide sequence of an infectious clone of the geminivirus
 RT beet curly top virus."
 RL EMBL J. 5:1761-1767(1986).
 CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.

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 CC -----

DR EMBL: X04144; -, NOT_ANNOTATED_CDS.
 DR InterPro: IPR001191; Gemini_AL1.
 DR Pfam: PF00799; Gemini_AL1; 1.
 DR PRINTS: PR00227; GEMCOATCIVL.
 DR PRINTS: PR00228; GEMCOATCIVL.
 DR Prodom: PD000736; Gemini_AL1; 1.
 DR ATP-binding. 222
 KW NP_BIND
 FT SEQUENCE 358 AA; 40889 MW; 39A45FE3C0B9C333 CRC64;

Query Match 59.6%; Score 217; DB 1; Length 358;

Best Local Similarity 55.7%; Pred. No. 7.2e-17;
 Matches 39; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

QY 1 TLWGEFQVDSARGGCGTSDNLLLEALNASSKEBALQIREKIPKYLFGFHNLNSML 60
 DB 110 TLWGEFQVDSARGGCGTSDNLLLEALNASSKEBALQIREKIPKYLFGFHNLNSML 169
 QY 61 DRIFPKTEPP 70
 DB 170 QKIFQRPDP 179

RESULT 12
 VAL1_TM0V STANDARD; PRT; 361 AA.
 AC O06657;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE AL1 PROTEIN.
 GN AL1.
 OS Tomato mottle virus (isolate Florida) (TM0V).
 OC Viruses: ssDNA viruses; Geminiviridae; Begomovirus.
 OX NCBI_TaxID=36449;
 RX MEDLINE=93107858; PubMed=1469361;
 RA Abouzid A.M., Polston J.E., Hiebert E.;
 RT "The nucleotide sequence of tomato mottle virus, a new geminivirus
 RT isolated from tomatoes in Florida."
 RL J. Gen. Virol. 73:3225-3229(1992).
 CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.

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 CC -----

DR EMBL: L14460; AAC32414.1; -
 DR PIR: J01870; J01870.
 DR InterPro: IPR001191; Gemini_AL1.
 DR Pfam: PF00799; Gemini_AL1; 1.
 DR PRINTS: PR00227; GEMCOATCIVL.
 DR PRINTS: PR00228; GEMCOATCIVL.
 DR Prodom: PD000736; Gemini_AL1; 1.
 KW ATP-binding. 222
 FT NP_BIND
 FT SEQUENCE 361 AA; 40516 MW; 8138B65CEBAC6950 CRC64;

Query Match 59.6%; Score 217; DB 1; Length 361;
 Best Local Similarity 55.7%; Pred. No. 7.2e-17;
 Matches 39; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

QY 1 TLWGEFQVDSARGGCGTSDNLLLEALNASSKEBALQIREKIPKYLFGFHNLNSML 60
 DB 110 TLWGEFQVDSARGGCGTSDNLLLEALNASSKEBALQIREKIPKYLFGFHNLNSML 169
 QY 61 DRIFPKTEPP 70
 DB 170 ERIFAKAPEP 179

RESULT 13
 VAL1_TYLCV STANDARD; PRT; 357 AA.
 AC P27259;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)

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DE AL1 PROTEIN (C1 PROTEIN).
GN C1.
OS Tomato yellow leaf curl virus (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxId=10832;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92024070; PubMed=1926771;
RA Navot N., Pichersky E., Zeidan M., Zamir D., Czosnek H.;
RT "Tomato yellow leaf curl virus: a whitefly-transmitted geminivirus
  with a single genomic component.";
RL Virology 185:151-161(1991).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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CC -----
DR EMBL; X15656; CA933688.1; -
DR PIR; D40779; Q0CVCI.
DR InterPro; IPR001191; Gemin1_AL1.
DR Pfam; PF00799; Gemin1_AL1; 1.
DR PRINTS; PR00227; GEMCOATV.L.
DR PRINTS; PR00228; GEMCOATV.L.
DR ProDom; PD000736; Gemin1_AL1; 1.
KW ATP-binding.
FT NP_BIND 219 226 ATP (POTENTIAL).
SQ SEQUENCE 357 AA; 40678 MW; 939AB68E1AB3B2A7 CRC64;

Query Match
Best Local Similarity 56.6%; Score 206; DB 1; Length 357;
Matches 39; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

OY 4 MGFFOYDGRSGRCGCTNSDNLLEALNASSKEPALQIREKIEKYLFOFHNSNLDRI 63
DB 111 FGVSQIDGRSGRCGOSANDAYALNASSKEPALNILEKAPKDYITLOFHNLSNLDRI 170

OY 64 F 64
DB 171 F 171

RESULT 14
VAL1_SLICV STANDARD; PRT; 347 AA.
ID P29048;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE AL1 PROTEIN.
OS Squash leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxId=10829;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91082449; PubMed=1984668;
RA Lazartowicz S.G., Jazdzins I.B.;
RT "Infectivity and complete nucleotide sequence of the cloned genomic
  components of a bipartite squash leaf curl geminivirus with a broad
  host range phenotype.";
RL Virology 160:58-69(1991).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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CC -----
DR EMBL; M38183; AAC32410.1; ALT_INIT.
DR PIR; C36785; Q0CVS1.
DR InterPro; IPR001191; Gemin1_AL1.
DR Pfam; PF00799; Gemin1_AL1; 1.
DR PRINTS; PR00227; GEMCOATV.L.
DR PRINTS; PR00228; GEMCOATV.L.
DR ProDom; PD000736; Gemin1_AL1; 1.
KW ATP-binding.
FT NP_BIND 218 225 ATP (POTENTIAL).
SQ SEQUENCE 347 AA; 39110 MW; AFDAEBDE12110E CRC64;

Query Match
Best Local Similarity 34.3%; Score 125; DB 1; Length 347;
Matches 25; Conservative 15; Mismatches 22; Indels 4; Gaps 1;

OY 5 GFQFVYDGRSGRCGCTNSDNLLEALNASSKEPALQIREKIEKYLFOFHNSNLDRI 64
DB 116 GQKYVSG-----GSKSKNDYHNNAVAGSAGELDITIKAGDKRTFLVYHNLLANVERLF 171

OY 65 DKTRPP 70
DB 172 QKPPPP 177

RESULT 15
RSMC_ECOLI STANDARD; PRT; 342 AA.
ID P39406;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE RIBOSOMAL RNA SMALL SUBUNIT METHYLTRANSFERASE C (EC 2.1.1.52) (RNA
  DE (GUANINE-N2)-METHYLTRANSFERASE) (16S RNA M2G1207 METHYLTRANSFERASE).
GN RSMC OR B4371.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxId=562;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=K12 / MG1655;
RX MEDLINE=95334362; PubMed=7610040;
RA Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
  Blattner F.R.;
RT "Analysis of the Escherichia coli genome VI: DNA sequence of the
  region from 92.8 through 100 minutes.";
RL Nucleic Acids Res. 23:2105-2119(1995).
RN [2]
RP SEQUENCE OF 1-19, AND CHARACTERIZATION.
RX MEDLINE=99091632; PubMed=9873033;
RA Tschirne J.S., Nurse K., Poplenick P., Ofengand J.;
RT "Purification, cloning, and characterization of the 16S RNA m2G1207
  RT methyltransferase from Escherichia coli.";
RL J. Biol. Chem. 274:924-929(1999).
CC -1- FUNCTION: SPECIFICALLY METHYLATES THE GUANOSINE IN POSITION 1207
  OF 16S RNA IN THE 30S PARTICLE.
CC -1- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + RNA = S-ADENOSYL-L-
  HOMOCYSTEINE + RNA CONTAINING N2-METHYLGUANINE.
CC -1- COFACTOR: REQUIRES MAGNESIUM FOR ACTIVITY.
CC -1- SIMILARITY: BELONGS TO THE METHYLTRANSFERASE SUPERFAMILY. RSMC
  SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).

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CC -----
 DR EMBL: U14003: AAA97267.1: -.
 DR EMBL: AE000507: AAC77324.1: -.
 DR EcoGene: EG12596: rsmc.
 DR InterPro: IPR002052: N6_Mtase.
 DR InterPro: IPR000051: SAM_bind.
 DR PROSITE: PS00092: N6_MTASE; UNKNOWN_1.
 KW rRNA processing; Transferase; Methyltransferase; Magnesium;
 FT Complete proteome.
 FT INIT_MET 0
 SQ SEQUENCE 342 AA; 37493 MM; C7A318155700302D CRC64;

Query Match 17.3%; Score 63; DB 1; Length 342;
 Best Local Similarity 31.1%; Pred. No. 9;
 Matches 14; Conservative 7; Mismatches 16; Indels 8; Gaps 1;

QY 4 WGEFOVDGRS-----ARGGCGQTSNDLLLEALNASSKREALQI 40
 |||: ||| : | | : ||| : | : | :
 DB 158 WGEYSVDGILTVKTLPGVFSRDGIDVGSQLLSTLTFPHRTKGKVIDV 202

Search completed: January 3, 2002, 15:57:18
 Job time: 1104 sec

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009727
ID 009727 PRELIMINARY; PRT; 226 AA.
AC 009727;
DT 01-JUL-1997 (TREMblrel. 04, Created)
DT 01-JUL-1997 (TREMblrel. 04, last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, last annotation update)
DE REP PROTEIN (FRAGMENT).
GN REP.
OS leonurus mosaic virus.
OC viruses: ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=58177;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LEMV- BRAZIL 1;
RA Faria J.C., Maxwell D.P.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: U92532; AAB5157.1; -.
DR InterPro: IPR001191; Geminl_AL1.
DR Pfam: PF00799; Geminl_AL1.
DR PRINTS: PR00227; GEMCOATL1.
DR ProDom: PD000736; Geminl_AL1.
FT NON_TER 226 226
SQ SEQUENCE 226 AA; 25617 MW; 73CDB6E766083FC5 CRC64;

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Query Match 77.2%; Score 281; DB 12; Length 226;
Best Local Similarity 77.1%; Pred. No. 7.7e-23;
Matches 54; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

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QY 1 TLVWGEFQVQGRSARGCGCTSNLLEALNASSKEEALQIREKIPKYLFOFHNLNSNL 60
   1: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 111 TIEWGEFQVQGRSARGCGCTVNDAAAEALNAPDKRTALQIIRKLEPKYLFQFHNLNSNL 170
   1: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 DRIFDKTPEP 70
   1: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 171 DRIFAKAPEP 180

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RESULT 3
Q9WHF6 PRELIMINARY; PRT; 226 AA.
ID Q9WHF6;
AC Q9WHF6;
DT 01-NOV-1999 (TREMblrel. 12, Created)
DT 01-NOV-1999 (TREMblrel. 12, last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, last annotation update)
DE REPLICATION-ASSOCIATED PROTEIN (FRAGMENT).
GN REP.
OS tomato mild mottle geminivirus.
OC viruses: ssDNA viruses; Geminiviridae; Unclassified Geminiviridae.
OX NCBI_TaxID=92943;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HN96-H5KW;
RA Nakha M.K., Mejia L., Ramirez P., Karkashian J.P., Doyle M.M.,
RA Maxwell D.P.;
RT "Molecular characterization and DNA-based detection methods for
RT vegetable-infecting geminiviruses in Central America.";
RT Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: A131071; AAD3471.1; -.
DR InterPro: IPR001191; Geminl_AL1.
DR Pfam: PF00799; Geminl_AL1.
DR PRINTS: PR00227; GEMCOATL1.
DR ProDom: PD000736; Geminl_AL1.
FT NON_TER 226 226
SQ SEQUENCE 226 AA; 25941 MW; 2EA4116712871A23 CRC64;

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Query Match 77.2%; Score 281; DB 12; Length 226;
Best Local Similarity 72.9%; Pred. No. 7.7e-23;
Matches 51; Conservative 12; Mismatches 7; Indels 0; Gaps 0;
QY 1 TLVWGEFQVQGRSARGCGCTSNLLEALNASSKEEALQIREKIPKYLFOFHNLNSNL 60
   1: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Db 111 TIEWGEFQIDGRSARGCGCTANDAAAEALNASSKEEAMRIKELPKRFLQYHNLSNL 170
QY 61 DRIFDKTPEP 70
   1: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 171 DRIFAKAPEP 180

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RESULT 4
Q67574 PRELIMINARY; PRT; 361 AA.
ID Q67574;
AC Q67574;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, last annotation update)
DE PUTATIVE REPLICATIVE PROTEIN.
GN AL1.
OS Bean golden mosaic virus.
OC viruses: ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10839;
RN [1]
RP SEQUENCE FROM N.A.
RA Gilbertson R.L., Faria J.C., Hanson S.F., Morales F.J., Ahlquist P.G.,
RA Maxwell D.P., Russell D.R.;
RL Phytopathology 81:980-985(1991).
RN [2]
RP SEQUENCE FROM N.A.
RA Gilbertson R.L., Hidayat S.H., Martinez R.T., Leong S.A., Faria J.C.,
RA Morales F.J., Maxwell D.P.;
RL Plant Dis. 75:336-342(1991).
RN [3]
RP SEQUENCE FROM N.A.
RA Gilbertson R.L., Faria J.C., Ahlquist P.G., Maxwell D.P.;
RL Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.
DR EMBL: M88686; AAA46312.1; -.
DR InterPro: IPR001191; Geminl_AL1.
DR Pfam: PF00799; Geminl_AL1.
DR PRINTS: PR00227; GEMCOATL1.
DR ProDom: PD000736; Geminl_AL1.
SQ SEQUENCE 361 AA; 41041 MW; 0094C7ACAF06E788 CRC64;

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Query Match 77.2%; Score 281; DB 12; Length 361;
Best Local Similarity 77.6%; Pred. No. 1.3e-22;
Matches 52; Conservative 8; Mismatches 7; Indels 0; Gaps 0;
QY 4 WEEFQVQGRSARGCGCTSNLLEALNASSKEEALQIREKIPKYLFOFHNLNSNLDR1 63
   1: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 113 WGFQVQGRSARGCGCTANDAAAEALNASSKEEAMQIREKLPKFLQYHNLSNLDR1 172
   1: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 64 FDKTPEP 70
   1: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 173 FTKAPDP 179

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RESULT 5
Q9QDB1 PRELIMINARY; PRT; 225 AA.
ID Q9QDB1;
AC Q9QDB1;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, last annotation update)
DE REPLICATION ASSOCIATED PROTEIN (FRAGMENT).
GN REP.
OS cowpea golden mosaic geminivirus.
OC viruses: ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=69263;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CGW-BR;
RA Faria J.C.;
RT "Partial nucleotide sequence of cowpea golden mosaic geminivirus from
RT Brazil.";
SQ Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

```

DR EMBL: AF188708: AAF06318.1: -
 DR InterPro: IPR001191: Gemini_AL1.
 DR Pfam: PF00799: Gemini_AL1; 1.
 DR PRINTS: PR00227: GEMCOATAL1.
 DR ProDom: PD000736: Gemini_AL1; 1.
 DR NON_TER 225 225
 FT SEQUENCE 225 AA: 25766 MW: 1089CB6BDBD15B5D CRC64;

Query Match 76.6%; Score 279; DB 12; Length 225;
 Best Local Similarity 77.6%; Pred. No. 1.3e-22;
 Matches 52; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 4 MGFEQVDGRSARGCGCOTSDNLLLEALNASSKEFALQIREKIPKYLFOFHNLNSML 63
 DB 113 WGFQIDGRSARGGQOTANDAAEALNASSKEFALQIREKIPKYLFOFHNLNSML 172
 QY 64 FDKTPEP 70
 DB 173 FKKTPEP 179

RESULT 6
 Q9ELT8 PRELIMINARY: PRT; 314 AA.
 AC Q9ELT8:
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE REPLICATION ASSOCIATION PROTEIN.
 GN AC1.
 OS sweet potato leaf curl virus.
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OX NCBI_TaxID=100755;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lotrakul P., Valverde R.A., Clark C.A., Sim J., De la Torre R.;
 RT "Detection of a geminivirus infecting sweet potato in the United
 States.";
 RL Plant Dis. 82:1253-1257(1998).
 RN [2]
 RN SEQUENCE FROM N.A.
 RP Lotrakul P., Valverde R.A.;
 RL Submitted (Jul-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF288227; AAG01006.1;
 DR InterPro: IPR001191; Gemini_AL1.
 DR Pfam: PF00799; Gemini_AL1; 1.
 DR PRINTS: PR00227; GEMCOATAL1.
 DR ProDom: PD000736; Gemini_AL1; 1.
 DR NON_TER 314 AA: 35153 MW: 686220613046943F CRC64;
 SQ SEQUENCE 314 AA: 35153 MW: 686220613046943F CRC64;

Query Match 76.1%; Score 277; DB 12; Length 314;
 Best Local Similarity 79.4%; Pred. No. 3e-22;
 Matches 54; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 1 TLWGEFQVDGRSARGCGCOTSDNLLLEALNASSKEFALQIREKIPKYLFOFHNLNSML 60
 DB 110 TITWGEFQVDGRSARGGQOTANDAAEALNASSKEFALQIREKIPKYLFOFHNLNSML 169
 QY 61 DRIFDKTP 68
 DB 170 DRIFSKPP 177

RESULT 7
 Q9QSS5 PRELIMINARY: PRT; 364 AA.
 AC Q9QSS5:
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE REPLICATION INITIATION PROTEIN AC1.

GN AC1.
 OS sweet potato leaf curl virus.
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OX NCBI_TaxID=100755;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lotrakul P., Valverde R.A., Clark C.A., Sim J., De la Torre R.;
 RT "Detection of a geminivirus infecting sweet potato in the United
 States.";
 RL Plant Dis. 82:1253-1257(1998).
 DR EMBL: AF104036; AAD47173.1; -
 DR InterPro: IPR001191; Gemini_AL1.
 DR Pfam: PF00799; Gemini_AL1; 1.
 DR PRINTS: PR00227; GEMCOATAL1.
 DR ProDom: PD000736; Gemini_AL1; 1.
 DR NON_TER 364 AA: 40680 MW: 5F79752431A09D6E CRC64;
 SQ SEQUENCE 364 AA: 40680 MW: 5F79752431A09D6E CRC64;

Query Match 76.1%; Score 277; DB 12; Length 364;
 Best Local Similarity 79.4%; Pred. No. 3.5e-22;
 Matches 54; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 1 TLWGEFQVDGRSARGCGCOTSDNLLLEALNASSKEFALQIREKIPKYLFOFHNLNSML 60
 DB 110 TITWGEFQVDGRSARGGQOTANDAAEALNASSKEFALQIREKIPKYLFOFHNLNSML 169
 QY 61 DRIFDKTP 68
 DB 170 DRIFSKPP 177

RESULT 8
 Q98693 PRELIMINARY: PRT; 185 AA.
 AC Q98693:
 DT 01-FEB-1997 (TREMBlrel. 02, Created)
 DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE REP PROTEIN (FRAGMENT).
 GN AC1.
 OS sida golden mosaic virus.
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OX NCBI_TaxID=51034;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=JAMAICA;
 RA Roye M.E., McLoughlin W.A., Nakhla N.K., Maxwell D.P.;
 RL Plant Dis. 81:1251-1258(1997).
 DR EMBL: U67926; AAB97865.1; -
 DR InterPro: IPR001191; Gemini_AL1.
 DR Pfam: PF00799; Gemini_AL1; 1.
 DR PRINTS: PR00227; GEMCOATAL1.
 DR ProDom: PD000736; Gemini_AL1; 1.
 DR NON_TER 185 185
 FT SEQUENCE 185 AA: 20975 MW: 3913850A025A5BE1 CRC64;
 SQ SEQUENCE 185 AA: 20975 MW: 3913850A025A5BE1 CRC64;

Query Match 75.3%; Score 274; DB 12; Length 185;
 Best Local Similarity 70.0%; Pred. No. 3.6e-22;
 Matches 49; Conservative 12; Mismatches 9; Indels 0; Gaps 0;

QY 1 TLWGEFQVDGRSARGCGCOTSDNLLLEALNASSKEFALQIREKIPKYLFOFHNLNSML 60
 DB 89 TITWGEFQVDGRSARGGQOTANDAAEALNASSKEFALQIREKIPKYLFOFHNLNSML 148
 QY 61 DRIFDKTP 70
 DB 149 DRIFSKPP 158

RESULT 9
 P88975

RL J. Plant Res. 110:247-257(1997).
DR EMBL: AB001318; BAA34039.1; -
DR InterPro: IPR001191; Geminl_AL1.
DR Pfam: PF00799; Geminl_AL1.1.
DR PRINTS: PR00227; GEMCOATL1.
DR ProDom: PD000736; Geminl_AL1.1.
FT NON_TER 1 190
FT NON_TER 190
SQ SEQUENCE 190 AA; 21444 MW; AACIC2943E3F01AD CRC64;

Query Match 71.7%; Score 261; DB 12; Length 190;
Best Local Similarity 60.0%; Pred. No. 9, 4e-21;
Matches 51; Conservative 8; Mismatches 10; Indels 16; Gaps 1;

QY 1 TLVWGEFQVDGSRAGCGCTSDNLLLEALNASSKEPALQIIRKIPKYLFOFHNLSNL 60
DB 85 TLEWGTFOIDGSRAGCGCONADACAELNASSKAEALSIIRKILPKDFIFOYHNLSNL 144

OY 61 DRI-----FDKTPK 69
DB 145 DRIFAFPLEFVFCPTASSFDVPE 169

RESULT 13
Q9W827 PRELIMINARY; PRT; 190 AA.
AC Q9W827;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE C1 PROTEIN (FRAGMENT).
GN C1.
OS tobacco leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=67762;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-GORAL;
RA Ooi K., Ohshita S., Ishii I., Yahara T.;
RT "Molecular phylogeny of geminivirus infecting wild plants in Japan."
RL J. Plant Res. 110:247-257(1997).
DR EMBL: AB001303; BAA34010.1; -
DR InterPro: IPR001191; Geminl_AL1.
DR Pfam: PF00799; Geminl_AL1.1.
DR PRINTS: PR00227; GEMCOATL1.
DR ProDom: PD000736; Geminl_AL1.1.
FT NON_TER 1 190
FT NON_TER 190
SQ SEQUENCE 190 AA; 21444 MW; 93C3742A8EBDE7EB CRC64;

Query Match 71.4%; Score 260; DB 12; Length 190;
Best Local Similarity 60.0%; Pred. No. 1, 2e-20;
Matches 51; Conservative 8; Mismatches 10; Indels 16; Gaps 1;

QY 1 TLVWGEFQVDGSRAGCGCTSDNLLLEALNASSKEPALQIIRKIPKYLFOFHNLSNL 60
DB 85 TLEWGTFOIDGSRAGCGCONADACAELNASSKAEALSIIRKILPKDFIFOYHNLSNL 144

OY 61 DRI-----FDKTPK 69
DB 145 DRIFAFPLEFVFCPTASSFDVPE 169

RESULT 14
Q9Z0C4 PRELIMINARY; PRT; 208 AA.
AC Q9Z0C4;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE C1 AND C4 GENES, CLONE ABURA3-1, PARTIAL AND COMPLETE CDS (FRAGMENT).

GN C1.
OS tobacco leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=67762;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ABUR3;
RA Ooi K., Ohshita S., Ishii I., Yahara T.;
RT "Molecular phylogeny of geminivirus infecting wild plants in Japan."
RL J. Plant Res. 110:247-257(1997).
DR EMBL: AB001294; BAA33992.1; -
DR InterPro: IPR001191; Geminl_AL1.
DR Pfam: PF00799; Geminl_AL1.1.
DR PRINTS: PR00227; GEMCOATL1.
DR ProDom: PD000736; Geminl_AL1.1.
FT NON_TER 1 208
FT NON_TER 208
SQ SEQUENCE 208 AA; 23526 MW; 249CC31D8729C72D CRC64;

Query Match 71.4%; Score 260; DB 12; Length 208;
Best Local Similarity 60.0%; Pred. No. 1, 3e-20;
Matches 51; Conservative 8; Mismatches 10; Indels 16; Gaps 1;

QY 1 TLVWGEFQVDGSRAGCGCTSDNLLLEALNASSKEPALQIIRKIPKYLFOFHNLSNL 60
DB 102 TLEWGTFOIDGSRAGCGCONADACAELNASSKAEALSIIRKILPKDFIFOYHNLSNL 161

OY 61 DRI-----FDKTPK 69
DB 162 DRIFAFPLEFVFCPTASSFDVPE 186

RESULT 15
O39180 PRELIMINARY; PRT; 234 AA.
AC O39180;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE REPLICATION-ASSOCIATED PROTEIN (FRAGMENT).
OS potato yellow mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10827;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-TOMATO STRAIN;
RA Guzman P., Arredondo C.R., Emmatly D., Portillo R.J., Gilbertson R.L.;
RL Plant Dis. 81:312-312(1997).
DR EMBL: AF026553; AAB82605.1; -
DR InterPro: IPR001191; Geminl_AL1.
DR Pfam: PF00799; Geminl_AL1.1.
DR PRINTS: PR00227; GEMCOATL1.
DR ProDom: PD000736; Geminl_AL1.1.
FT NON_TER 234
FT NON_TER 234
SQ SEQUENCE 234 AA; 26486 MW; 9ED8F0697105CD19 CRC64;

Query Match 71.4%; Score 260; DB 12; Length 234;
Best Local Similarity 67.1%; Pred. No. 1, 5e-20;
Matches 47; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDGSRAGCGCTSDNLLLEALNASSKEPALQIIRKIPKYLFOFHNLSNL 60
DB 110 TLEWGTFOIDGSRAGCGCONADACAELNASSKAEALSIIRKILPKDFIFOYHNLSNL 169

OY 61 DRIEDKTPK 70
DB 170 DRIEKKAPND 179

Search completed: January 3, 2002, 15:56:26

Job time: 1122 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 3, 2002, 15:38:51 ; Search time 65.28 Seconds
(without alignments)
24.130 Million cell updates/sec

Title: US-09-289-346A-10

Perfect score: 364

Sequence: 1 TLVWGEFQVDRSARSGCQT.....FQFHNLNSNLDRIETKPEP 70

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PT05_COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	223	61.3	353	4	US-08-838-151A-44	Sequence 46, Appl
2	223	61.3	353	4	US-08-838-151A-46	Sequence 44, Appl
3	223	61.3	353	4	US-08-838-151A-49	Sequence 49, Appl
4	223	61.3	353	4	US-08-838-151A-52	Sequence 52, Appl
5	223	61.3	353	4	US-08-838-151A-55	Sequence 55, Appl
6	221	60.7	359	4	US-08-809-103B-2	Sequence 2, Appl
7	221	60.7	359	4	US-08-809-103B-4	Sequence 2, Appl
8	221	60.7	359	4	US-08-809-103B-6	Sequence 6, Appl
9	221	60.7	359	4	US-08-809-103B-8	Sequence 6, Appl
10	221	60.7	361	4	US-08-838-151A-2	Sequence 2, Appl
11	221	60.7	361	4	US-08-838-151A-4	Sequence 4, Appl
12	221	60.7	361	4	US-08-838-151A-6	Sequence 6, Appl
13	221	60.7	361	4	US-08-838-151A-8	Sequence 8, Appl
14	206	56.6	357	4	US-08-838-151A-24	Sequence 24, Appl
15	206	56.6	357	4	US-08-838-151A-27	Sequence 27, Appl
16	206	56.6	357	4	US-08-838-151A-30	Sequence 30, Appl
17	198	54.4	357	4	US-08-838-151A-20	Sequence 20, Appl
18	61	16.8	602	2	US-08-419-652-6	Sequence 6, Appl
19	61	16.8	771	1	US-07-923-976-6	Sequence 6, Appl
20	61	16.8	783	6	5422248-2	Patent No. 5422248
21	61	16.8	836	1	US-07-923-976-4	Sequence 4, Appl
22	61	16.8	863	1	US-07-923-976-8	Sequence 8, Appl
23	60.5	16.6	131	4	US-08-838-151A-14	Sequence 14, Appl
24	58.5	16.1	2161	1	US-07-745-206A-2	Sequence 2, Appl
25	58.5	16.1	2161	1	US-08-455-543A-49	Sequence 49, Appl
26	58.5	16.1	2161	1	US-08-455-543A-51	Sequence 51, Appl
27	58.5	16.1	2161	2	US-08-223-305C-49	Sequence 49, Appl

28	58.5	16.1	2161	2	US-08-223-305C-51	Sequence 51, Appl
29	58.5	16.1	2161	2	US-08-311-363-2	Sequence 2, Appl
30	56	15.4	323	1	US-07-667-276A-7	Sequence 7, Appl
31	56	15.4	844	3	US-09-029-267-20	Sequence 20, Appl
32	55	15.1	384	4	US-08-928-442-3	Sequence 3, Appl
33	55	15.1	751	4	US-09-036-987A-24	Sequence 24, Appl
34	55	15.1	751	4	US-09-370-700-24	Sequence 24, Appl
35	54.5	15.0	593	4	US-09-234-393-54	Sequence 54, Appl
36	54	14.8	244	1	US-08-910-973-22	Sequence 22, Appl
37	54	14.8	432	1	US-08-167-919A-11	Sequence 11, Appl
38	54	14.8	432	3	US-08-715-106-11	Sequence 11, Appl
39	54	14.8	1713	3	US-08-600-982-24	Sequence 24, Appl
40	54	14.8	1713	5	PCT-US94-10261A-24	Sequence 24, Appl
41	53.5	14.7	439	1	US-07-637-870-9	Sequence 9, Appl
42	53.5	14.7	439	1	US-07-637-389-6	Sequence 6, Appl
43	53.5	14.7	439	1	US-08-112-703-6	Sequence 6, Appl
44	53.5	14.7	3898	2	US-08-876-991-2	Sequence 2, Appl
45	53.5	14.7	3898	2	US-09-059-853-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-838-151A-44
; Sequence 44, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Lau, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Maxwell, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamov & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEO ID NO.: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-44

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Best Local Similarity 60.0%; Pred. No. 1.5e-21;
Matches 42; Conservative 12; Mismatches 16; Indels 0; Gaps 0;
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; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,103B
; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94.11040
; FILING DATE: 15-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR95/01192
; FILING DATE: 15-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: US894AL CNR TOM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 685-0573
; TELEX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-809-103B-8

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Query Match          60.7%; Score 221; DB 4; Length 359;
Best Local Similarity 56.5%; Pred. No. 2.8e-21;
Matches 39; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

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QY 2 LVWGEFQVGRSARGGCOTSDLLLEALNASSKEALQIREKIPKYLQFPHNLNSL 61
DB 111 LVWGFQIDGRSARGGCOTANDAYAKALNASSKSQLDYIKELAPRDVYLPHHNIRSL 170
QY 62 RIFDKTPRP 70
DB 171 KVEQVPPAP 179

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RESULT 10
US-08-838-151A-2
; Sequence 2, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Lau, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Gemlinivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A

```

```

; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-2

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Query Match          60.7%; Score 221; DB 4; Length 361;
Best Local Similarity 57.1%; Pred. No. 2.8e-21;
Matches 40; Conservative 15; Mismatches 15; Indels 0; Gaps 0;

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QY 1 TLWGEFQVGRSARGGCOTSDLLLEALNASSKEALQIREKIPKYLQFPHNLNSL 60
DB 110 TLWGFQIDGRSARGGCQSDANDSYAKALNASSVSQALAVLREQPKDVLQNHNIRSL 169
QY 61 RIFDKTPRP 70
DB 170 ERFAKAPRP 179

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RESULT 11
US-08-838-151A-4
; Sequence 4, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Lau, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Gemlinivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

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US-08-838-151A-4

Query Match 60.7%; Score 221; DB 4; Length 361;

Best Local Similarity 57.1%; Pred. No. 2.8e-21;

Matches 40; Conservative 15; Mismatches 15; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSRGSGCOTSDLLLEALNASSKEPALQITREKPEKYLFOFHNLNSNL 60

DB 110 TIEWGDFQIDGRSARGGQOSANDSYAKALNASSVQSALAVLREQPKDFVLQNHNRSL 169

QY 61 DRIFDKTPEP 70

DB 170 ERIFAKAPEP 179

RESULT 12

US-08-838-151A-6

Sequence 6, Application US/08838151A

Patent No. 6291743

GENERAL INFORMATION:

APPLICANT: Stout, John T

APPLICANT: Luu, Hang T

APPLICANT: Maxwell, Douglas

APPLICANT: Ahlquist, Paul

APPLICANT: Hanson, Steve

TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus

NUMBER OF SEQUENCES: 63

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dressler, Rocky, Milnamow & Katz

STREET: Two Prudential Plaza, Suite 4700

CITY: Chicago

STATE: Illinois

COUNTRY: U.S.A.

ZIP: 60601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/838,151A

FILING DATE:

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Mueller, Lisa V

REGISTRATION NUMBER: 38,978

REFERENCE/DOCKET NUMBER: SVS3801P0260

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-616-5400

TELEFAX: 312-616-5460

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 361 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-838-151A-6

Query Match 60.7%; Score 221; DB 4; Length 361;

Best Local Similarity 57.1%; Pred. No. 2.8e-21;

Matches 40; Conservative 15; Mismatches 15; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSRGSGCOTSDLLLEALNASSKEPALQITREKPEKYLFOFHNLNSNL 60

DB 110 TIEWGDFQIDGRSARGGQOSANDSYAKALNASSVQSALAVLREQPKDFVLQNHNRSL 169

QY 61 DRIFDKTPEP 70

DB 170 ERIFAKAPEP 179

RESULT 13

US-08-838-151A-8

Sequence 8, Application US/08838151A

Patent No. 6291743

GENERAL INFORMATION:

APPLICANT: Stout, John T

APPLICANT: Luu, Hang T

APPLICANT: Maxwell, Douglas

APPLICANT: Ahlquist, Paul

APPLICANT: Hanson, Steve

TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus

NUMBER OF SEQUENCES: 63

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dressler, Rocky, Milnamow & Katz

STREET: Two Prudential Plaza, Suite 4700

CITY: Chicago

STATE: Illinois

COUNTRY: U.S.A.

ZIP: 60601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/838,151A

FILING DATE:

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Mueller, Lisa V

REGISTRATION NUMBER: 38,978

REFERENCE/DOCKET NUMBER: SVS3801P0260

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-616-5400

TELEFAX: 312-616-5460

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 361 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-838-151A-8

Query Match 60.7%; Score 221; DB 4; Length 361;

Best Local Similarity 57.1%; Pred. No. 2.8e-21;

Matches 40; Conservative 15; Mismatches 15; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSRGSGCOTSDLLLEALNASSKEPALQITREKPEKYLFOFHNLNSNL 60

DB 110 TIEWGDFQIDGRSARGGQOSANDSYAKALNASSVQSALAVLREQPKDFVLQNHNRSL 169

QY 61 DRIFDKTPEP 70

DB 170 ERIFAKAPEP 179

RESULT 14

US-08-838-151A-24

Sequence 24, Application US/08838151A

Patent No. 6291743

GENERAL INFORMATION:

APPLICANT: Stout, John T

APPLICANT: Luu, Hang T

APPLICANT: Maxwell, Douglas

APPLICANT: Ahlquist, Paul

APPLICANT: Hanson, Steve

TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus

NUMBER OF SEQUENCES: 63

CORRESPONDENCE ADDRESS:

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Date: Jan 3, 2002 8:17 PM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

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Search information block:

Query: US-09-289-346a-2
Query length: 70
Database: GenEmbl.*
Database sequences: 1472140
Database length: 341344837
Search time (sec): 7316.720000

Score list:

Sequence	Strd Orig	ZScore	EScore	len	Documentation
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gb_v1.AF291705	-	281.00	666.27	7.8e-29	2622
gb_v1.LM092532	-	281.00	633.82	5.0e-27	1193
gb_v1.AF131071	-	281.00	632.75	5.7e-27	1345
gb_v1.MB6A8AL	-	279.00	623.16	2.2e-26	2617
gb_v1.AF188708	-	277.00	623.32	1.9e-26	1365
gb_v1.AF184036	-	277.00	623.21	1.9e-26	1383
gb_v1.AF104427	-	273.00	616.82	4.4e-26	2828
gb_v1.SG67926	-	273.00	624.41	1.7e-26	554
gb_v1.IY132548	-	273.00	607.74	1.4e-25	2763
gb_v1.MG75278	-	266.00	607.74	1.4e-25	447
gb_v1.AE350330	-	266.00	597.52	5.3e-25	1405
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gb_v1.AB001318	-	257.00	584.67	2.7e-24	570
gb_v1.AB001324	-	256.00	582.34	3.7e-24	570
gb_v1.AB001294	-	256.00	581.52	4.1e-24	625
gb_v1.AE350330	-	256.00	568.24	2.2e-23	2767
gb_v1.AB001296	-	254.00	576.88	7.4e-24	625
gb_v1.AB001297	-	254.00	576.88	7.4e-24	625
gb_v1.AB001298	-	252.00	572.23	1.3e-23	625
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gb_v1.CMAVJ3191	-	242.00	535.45	1.5e-21	2861
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gb_v1.AB014347	-	241.00	533.33	2.0e-21	2787
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seq_name: gb_v1.MTGA
seq_documentation_block: 2588 bp ss-DNA circular VRL 02-AUG-1993
LOCUS MTGA
DEFINITION Tomato golden mosaic virus, component A of complete genome.
ACCESSION K02029
VERSION K02029.1 GI:332213
KEYWORDS coat protein; complete genome; unidentified reading frame.
SOURCE TGMV cloned ds-DNA, clone PBH404.
ORGANISM Tomato golden mosaic virus
VIRUSES: ssDNA viruses; Geminiviridae; Begomovirus.
REFERENCE 1 (bases 1 to 2588)
AUTHORS Hamilton,W.D. O., Stein,V.E., Coulters,R.H.A. and Buck,K.W.
TITLE Complete nucleotide sequence of the infectious cloned DNA components of tomato golden mosaic virus. Potential coding regions and regulatory sequences
EMBO J. 3, 2197-2205 (1984)
COMMENT Geminiviruses are characterized by twin isometric virions, major capsid polypeptides of about 28 kd, and ss-DNA genomes. The genomes of cassava latent virus (CLV) and tomato golden mosaic virus (TGMV) consist of two circular components, while that of maize streak virus (MSV) consists of a single circle.
[1] Identifies the following additional open reading frames on the complementary strand that would code for proteins with >10 kd:
A11 -- 13-1543 (passing through origin)
A12 -- 1601-1212
A13 -- 1465-1067

The sequence at 1-235 is highly homologous to an equivalent region on component B; it doesn't appear to code for protein and has the potential to form a stable hairpin [1]. An analogous region is found in CSV.
The vitron-sense (+) strand is shown below.

FEATURES

source location/Qualifiers

CDS 1..2588
/organism="tomato golden mosaic virus"
/db_xref="taxon:10831"
327..1070
/note="coat protein (AR1)"
/codon_start=1
/protein_id="AAA4582.1"
/db_xref="GI:332214"

BASE COUNT 672 a 513 c 605 g 798 t
ORIGIN 140 bp upstream of HpaII site; beginning of A-B homology region.
alignment_scores: quality: 349.00 length: 70
ratio: 5.132 gaps: 0
Percent Similarity: 97.143 Percent Identity: 95.714

alignment block:

US-09-289-346a-2 x MTGA/rev ..

Align seq 1/1 to reverse of: MTGA from: 1 to: 2588

1 ThreueValrppgylguphegnvalaspclvalaalaalaglyl 17
|||||
2271 ACTTTGATGAGGAGATTCACGCTGCACGCTGAAGTCTTAAGAGG 2272
17 yCySglnThrSerAsnAspAlaAlaAlaAlaAlaAlaSerSert 34
|||||
2221 TTGCAAAACATCTAACGACGCTGACGAGGCTTAAGTCTTCTTCA 2172

KEYWORDS Tomato rugose mosaic virus.

SOURCE ssDNA viruses: Geminiviridae: Begomovirus.

ORGANISM 1 (bases 1 to 2622)

REFERENCE Fernandes,J.J., Fontes,E.P.B., Brommonschenkel,S.H., Carvalho,M.G., Zambolim,E.M. and Zerbini,F.M.

AUTHORS Molecular Cloning and Characterization of Tomato rugose mosaic virus (TRMV), a Begomovirus isolated from tomatoes at Triangulo Mineiro, Minas Gerais, Brazil

TITLE Unpublished

JOURNAL 2 (bases 1 to 2622)

REFERENCE Fernandes,J.J. and Zerbini,F.M.

AUTHORS Direct Submission

TITLE Submitted (31-JUL-2000) Dept. de Fitopatologia, Universidade Federal de Viçosa, Av. P.H. Kolfs, s/n - Centro, Viçosa, MG 36571-000, Brazil

JOURNAL Location/Qualifiers

FEATURES 1. 2622

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/villon /db_xref="taxon:134599"

/country="Brazil: Uberlandia, Triangulo Mineiro, Mans Gerais"

/note="Previously referred to as Tomato geminivirus Uberlandia TRMV"

rep_origin 1. 227

gene /note="common region"

complement(240..992)

/gene="AC4"

complement(240..992)

CDS /gene="AC4"

/codon_start=1

/product="putative AC4 protein"

/protein_id="AAG15549.1"

/db_xref="GI:10281649"

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342..1097

gene /gene="AV1"

342..1097

CDS /gene="AV1"

/note="CP"

/codon_start=1

/product="capsid protein"

/protein_id="AAG15545.1"

/db_xref="GI:10281645"

/translation="MPKRDAPRHMNSTSKISRGVNSBRAGVGRSKATDVRPM YRPRIVRMRYRTPDVRCGCEPKVQSFQRDISHTRKVMQVSDVTRNGITTHAVGK RRCVKSIVYILGKIMDENIKLKNHTNSAMFWLVRDRRPYGFMDGQVFNMDNEPST ATVKNDLDRDFQVHMKFYAKVTGGQYASNEGLVRFKVMVNNVVYVNHQEAQKYLENHT ENALLIYACTASNPYVATLKRIFYDSITN"

complement(1094..1492)

gene /gene="AC3"

complement(1094..1492)

CDS /gene="AC3"

/note="REN"

/codon_start=1

/product="replication-enhancer protein"

/protein_id="AAG15548.1"

/db_xref="GI:10281648"

/translation="MDSRTGELITAHQAENGYYTWEISNPLYFKMYNVEDIYTRTRV YHVQIRFNNHLRVLGLHKAVALNFQIWTFTSLRASQMTYLNRFKYLIMLYIDQLGVISV NNVIRAVRPATPQVNAVLENHSTKVKIY"

complement(1239..1628)

gene /gene="AC2"

complement(1239..1628)

CDS /gene="AC2"

/note="TRAP"

/codon_start=1

/product="trans-activation protein"

/protein_id="AAG15547.1"

/db_xref="GI:10281647"

/translation="MHNSSSTPPSIKYOHRAAKRRAIRRRRIDLCCGSLFVHIDCA CHGFTNRGCTHCTSGREWRVYIGNTKSLFDVQVRGHTIHEDSLPRPNTVQVQPEE STGSPQGLPDLDDIPESFMDIEK"

complement(join(1570..2622,1..6))

gene /gene="AC1"

complement(join(1570..2622,1..6))

CDS /gene="AC1"

/note="Rep"

/codon_start=1

/product="replication-associated protein"

/protein_id="AAG15546.1"

/db_xref="GI:10281646"

/translation="MPSATRRQIRAKNYFLTPPKCSISKERALSQLNLTPTNKKF IKVCRELHENGEPFLHVLLOEGNCCNORFPLVSPRSTHFPNIOAKSSSDVK SYVDKDGDTIEGFEQIDGRSARGCOTANDAAALNAPSKOILQIIRKMPKFL FQFHNLNSNLRIRFARPEPAPAPPPPLSSFTNVPEMDMDADYRGCAARPPRPIS IIRBDSRTGKTMRARALGARNYLSGHLDFNPRVYSNRYEVVIDIAPHYLKLKHK ELIGARQWQSNCKTGKPVQIKGIPICIVLCNPGEGASYKCPFLDKENSALSSWTKHN AQFIPLNPLVQSSSTSGC"

BASE COUNT 684 a 562 c 600 g 776 t

ORIGIN

alignment_scores: Quality: 298.00 Length: 70

Ratio: 4.656 Gaps: 0

Percent Similarity: 91.429 Percent Identity: 78.571

alignment_block:

US-09-289-346a-2 x AF291705/rev ..

Align seq 1/1 to reverse of: AF291705 from: 1 to: 2622

1 ThleuValTrrpGlyGluPhgInValAspCylAlaAlaAlaAlaCylG 17

||||: |||||||||:|||||: ||||| |||||

2298 ACTATCGAATGGGGGGAATTCGCAATCGACGCGAAGAGCTGTAGAGCGG 2249

17 YCYSGITThrSerAsnAspAlaAlaAlaAlaAlaAlaAlaAlaSerSer 34

|||||||:|||||||:|||||||: ||||| |||||

2248 TTGCCACACACCTACGACCGTCCGCGACGAGACCTTAACGACCTTCCA 2199

34 YSGIUGIAlaLeuGlnIleIleArgGluIuysIlePioGluIuysTyrLeu 50

||||: |||||||||:|||||||: ||||| |||||

2198 AAGACATCGCCTTGACAGATATCCGGAGAAAGATCGCGAAAGTCTTA 2149

51 PhgIInpHeHtsAnLeuAsnSerAsnLeuAspArgIlePhaAspIuys 67

|||||||:|||||||:|||||||: ||||| |||||

2148 TTYCAGTTTCACATCTTAATAGTATTTAGATGATATTTGCCAAGGC 2099

67 rPioGluPro 70

|||||||

2098 TCCGAGACCA 2089

seq_name: gb_v1:LM092532

seq_documentation_block: 1193 bp DNA VRL 01-APR-1997

LOCUS LM092532

DEFINITION Leonurus mosaic virus Rep protein (rep) and coat protein (cp)

ACCESSION 092532

VERSION 092532

KEYWORDS genes, partial cds.

ORGANISM Leonurus mosaic virus.

SOURCE Viruses: ssDNA viruses: Geminiviridae: Begomovirus.

REFERENCE 1 (bases 1 to 1193)

AUTHORS Faria,J.C. and Maxwell,D.P.

TITLE Variability in geminivirus associated with Phaseolus vulgaris in Brazil

us-09-289-346a-2 x AF131071/rev ..

Align seg 1/1 to reverse of: AF131071 from: 1 to: 1345

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1 ThrLeuValTrpGlyGluPheGlnValAspGlyAlaAlaAlaGlyGly 17
||||: |||||||||:|||||: |||||: |||||
348 ACATCGAATGGGAGAAATTCAGATGACGCGGAGATGCTGCTAAGAGAGG 299
17 YcYsGlnThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerL 34
||||: |||||||||:|||||: |||||: |||||
298 TCAGCAACGACTAACGACGCTGCCGACGAGGCCCTAAATGCCCTTCGA 249
34 YsgIuGluAlaLeuGlnIleLeuArgLulysIleProGluLysTyrLeu 50
||||: |||||||||:|||||: |||||: |||||
248 AACAGAAAGCCATGCGAATTTATTAAAGAGAGCTCCCAAGAGCTTCTT 199
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTrh 67
||||: |||||||||:|||||: |||||: |||||
198 TTTCATATATACAAACCTGTCTAGTAACTGAGACGATATTTCGCTAAGGC 149
67 rPrOGluPro 70
||||: |||||||||
148 TCCGGAACCG 139

seq_name: gb_vi:MBGARAL

seq_documentation_block:
LOCUS MBGARAL 2617 bp ss-DNA circular VRL 02-AUG-1993
DEFINITION Bean golden mosaic geminivirus viral coat protein (ARI) gene,
complete cds; putative replicative protein (AL1) gene, putative
cds; AL2 gene, complete cds; and AL3 gene, complete cds.
ACCESSION M86886
VERSION M86886.1 GI:331462
KEYWORDS coat protein; replicative protein.
SOURCE Bean golden mosaic virus (individual isolate Brazil, strain type 1)
ORGANISM bean golden mosaic virus
VIRUSES: ssDNA viruses; Geminiviridae; Begomovirus.
REFERENCE
1 (sites)
AUTHORS Gilbertson,R.L., Farla,J.C., Hanson,S.F., Morales,F.J.,
Ahluwist,P.G., Maxwell,D.P. and Russell,D.R.
TITLE Cloning of the Complete DNA Genomes of Four Bean-Infecting
Geminiviruses and Determining Their Infectivity by Electric
Discharge Particle Acceleratio
JOURNAL Phycopathology 81, 980-985 (1991)
REFERENCE
2 (sites)
AUTHORS Gilbertson,R.L., Hidayat,S.H., Martinez,R.T., Leong,S.A., Farla,J.C.,
Morales,F.J. and Maxwell,D.P.
TITLE Differentiation of bean-infecting geminiviruses by nucleic acid
hybridization probes and aspects of bean golden mosaic in Brazil
JOURNAL Plant Dis. 75, 336-342 (1991)
REFERENCE
3 (bases 1 to 2617)
AUTHORS Gilbertson,R.L., Farla,J.C., Ahluwist,P.G. and Maxwell,D.P.
TITLE Genetic diversity in geminiviruses causing bean golden mosaic
disease: The nucleotide sequence of the infectious cloned DNA
components of a Brazilian isolate of bean golden mosaic geminivirus
unpublished (1992)
FEATURES
source
1. .2617
Location/Qualifiers
/organism="bean golden mosaic virus"
/proviral
/isolate="Brazil"
/strain="type 1"
/db_xref="taxon:10839"
/dev_stage="Replicative form"
/gemline
1. .181
/standard_name="Common Region"
/note="putative"
/function="Putative origin of replication"
358. .1113
/gene="ARI"
358. .1113
CDS
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/gene="ARI"
/note="putative"
/codon_start=1
/function="coat protein"
/product="coat protein"
/protein_id="AAA46313.1"
/db_xref="GI:331464"
/translation="MPKRDADMRHMGSTKTSRSANFSPRGNGPKYKKAEMVNRPM
YRKPRITRLRGPDVPRGCEPKQVOSTBORHDVSHVCKVMQVSPVTKGKCTTHVCK
RFGVKSVALILKQIMDENIKLKNHTNSVFWLVRDRRPRTGTPMDGQVFNMDNPEST
ATVKNDSDLRQFMHKKFYGKYVGQVASEGALVYRFWKVNVVYVYNHDEAGKYENHT
ENALLYMACTHASNRYVATLKRIRYFDSLTN"
complement(1110. .1508)
/gene="AL3"
complement(1110. .1508)
/gene="AL3"
complement(1110. .1508)
/note="putative"
/codon_start=1
/protein_id="AAA46314.1"
/db_xref="GI:331465"
/translation="MDSRTGERITRQAEENGYIWEISNPLYFKKYNVEDLOTYTRV
YHLQIRFNHNLKNKLGHLKAFLNQVMTSLQASGTTYLNRPKYLVLVLDRIQVISTL
NNVIRAVRPATDKSYNVVYLNENHETKRYFY"
complement(1255. .1644)
/gene="AL2"
complement(1255. .1644)
/note="putative"
/codon_start=1
/protein_id="AAA46315.1"
/db_xref="GI:331466"
/translation="MRNSSSTPPSIKQVRAKRAIRRRRVDECGCTIYVHNS
GHGFTGRHHTCSGEMKRYLIGDKSPFQVQVRGSTIHMDOSTIPPEVTVOPOPE
QVGSVQGFPEPESLDDISSFEWDLIFK"
complement(1556. .2617)
/gene="AL1"
complement(1556. .2617)
/gene="AL1"
complement(1556. .2617)
/note="putative"
/codon_start=1
/function="viral replication"
/product="replicative protein"
/protein_id="AAA46312.1"
/db_xref="GI:331463"
/translation="MPPKRKTKANKNFITYPQCSITKESALBDOLNLOTPEVKKYI
RICREIHENGEPHIALIQEGKFOQTCNCFVDLHPPTTSVSHANIQSAKSSOVKS
YIEKGDYIEWGHFOVDGSRARGOQTNDASALNMSKDEAMQIIEKLPKFLF
OYHNSLNDRIETKAPDPWSPYHLSTFTNVPREMAVDYFGRGAARPERPISI
ITEGSRKGTMMARALGTHNYLSGHLDFNSVFNHAEVNYIDIDAPHYLTKHKE
LMGAKQDNQSNCKRYKPYQIKGISYIYCNPEGASYKCFIDREMAALKMTIHTNA
KFIPLNSPLOSSTQCESTMQTISR"
BASE COUNT 677 a 491 c 592 g 857 t
ORIGIN

alignment_scores:
Quality: 279.00 Length: 67
Ratio: 4.429 Gaps: 0
Percent Similarity: 94.030 Percent Identity: 76.119

alignment_block:
US-09-289-346A-2 x MBGARAL/rev ..

Align seg 1/1 to reverse of: MBGARAL from: 1 to: 2617

4 TrpGlyGluPheGlnValAspGlyAlaAlaAlaGlyGlyCysGlnTh 20
||||: |||||||||:|||||: |||||: |||||
2305 TGGGCTCATTTTCAAGTCGACGAGATCTGCTAGAGAGAGTCAACGAC 2256

20 rSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerLysGluGlu 37
||||: |||||||||:|||||: |||||: |||||
2255 AGCTAATGATCGCGCATCGAAGCATGGAATGCTTCTTCAAGAGAGAG 2206
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37 1aleuGlnIle1leAArgLulysIleProGluLulysTyrLeuPheGlnPhe 53
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2205 CCATGCAATATATCAAGAAAGTACCGAAAGTTCTCTTCCAAATAT 2156
54 HisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysThrProGluPr 70
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2155 CACATTTATTCACGATGACCTGATGAAATATTCACAAAGCTCCGATCC 2106
70 o 70
2105 G 2105

seq_name: gb_v1:AF188708
seq_documentation_block:
LOCUS AF188708 1365 bp DNA VRL 07-NOV-1999
DEFINITION Cowpea golden mosaic geminivirus replication associated protein
(rep) and coat protein (cp) genes, partial cds.
ACCESSION AF188708
VERSION AF188708.1 GI:6273115
KEYWORDS
SOURCE cowpea golden mosaic geminivirus.
ORGANISM cowpea golden mosaic geminivirus
REFERENCE 1 (bases 1 to 1365)
AUTHORS Faria,J.C.
TITLE Partial nucleotide sequence of cowpea golden mosaic geminivirus
from Brazil
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1365)
AUTHORS Faria,J.C.
TITLE Direct Submission
JOURNAL Submitted (21-SEP-1999) Biotechnology Laboratory, EMBRAPA, Caixa
Postal 179, Goiania, GO 75375, Brazil
FEATURES
Source
1..1365
/organism="cowpea golden mosaic geminivirus"
/strain="CGMY-BR"
/specific_host="cowpea"
/db_xref="taxon:69263"
complement(<1..676)
/gene="rep"
complement(<1..676)
/gene="rep"
/note="AC1"
/codon_start=1
/product="replication associated protein"
/protein_id="AF06318.1"
/db_xref="GI:6273117"
/translatation="MPPKRFKINAKNYELTYPOCSIGKSAIELOTLQTPYNNKYI
RVCRLEHNEGEPHLHALIOEKGFCOCTNCRLPQKPHPSVSHPIIOGAKSSDVKS
YIEKGDYVEMWGHQIDGSRAGCOOTINDASSEANASSKEAMQITIEKPEKPLF
OYHNLSNLDRIKPKPEPMSPPQLSFTINVKQMDWADDFGDAARPERPVSIT
IEGDSR"
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674..820
1021..>1365
/gene="cp"
1021..>1365
/gene="cp"
/note="AV1"
/codon_start=1
/product="coat protein"
/protein_id="AF06317.1"
/db_xref="GI:6273116"
/translatation="MYKRDAPMRHMSGTSKVSRTNNFSPRSGGCPKYKKAEMMRPM
YKPRIRYMRKSRSDPRGCEGPCVKVSPQKHVSHIGVICLSDVTGCGITTHRVGK
RFCVSVYILGK"
BASE COUNT 339 a 259 c 332 g 435 t
ORIGIN
alignment_scores:
Quality: 277.00 Length: 67

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Ratio: 4.541 Gaps: 0
Percent similarity: 91.045 Percent identity: 76.119
alignment_block:
US-09-289-346A-2 x AF188708/rev ..
Align seg 1/1 to reverse of: AF188708 from: 1 to: 1365

4 TrpGlyGlnPheGlnValAspGlyAlaAlaAlaIaGlyGlyCysGln 20
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
340 TGGGTCATTTTCAATCGACGAGATCTCTAGACGAGGTCACGAC 291
20 rSerAsnAspAlaAlaIaGlnAlaLeuAsnAlaSerSerLysGlnL 37
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
290 AATTATATCATCGACATCGACGCGCTTAATGCTTCTTCAAGACGAC 241
37 1aleuGlnIle1leAArgLulysIleProGluLulysTyrLeuPheGlnPhe 53
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
240 CCATGCAATATATCAAGAAAGTACCGAGAGAGTTCTCTTCCAGTAT 191
54 HisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysThrProGluPr 70
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
190 CACACTTATTCACGATGACCTGATGATATTCAAAAGCCTCCGAAAC 141
70 o 70
140 A 140

seq_name: gb_v1:AF288227
seq_documentation_block:
LOCUS AF288227 1383 bp DNA VRL 20-AUG-2000
DEFINITION Sweet potato leaf curl virus replication association protein (AC1)
and AC4 (AC4) genes, complete cds.
ACCESSION AF288227
VERSION AF288227.1 GI:9858125
KEYWORDS
SOURCE sweet potato leaf curl virus.
ORGANISM sweet potato leaf curl virus
REFERENCE 1 (bases 1 to 1383)
AUTHORS Lotrakul,P., Valverde,R.A., Clark,C.A., Sim,J. and De la Torre,R.
TITLE Detection of a geminivirus infecting sweet potato in the United
States
JOURNAL Plant Dis. 82, 1253-1257 (1998)
REFERENCE 2 (bases 1 to 1383)
AUTHORS Lotrakul,P. and Valverde,R.A.
TITLE Direct Submission
JOURNAL Submitted (18-JUL-2000) Plant Pathology and Crop Physiology,
Louisiana State University, 302 Life Sciences Bldg., Baton Rouge,
LA 70803, USA
FEATURES
Source
1..1383
/organism="sweet potato leaf curl virus"
/db_xref="taxon:100755"
/note="subgenomic DNA"
complement(285..1229)
/gene="AC1"
complement(285..1229)
/gene="AC1"
/note="AL1"
/codon_start=1
/product="replication association protein"
/protein_id="AAC01006.1"
/db_xref="GI:9858126"
/translatation="MAPPKRFKIQAKNFITYPRCSLSKEDCLAOLNIOFPSNNKYI
HVARLEHDEGEPHLVLVQFEGKFCOCTNSRFPDLVSPNSNHFHPIIOGAKSSDVKS
YVAKDQDTTGEFOVYDSARGGCOOTANDAAEAALNPGSKFAALQITREKPEYLF
OFHNLYSNLDRIFFSPPSVYSSPSSSPNNAVPIITDMAAEVWDSARPDPSIV
IEGPRIGKTYVARSIGPHNYICGHLDDSPKYSNSANYNVIDVNPOTLKHFKFPMG
AQRDQSNCKYKGPVKIRKAVRPTEGLAIVMKPCHTA"
complement(815..1072)
/gene="AC4"
gene

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/gene="AC4"
/notes="AL4"
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/product="AC4"
/protein_id="AAD47174.1"
/db_xref="GI:5702164"
/translation="MGNLTSMCMSCSSKANSASOIAIDSSITSHRTDRITFTPTSRRLNP
AMSSPTSRITGIPSGVNSRSTADILEASRLLTTPQRL"
BASE COUNT      741 a      606 c      675 g      806 t
ORIGIN

alignment_scores:
  Quality: 277.00      Length: 68
  Ratio: 4.541      Gaps: 0
  Percent Similarity: 89.706      Percent Identity: 79.412

alignment_block:
US-09-289-346A-2 x AF104036/rev ..

Align seg 1/1 to reverse of: AF104036 from: 1 to: 2828

1  ThrleuValTrpGlyGluPheGlnValAspGlyAlaAlaAlaGlyG1 17
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
2354 ACCATCAGCTGGGTGCAATTCAGTCAGCGCAGATCTCTAGAGAGG 2305
17  YcysGlnThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerL 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
2304 CCACGAGCTCTACGACGCGCGCAGGCTCTAAACGACGAGTCTTA 2255
34  YsglGluAlaLeuGlnIlelleArgGluLysIleProGluLysTyrLeu 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
2254 AAGAGAGCTGGCTTGCATAATATCAGCGAGAACCTCCGAAATATTTTA 2205
51  PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
2204 TTTCATATTTCATTAATTAGTAGTAATTAGATGATTTTCTCTCC 2155
67  rPro 68
|||||
2154 ACCT 2151

seq_name: gb_v1:SGU67926

seq_documentation_block:
LOCUS      SGU67926      554 bp      DNA
DEFINITION Sida golden mosaic geminivirus Rep protein (AC1) gene, partial cds.
ACCESSION  U67926
VERSION    067926.1 GI:1546801
KEYWORDS   sida golden mosaic virus.
SOURCE     sida golden mosaic virus.
ORGANISM   Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
REFERENCE  1 (bases 1 to 554)
AUTHORS    Roye,M.E., McLaughlin,W.A., Nakhlia,N.K. and Maxwell,D.P.
TITLE      Genetic Diversity among geminiviruses associated with the weed
           species Sida spp. Macroptilium lathyroides, and Wissadula
           ampelasma from Jamaica
JOURNAL    Plant Dis. 81, 1251-1258 (1997)
AUTHORS    Roye,M.E., McLaughlin,W.A. and Maxwell,D.P.
TITLE      Direct Submission
JOURNAL    Submitted (23-AUG-1996) Plant Pathology, University of Wisconsin,
           1630 Linden Drive, Madison, WI 53706-1598, USA
FEATURES   Location/Qualifiers
            1..554
            /organism="sida golden mosaic virus"
            /strain="Jamaica"
            /isolate="Jamaica, May 1993"
            /db_xref="taxon:51034"
            /note="DNA A component"
            /complement(1..554)
            /gene="AC1"
gene

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CDS      complement(1..554)
/gene="AC1"
/notes="replication-associated protein"
/codon_start=1
/product="Rep protein"
/protein_id="AAB97865.1"
/db_xref="GI:1546802"
/translation="SISKREALSLOTLKTPVKKFKIKICRELHNGEPHLVLIQFE
GRYKNTNNRPPLVSPPTBSVHPHPNIGCAKSSDYKSVKRDGDTIENGVCQIDERSA
RGQDOTADDAEALNSGKEDALKIREKLPERYLFOYHNLSSNIDRIFSKPEPWS
HPFLPSEFAVPGQMOMEWADYFGR"
BASE COUNT      121 a      127 c      139 g      167 t
ORIGIN

alignment_scores:
  Quality: 274.00      Length: 70
  Ratio: 4.281      Gaps: 0
  Percent Similarity: 91.429      Percent Identity: 70.000

alignment_block:
US-09-289-346A-2 x SGU67926/rev ..

Align seg 1/1 to reverse of: SGU67926 from: 1 to: 554

1  ThrleuValTrpGlyGluPheGlnValAspGlyAlaAlaAlaGlyG1 17
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
290 ACCATCAGATGGGGGTGTTCCAGATCGACGAGAGAGTCTCTGGAGG 241
17  YcysGlnThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerL 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
240 TCAGCAACAGCTATACGACGAGCGCCGAGCATGTAATTCGAGACAA 191
34  YsglGluAlaLeuGlnIlelleArgGluLysIleProGluLysTyrLeu 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
190 AGGAGGATGCGACGAAATCATCAGAGAGAGATTACGAGAAAGTATVCTC 141
51  PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
140 TTTCAGTATCACAACCTATATCCAGTATATCGATAGCATTTTCAGTAAGCC 91
67  rProGluPro 70
|||||
90 TCCAGAACCG 81

seq_name: gb_v1:YIE132548

seq_documentation_block:
LOCUS      YIE132548      2763 bp      DNA      circular      VRL
DEFINITION Ipomoea yellow vein virus V2, V1, C3 and C2 genes.
ACCESSION  AJ132548
VERSION    AJ132548.1 GI:4210720
KEYWORDS   C2 gene; C2 protein; C3 gene; C3 protein; coat protein; V1 gene; V2
           gene; V2 protein.
SOURCE     Ipomoea yellow vein virus.
ORGANISM   Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
REFERENCE  1 (bases 1 to 2763)
AUTHORS    Banks,G.K.
TITLE      Direct Submission
JOURNAL    Submitted (26-JAN-1999) Banks G.K., Virus Research, John Innes
           Centre, Norwich Research Park, Colney Lane, Norwich, NR4 6UL, UK
AUTHORS    Banks,G.K., Bedford,I.D., Beitia,F.J., Cerezo,F.R. and Markham,P.G.
TITLE      A novel geminivirus of Ipomoea indica (Convolvulaceae) from southern
           Spain
JOURNAL    Unpublished
FEATURES   Location/Qualifiers
            1..2763
            /organism="Ipomoea yellow vein virus"
            /viroion
            /specific_host="Ipomoea indica"
            /db_xref="taxon:87832"

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          /gene="V2"
CDS        995..1390
          /gene="V2"
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          /protein_id="CA10695.1"
          /db_xref="GI:4210721"
          /translation="MTLLYKDSQSDCRAMCPSTAEWMDPLONLPDLYGPRCMLSVKY
          LOGILKKERPTGLCEPLCSLIRIRVQYDRANRFAEISSLMGETKTESELDSTY
          RALMECCPNCCKPLCPGFKRPDEKEG"
gene      1215..1979
          /gene="V1"
          /codon_start=1
          /product="coat protein"
          /protein_id="CA10696.1"
          /db_xref="GI:4210722"
          /translation="MTGRIRVSPRFPHYGGROVRSNLETAIVPYTGNAVPIAARSY
          VPSRSGVMKRGRDRIPKCGVCKIDYERKMVPHTGTCVSDFRGGLTHRL
          GKRVCIKMSIDGKYMDDNNAKRDHTNITTWLIRDRPKDPLNFGOIFWTYNEP
          TTAKTMDLRDMOVLKRFVTVSGSPYSHKQALIRKFKCLYNHVTYNHKEEAKYE
          NQLENALMLYSASHSNPVYQTLRCRAVFYDSHKN"
gene      complement(1976..2413)
CDS        /gene="C3"
          /complement(1976..2413)
          /codon_start=1
          /product="C3 protein"
          /protein_id="CA10697.1"
          /db_xref="GI:4210723"
          /translation="MDSRGEESLSHAQTRAAEFNNPNSVQOTAPFHRLMYVTNN
          LDSKTIKMYQLOVNHNRNREIGFOKITFQSRITQPIRLGALPNTWGISNRLKWLICNS
          LASLGYSFLPNLVYIRHLPOQCLMEVEVDVDDKIDIKVLLY"
gene      complement(2127..2576)
          /gene="C2"
          /complement(2127..2576)
          /codon_start=1
          /product="C2 protein"
          /protein_id="CA10698.1"
          /db_xref="GI:4210724"
          /translation="MSTAPSGYKRRKCPAOPERPHAAKKRORRTPPRPIYVKGCGCS
          AFITNDCKFORGFTHRGVTKKSTDESSRILQDSYVCGSDCTIPSTTDVCPYKQPRLK
          DHESAASSQPEDEGNMIPEDLPRIPDHTNASDWCYSOLDWYFQSP"
BASE COUNT 734 a 570 c 671 g 788 t
ORIGIN

alignment_scores:
  Quality: 273.00      Length: 68
  Ratio: 4.550        Gaps: 0
  Percent Similarity: 88.235   Percent Identity: 76.471

alignment_block:
US-09-289-346a-2 x IYE132548/rev ..

Align seg 1/1 to reverse of: IYE132548 from: 1 to: 2763

1  ThrLeuValTrrpGlyGluPheGluValAspGlyValAlaAlaAlaGlyG1 17
   |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
469 ACCGTCATATGAGGGGTGAATTCAGATCGACGCGCATCTGCTAGAGAGG 420

17 yCySGlnThrSerAsnAspAlaAlaAlaGluAlaLeuAsnAlaSerSer1 34
   |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
419 TCACACAGCTGCTTAACGACGACGCGCAGAGCGCTTAACGCGCATGTTCTA 370

34 ySGluGluAlaLeuGlnIleIleArgGlyLysIleProGluLysTyrLeu 50
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
369 AAGAAAGCTGGCTGCAATATATCAGGAGAAACCTCGAAAAAATATT7TA 320

51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTth 67

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seq_name: gb_v1:MGU75278
seq_documentation_block:
LOCUS      MGU75278          447 bp      DNA          VRL          27-NOV-1996
DEFINITION Macropitillum golden mosaic geminivirus replication-associated
            protein (Ac1) gene, partial cds.
ACCESSION  U75278
VERSION    U75278.1  GI:1688188
KEYWORDS   Macroptillum golden mosaic geminivirus.
SOURCE     Macropitillum golden mosaic geminivirus.
            Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
ORGANISM   1 (bases 1 to 447)
            Diversity and phylogeny of whitefly-transmitted geminiviruses from
            Jamaica
            Thesis (1996)
            2 (bases 1 to 447)
            Roye, M.E., McLaughlin, W.A. and Maxwell, D.P.
            Three distinct geminiviruses infecting M. latihyoides from Jamaica
            but not BGMV
            Unpublished (1996)
JOURNAL    3 (bases 1 to 447)
            Roye, M.E., McLaughlin, W.A. and Maxwell, D.P.
            Direct Submission
            Submitted (17-OCT-1996) Biochemistry, University of the West
            Indies, Mona, Kingston 7, Jamaica
            Location/Qualifiers
FEATURES   1..447
            /organism="Macropitillum golden mosaic geminivirus"
            /strain="Jamaican"
            /isolate="2"
            /db_xref="taxon:51676"
            /clone="PMGJA2"
            /complement(1..447)
            /gene="AC1"
            /complement(<1..>447)
            /gene="AC1"
            /codon_start=1
            /product="replication-associated protein"
            /protein_id="AAB36919.1"
            /db_xref="GI:1688189"
            /translation="HVLIQFOGKFNCTNRLFDIYSPSRSAFHPRNIQGAKSSDPYKS
            YEKDGDITENKGVFOIDGRSARGGQOTSNDAAAEALNSGTREANRITYEKLPKPFLE
            OYHNLSNDRLEFMKDPFPAWPPPLSFTFNVDEDEWATNVEFGG"
BASE COUNT 97 a 112 c 110 g 128 t
ORIGIN

alignment_scores:
  Quality: 266.00      Length: 70
  Ratio: 4.290        Gaps: 0
  Percent Similarity: 88.571   Percent Identity: 68.571

alignment_block:
US-09-289-346a-2 x MGU75278/rev ..

Align seg 1/1 to reverse of: MGU75278 from: 1 to: 447

1  ThrLeuValTrrpGlyGluPheGluValAspGlyValAlaAlaAlaGlyG1 17
   |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
294 ACCATTCGAATGGGAGCTGTTCCAGATCGACGAGAAAGAGTGTGAGGCGG 245

17 yCySGlnThrSerAsnAspAlaAlaAlaGluAlaLeuAsnAlaSerSer1 34
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
244 TCACCAACATCTAAGCATGCGCGCGGAGAACGCAATVTAATTCGAGCAA 195

```

seq_name: gb_v1:AF098940	seq_documentation_block:	LOCUS	AF098940	1405 bp	DNA	VRL	04-MAR-1999
DEFINITION	Macropitillium golden mosaic geminivirus strain Jamaica	DEFINITION	Macropitillium golden mosaic geminivirus strain Jamaica	1	partial cds.		
ACCESSION	AF098940	ACCESSION	AF098940	1	partial cds.		
VERSION	AF098940.1	VERSION	AF098940.1	1	partial cds.		
KEYWORDS		KEYWORDS					
SOURCE		SOURCE					
ORGANISM	Macropitillium golden mosaic geminivirus.	ORGANISM	Macropitillium golden mosaic geminivirus.				
REFERENCE	1 (bases 1 to 1405)	REFERENCE	1 (bases 1 to 1405)				
AUTHORS	Roye, M.E., McLaughlin, W.A. and Maxwell, D.P.	AUTHORS	Roye, M.E., McLaughlin, W.A. and Maxwell, D.P.				
TITLE	Molecular characterization of two distinct geminiviruses infecting M. lathyroides from Jamaica	TITLE	Molecular characterization of two distinct geminiviruses infecting M. lathyroides from Jamaica				
JOURNAL	Unpublished	JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 1405)	REFERENCE	2 (bases 1 to 1405)				
AUTHORS	Roye, M.E., McLaughlin, W.A. and Maxwell, D.P.	AUTHORS	Roye, M.E., McLaughlin, W.A. and Maxwell, D.P.				
TITLE	Direct Submission	TITLE	Direct Submission				
JOURNAL	Submitted (14-OCT-1998)	JOURNAL	Submitted (14-OCT-1998)				
FEATURES	West Indies, Mona, Kingston 7, Jamaica	FEATURES	West Indies, Mona, Kingston 7, Jamaica				
Source	Location/Qualifiers	Source	Location/Qualifiers				
1. .1405	/organism="Macropitillium golden mosaic geminivirus"	1. .1405	/organism="Macropitillium golden mosaic geminivirus"				
	/strain="Jamaica strain 1"		/strain="Jamaica strain 1"				
	/specific_host="Macropitillium lathyroides"		/specific_host="Macropitillium lathyroides"				
	/db_xref="taxon:51676"		/db_xref="taxon:51676"				
	/country="Jamaica"		/country="Jamaica"				
	/clone="pmGJA3"		/clone="pmGJA3"				
	/complement(<1. .701)		/complement(<1. .701)				
	/gene="rep"		/gene="rep"				
	/complement(<1. .701)		/complement(<1. .701)				
	/gene="rep"		/gene="rep"				
	/codon_start=1		/codon_start=1				
	/product="replication associated protein"		/product="replication associated protein"				
	/protein_id="AADI7850.1"		/protein_id="AADI7850.1"				
	/db_xref="GI:4336586"		/db_xref="GI:4336586"				
	/translation="MPKRGSPSIRAKNYFLTYPOCSITLKEBASOLINLMPYVKKPFIKICEFHEDGPHLVLIOFGKFNCTNNRFLDLYPSRSASHFHPNIOGKSSSDVASVYENDGPTITGVGYOITDGRSARGCOQNSDAAALNSGTFEAMRIYKEKLPKPLFQYHLSNSLDRITFKDKPEWMPVPPPLSSFTVPEDEMADYFGPNSAKRPERPKSITIVEDSRTRGRTMAC"		/translation="MPKRGSPSIRAKNYFLTYPOCSITLKEBASOLINLMPYVKKPFIKICEFHEDGPHLVLIOFGKFNCTNNRFLDLYPSRSASHFHPNIOGKSSSDVASVYENDGPTITGVGYOITDGRSARGCOQNSDAAALNSGTFEAMRIYKEKLPKPLFQYHLSNSLDRITFKDKPEWMPVPPPLSSFTVPEDEMADYFGPNSAKRPERPKSITIVEDSRTRGRTMAC"				
	702. .1030		702. .1030				
	/note="intergenic region"		/note="intergenic region"				
	1031. .>1405		1031. .>1405				
	/gene="cp"		/gene="cp"				
	1031. .>1405		1031. .>1405				
	/gene="cp"		/gene="cp"				
	/codon_start=1		/codon_start=1				
	/product="coat protein"		/product="coat protein"				
	/protein_id="AADI7849.1"		/protein_id="AADI7849.1"				
	/db_xref="GI:4336585"		/db_xref="GI:4336585"				
	/translation="MPKRDGSMWRTTPGVAKVSRRLNPSKRGYGGPNSKAOEWVNRPM"		/translation="MPKRDGSMWRTTPGVAKVSRRLNPSKRGYGGPNSKAOEWVNRPM"				

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YRKRRIRTRLTSPDVPARGCEPCKVQGEQRHDSHGKXWMCISDVTRGVITHRVCN
RRCVKFYIILGKTMDENINNSC"
BASE COUNT      328 a      333 c      357 g      306 t      1 others
ORIGIN

alignment_scores:
    Quality:     266.00          Length:       70
                Ratio:     4.290         Gaps:        0
Percent Similarity: 88.571      Percent Identity: 68.571

alignment_block:
US-09-289-346A-2 x AF098940/rev ..

Align seg 1/1 to reverse of: AF098940 from: 1 to: 1405

1 ThrLeuValTrpPolylgUnpheginValaspGlyAlaAlaAlaAglygl 17
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
374 ACCATCGAGTGGGGAGTGTTCCGATCGACGGAGAAGTGTCTGAAGCGG 325
17 yCyScgtInTrSerAsnAspAlaAlaLaGlualalaEuasnAlaSerSerL 34
1 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
324 TCAGCAAAATCTTAACGATGCACGCCCGAAGATTMAATTCGTGAACA 275
34 ySglndUluLalenglnllelArGLuLystrleProglunLystrllu 50
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
274 AGAGAGCGCGCATGAGATAGTCAAGAGAGAAGTGGCGGAATAAGTTTC 225
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIllepheAspLysTh 67
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
224 TTTCATATTCACACACTATTCGACTAACCTGAGATTTTCATGAAGA 175
67 rProGIUpTo 70
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
174 TCCGGAACCA 165

seq_name: gb_v1:AF026553

seq_documentation_block:
LOCUS           AF026553              1165 bp            DNA                   VRL                    03-NOV-1997
DEFINITION      Potceto yellow mosaic virus Tomato strain AV1 and AC1 genes, partial cds.
VERSION         AF026553.1
KEYWORDS        AF026553.1 GI:2583073
SOURCE          Geminiviridae.
ORGANISM        Geminiviridae
                 Viruses: ssDNA viruses.
REFERENCE       1 (bases 1 to 1165)
AUTHORS        Guzman,P., Arredondo,C.R., Emmatty,D., Portillo,R.J. and
                 Gilbertson,R.L.
TITLE          Partial Characterization of Two Whitefly-Transmitted Geminiviruses
               Infecting Tomatoes in Venezuela
JOURNAL         Plant Dis. 81, 312-312 (1997)
AUTHORS        2 (bases 1 to 1165)
               Guzman,P., Arredondo,C.R., Emmatty,D., Portillo,R.J. and
               Gilbertson,R.L.
TITLE          Direct Submission
JOURNAL         Submitted (24-SEP-1997) Plant Pathology, University of
               California-Davis, Department of Plant Pathology, Davis, CA 95616,
               USA

FEATURES             Location/Qualifiers
     source           1..1165
                     /organism="Geminiviridae"
                     /strain="Tomato strain"
                     /db_xref="taxon:10811"
                     /note="Bipartite genome; whitefly-transmitted; DNA-A
                     fragment obtained by PCR from tomato sample from State of
                     Monagas (Venezuela)"
                     complement(1..153)
                     /note="capsid protein"
                     /codon_start=1
                     /product="AV1"

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2216 AGCTAATGATGCTGCCGAGAGCCCTTAATGAGTTCCAGCTGACGAG 2167
37 1aleuGlnIleIleArgGluIysIleProGluIysTyrLeuPheGlnPhe 53
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2166 CTTTAGCATATTAATGAGAAAGAACTCCCTTAAGATTATTTTCAATAT 2117
54 HisAsnLeuAsnSerAsnLeuAspArgIlePheAspIysThrPro 68
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2116 CATATATTAATGATTAATTTAGATAGATTCTT.....ACACCT 2078
seq_name: /cgnl_8/gcgdata/geneseq/geneseqn/NA1995.DAT:AAQ84371

seq_documentation_block:
ID   AAQ84371 standard; DNA; 434 BP.
XX
AC   AAQ84371:
XX
DT   19-AUG-1995 (first entry)
XX
DE   Gemini virus-specific polyribozyme-E target sequence.
XX
KW   ribozyme target sequence: polyribozyme-E;
KM   tomato leaf curl virus; RNA cleavage; tomato transgenic plant;
KW   virus disease-resistance; ss.
XX
OS   Tomato leaf curl virus.
XX
FH   key
FT   misc_feature
   13..43
   /tag= a
   /note= "ribozyme R1 target sequence"
FT   misc_feature
   25..28
   /tag= b
   /note= "ribozyme R1 cleavage site"
FT   misc_feature
   312..342
   /tag= c
   /note= "ribozyme R2 target sequence"
FT   misc_feature
   325..327
   /tag= d
   /note= "ribozyme R2 cleavage site"
FT   misc_feature
   384..414
   /tag= e
   /note= "ribozyme R3 target sequence"
FT   misc_feature
   397..399
   /tag= c
   /note= "ribozyme R3 cleavage site"
XX
XX   WO9503404-A.
XX   PN
XX   PD
XX   02-FEB-1995.
XX
PF   22-JUL-1993; 93WO-EP01946.
XX
PR   22-JUL-1993; 93AU-0047014.
PR   22-JUL-1993; 93WO-EP01946.
XX
XX   (BIOC-) BIOCEM SA.
XX   PA   (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX   PI   Baudino S, Comeau D, Dry IB, Gruber V, Lenee P;
XX   PI   Mason J, Rezaiian MA, Rigen JE, Rezanan MA;
XX   DR
XX   WPI: 1995-075232/10.
XX
PT   Synthetic DNA virus ribozyme(s) - reduce replication, infection
PT   and/or assembly of viruses by cleaving target virus sequence,
PT   useful for preparing resistant plants, esp tomatoes.
XX
PS   Example 10; Fig 11b; 90pp; English.
XX
CC   The sequence is a tomato leaf curl virus target sequence for
CC   polyribozyme-E, which hybridizes to and cleaves the sequence and
CC   thereby reduces replication, infection and/or assembly of the virus

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CC   substantially. The ribozyme may be expressed in a transgenic plant,
CC   e.g. tomato, to confer virus disease-resistance.
XX
SQ   Sequence 434 BP; 126 A; 86 C; 91 G; 131 T; 0 other;

alignment_scores:
      Quality: 229.00      Length: 85
      Ratio: 3.754      Gaps: 1
Percent Similarity: 71.765      Percent Identity: 52.941

alignment_block:
us-09-289-346a-2 x AAQ84371
Align seg 1/1 to: AAQ84371 from: 1 to: 434

1  ThrLeuValTrpGlyIupPheGlnValAspGlyAlaAlaAlaIagIyl 17
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
95  ACCCTCGAATGGGAGAGATTTCAGATCGATGAGCATCTCGAAGAGGG 144
17  yCysGlnThrSerAsnAspAlaAlaIagIuAlaLeuAsnAlaSerL 34
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
145  ACAACAATCAGCCCAATGACGCTTACGCCAGCGCTTAACACTGGAAGTA 194
34  ySGIuGluAlaLeuGlnIleIleArgGluIysIleProGluIysTyrLeu 50
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
195  AGTCAGAGGCTCTTAACGCTCTTAGGCAATTAAGCCCTTAAGATTATGTT 244
51  PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIle..... 63
   ::||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
245  TTACAAATTTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTA 294
64  .....PheAspIysThrP 68
295  GTTGAGGTTTATGTTCTCTTTTATATCTTCTTGTGATGAGATTC 344
68  roGlu 69
   |||||
345  CAGAA 349

seq_name: /cgnl_8/gcgdata/geneseq/geneseqn/NA1995.DAT:AAQ84372

seq_documentation_block:
ID   AAQ84372 standard; DNA; 479 BP.
XX
AC   AAQ84372:
XX
DT   19-AUG-1995 (first entry)
XX
DE   Gemini virus-specific polyribozyme-F target sequence.
XX
KW   ribozyme target sequence: polyribozyme-F;
KM   tomato leaf curl virus; RNA cleavage; tomato transgenic plant;
KW   virus disease-resistance; ss.
XX
OS   Tomato leaf curl virus.
XX
FH   key
FT   misc_feature
   46..96
   /tag= a
   /note= "ribozyme R4-R5 target sequence"
FT   misc_feature
   58..60
   /tag= b
   /note= "ribozyme R4 cleavage site"
FT   misc_feature
   81..83
   /tag= c
   /note= "ribozyme R5 cleavage site"
FT   misc_feature
   355..386
   /tag= d
   /note= "ribozyme R2 target sequence"
FT   misc_feature
   370..372
   /tag= c
   /note= "ribozyme R2 cleavage site"
XX

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FT misc_feature 429..459
FT /*tag= e
FT /note= "ribozyme R3 target sequence"
FT misc_feature 442..444
FT /*tag= d
FT /note= "ribozyme R3 cleavage site"
PN W09503404-A.
XX 02-FEB-1995.
XX 22-JUL-1993; 93WO-EP01946.
XX 22-JUL-1993; 93AU-0047014.
XX 22-JUL-1993; 93WO-EP01946.
XX (BIOC-) BIOCEM SA.
XX (CSTR) COMMONWEALTH SCI & IND RES ORG.
XX Baudino S, Comeau D, Dry IB, Gruber V, Lence P;
XX Mason J, Rezalian MA, Rigden JE, Rezanan MA;
XX WPI: 1995-075232/10.
XX
XX Synthetic DNA virus ribozyme(s) - reduce replication, infection
XX and/or assembly of viruses by cleaving target virus sequence,
XX useful for preparing resistant plants, esp tomatoes.
XX
XX Example 10; Fig 11c; 90pp; English.
XX
XX The sequence is a tomato leaf curl virus target sequence for
XX poliribozyme-F, which hybridizes to and cleaves the sequence and
XX thereby reduces replication, infection and/or assembly of the virus
XX substantially. The ribozyme may be expressed in a transgenic plant,
XX e.g. tomato, to confer virus disease-resistance.
XX
SQ Sequence 479 BP; 145 A; 95 C; 97 G; 142 T; 0 other;

alignment_scores:
Quality: 229.00 Length: 85
Ratio: 3.754 Gaps: 1
Percent Similarity: 71.765 Percent Identity: 52.941

alignment_block:
US-09-289-346A-2 x AAQ84372 ..
Align seg 1/1 to: AAQ84372 from: 1 to: 479

1 ThleuValTrpGlyGluPheGlnValAspGlyAlaAlaAlaAlaGlyG1 17
||||| ||||||||| ||||||| :||| ||||
140 ACCCTCGAATGGGAGGAGTTTCAGATCGATCGATCGATCGAAGAGGGG 189
17 yCysGlnThrSerAsnAspAlaAlaAlaGluAlaLeuAsnAlaSerSer1 34
| ||||| ||||||| ||||| :||| ||||
190 ACACACATCATGCCATGACGCTTACGCCGCGCTTAACACACTGGAAGTA 239
34 ysgGluAlaLeuGlnIleIleArgGluIuysIleProGluIuysTyLeu 50
| ||||| ||||||| ||||| :||| ||||
240 AGTCAGAGGCTCTTAACGCTCTTAGGGAATTAGCCCTTAAGCATTAAGT 289
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIle..... 63
| ||||| ||||||| ||||||| |||||
290 TTACAAATTTCATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 339
64 ..... PheAspIuysThrP 68
||||| :|||
340 CTTCGAGATTATGTTCTTCCTTTTATCTCTTCTTTGATCGAAGTTC 389
68 roGlu 69
|||||
390 CAGAA 394

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seq_name: /cgnl_8/gcgdata/geneseq/geneseqn/NA1995.DAT:AAQ84375
seq_documentation_block:
ID AAQ84375 standard; DNA; 550 BP.
XX
XX AAQ84375;
XX
XX 19-AUG-1995 (first entry)
XX
XX Tomato leaf curl virus Australian strain DNA sequence.
XX
XX Tomato leaf curl virus; Australia strain; plant disease; ds.
XX
XX Tomato leaf curl virus (Australia).
XX
XX W09503404-A.
XX 02-FEB-1995.
XX 22-JUL-1993; 93WO-EP01946.
XX 22-JUL-1993; 93AU-0047014.
XX 22-JUL-1993; 93WO-EP01946.
XX (BIOC-) BIOCEM SA.
XX (CSTR) COMMONWEALTH SCI & IND RES ORG.
XX Baudino S, Comeau D, Dry IB, Gruber V, Lence P;
XX Mason J, Rezalian MA, Rigden JE, Rezanan MA;
XX WPI: 1995-075232/10.
XX
XX Synthetic DNA virus ribozyme(s) - reduce replication, infection
XX and/or assembly of viruses by cleaving target virus sequence,
XX useful for preparing resistant plants, esp tomatoes.
XX
XX Disclosure; Fig 1; 90pp; English.
XX
XX The sequence represents the complementary sense DNA strand of an
XX Australian strain of tomato leaf curl virus. Ribozymes specific
XX for this sequence may be used in generation of transgenic plants
XX with disease-resistance.
XX
SQ Sequence 550 BP; 148 A; 120 C; 134 G; 142 T; 6 other;

alignment_scores:
Quality: 228.50 Length: 86
Ratio: 3.746 Gaps: 1
Percent Similarity: 70.930 Percent Identity: 52.326

alignment_block:
US-09-289-346A-2 x AAQ84375 ..
Align seg 1/1 to: AAQ84375 from: 1 to: 550

1 ThleuValTrpGlyGluPheGlnValAspGlyAlaAlaAlaAlaGlyG1 17
||||| ||||||||| ||||||| :||| ||||
201 ACCCTCGAATGGGAGAGGTTTCAGATCGATCGATCGATCGAAGAGGGG 250
17 yCysGlnThrSerAsnAspAlaAlaAlaGluAlaLeuAsnAlaSerSer1 34
| ||||| ||||||| ||||| :||| ||||
251 ACACACATCATGCCATGACGCTTACGCCGCGCTTAACACACTGGAAGTA 300
34 ysgGluAlaLeuGlnIleIleArgGluIuysIleProGluIuysTyLeu 50
| ||||| ||||||| ||||| :||| ||||
301 AGTCAGAGGCTCTTAACGCTCTTAGGGAATTAGCCCTTAAGCATTAAGT 350
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIle..... 63
| ||||| ||||||| ||||||| |||||
351 TTACAAATTTCATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 400
64 ..... PheAspIuysT 67

```



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1 ThrlenuAlTrpGlyGluPheGlnValAspGlyValAlaAlaAlaIaGly1 17
||||: ||||||:||||||||||||| :||| ||||
328 ACAATCGAATGGGACAAATTCGAATGCGACGCGCATCTCGACAGAGG 377
17 YcysGlnThrSerAsnAspAlaAlaAlaGluAlaLeuAsnAspSerL 34
| ||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
378 TCAGCACTCTGCCAACGATCATTCGAAGGCGTTAAACGACGATTCAA 427
34 YSGluGluAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeu 50
||||:||||| ||||:|||||:|||||:|||||:|||||:|||||
428 TTGAATCTGCTTGACAATATTGAAGAGAACACCGAAAGATTACGTC 477
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
478 CTTCAACATCATCAACATCCGTTCTAATCTCGAACGATCTTCGTAAGT 527
67 rProGluPro 70
:|||||||
528 GCCGGAAACCA 537

seq_name: /cgnl_8/gcgdata/geneseq/geneseqn/NA1997.DAT:AAAT93292
seq_documentation_block:
ID AAAT93292 standard; DNA; 1062 BP.
XX
AC AAAT93292;
XX
DT 27-APR-1998 (first entry)
XX
DE Bean golden mosaic geminivirus CI mutant ORF BGAC228.
XX
KW Geminivirus; BGWV; CI gene; transdominant mutation;
XX Transgenic plant; disease resistance; ss; cyclic; circular.
XX Bean golden mosaic virus type II isolate Guatemala.
XX
OS WO9739110-A1.
XX
PN 23-OCT-1997.
XX
PD 15-APR-1997; 97WO-US06300.
XX
PF 16-APR-1996; 96US-0015517.
XX
PR (SEMI-) SEMINIS VEGETABLE SEEDS INC.
XX PA (WISC ) WISCONSIN ALUMNI RES FOUND.
XX PI Ahlquist PG, Hanson SF, Luu HT, Maxwell DP, Stout JT;
XX
DR WPI: 1997-526447/48.
DR P-PSDB; AAW34334.
XX
PT Transgenic plants expressing geminivirus AC1 and CI wild-type and
PT mutant genes - have increased resistance to geminivirus infection
PT e.g. tomato mottle virus, tomato yellow leaf curl virus or bean
PT golden mosaic geminivirus
XX
PS Claim 13; Page 111-112; 132pp; English.
XX
CC This DNA sequence comprises construct BGAC228 that codes for a
CC transdominant lethal mutant (see AAW34334) of the CI protein (see
CC AAW34338) of bean golden mosaic virus (BGWV). It was obtained by
CC Kunze mutagenesis of the wild-type CI gene (see AAAT93314). CI is
CC required for replication. The invention involves production of
CC transgenic plants containing DNA comprising geminivirus CI or AC1
CC wild-type or mutant sequences that negatively interfere in trans
CC with geminiviral replication during infection. Such transgenic
CC plants are resistant to viral infection. The AC1/CI genes are
CC especially from BGWV, tomato mottle virus or tomato yellow leaf
CC curl virus (see AAAT93282-93) and encode polypeptides (see AAW34324-35)
CC that have mutations in the highly conserved DNA-nicking and/or the
CC NTP-binding domains.

```

```

XX
SQ Sequence 1062 BP; 338 A; 247 C; 218 G; 259 T; 0 other;
alignment_scores:
Quality: 215.00 Length: 70
Ratio: 3.644 Gaps: 0
Percent Similarity: 84.286 Percent Identity: 57.143
alignment_block:
US-09-289-346a-2 x AAAT93292 ..
Align seq 1/1 to: AAAT93292 from: 1 to: 1062
1 ThrlenuAlTrpGlyGluPheGlnValAspGlyValAlaAlaAlaIaGly1 17
||||: ||||||:||||||||||||| :||| ||||
328 ACAATCGAATGGGACAAATTCGAATGCGACGCGCATCTCGACAGAGG 377
17 YcysGlnThrSerAsnAspAlaAlaAlaGluAlaLeuAsnAspSerL 34
| ||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
378 TCAGCACTCTGCCAACGATCATTCGAAGGCGTTAAACGACGATTCAA 427
34 YSGluGluAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeu 50
||||:||||| ||||:|||||:|||||:|||||:|||||:|||||
428 TTGAATCTGCTTGACAATATTGAAGAGAACACCGAAAGATTACGTC 477
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
478 CTTCAACATCATCAACATCCGTTCTAATCTCGAACGATCTTCGTAAGT 527
67 rProGluPro 70
:|||||||
528 GCCGGAAACCA 537

seq_name: /cgnl_8/gcgdata/geneseq/geneseqn/NA1997.DAT:AAAT93293
seq_documentation_block:
ID AAAT93293 standard; DNA; 1062 BP.
XX
AC AAAT93293;
XX
DT 27-APR-1998 (first entry)
XX
DE Bean golden mosaic geminivirus CI mutant ORF BGAC262.
XX
KW Geminivirus; BGWV; CI gene; transdominant mutation;
XX Transgenic plant; disease resistance; ss; cyclic; circular.
XX Bean golden mosaic virus type II isolate Guatemala.
XX
OS WO9739110-A1.
XX
PN 23-OCT-1997.
XX
PD 15-APR-1997; 97WO-US06300.
XX
PF 16-APR-1996; 96US-0015517.
XX
PR (SEMI-) SEMINIS VEGETABLE SEEDS INC.
XX PA (WISC ) WISCONSIN ALUMNI RES FOUND.
XX PI Ahlquist PG, Hanson SF, Luu HT, Maxwell DP, Stout JT;
XX
DR WPI: 1997-526447/48.
DR P-PSDB; AAW34335.
XX
PT Transgenic plants expressing geminivirus AC1 and CI wild-type and
PT mutant genes - have increased resistance to geminivirus infection
PT e.g. tomato mottle virus, tomato yellow leaf curl virus or bean
PT golden mosaic geminivirus
XX
PS Claim 13; Page 115-116; 132pp; English.
XX

```



```

XX XX Sardinian tomato yellow leaf curl virus mutated C1 gene (K227H).
DE XX
KM Nucleotide triphosphate binding site; DNA helicase; RNA helicase;
KM modification; mutation; viral replication; deficient; inhibition;
KM viral resistance; geminivirus; tomato yellow leaf curl virus;
KM Sardinian isolate; STYLCV; transgenic plant; P-loop; C1 gene;
KM All gene; ss.
XX XX
OS Sardinian tomato yellow leaf curl virus.
XX XX
XX Key Location/Qualifiers
FH CDS 1..1080
FT /*tag= a
FT /product= Rep_(K227H)
FT /note= "encodes Rep protein in which wild-type Lys
FT at position 227, i.e. within the NTP-
FT binding site, is replaced by His"
XX XX
PN WO9608573-A1.
XX XX
XX 21-MAR-1996.
XX XX
XX 15-SEP-1995; 95WO-FR01192.
XX XX
XX 15-SEP-1994; 94FR-0011040.
XX XX
XX (CNRS ) CENT NAT RECH SCI.
XX XX
XX Gronenborn B;
XX XX
XX WPI: 1996-179947/18.
XX XX
XX P-PSDB; AAR88871.
XX XX
XX Prod. of virus-resistant transgenic plants - using mutated genomic
XX sequence from phytopathogenic DNA virus
XX XX
XX Disclosure: Fig 13; 93pp; French.
XX XX
XX Mutation of consensus amino acids in the NTP-binding site of
XX geminivirus Rep protein is used to produce replication deficient
XX viruses. The mutated viral nucleic acid is used for producing
XX transgenic plants that are resistant to, or tolerant of, the native
XX virus. The present sequence encodes a mutant form of the Rep (or C1)
XX protein from the Sardinian isolate of tomato yellow leaf curl virus
XX (STYLCV) in which the wild-type Lys227 residue has been changed to a
XX His residue; transgenic Nicotiana benthamiana plants generated by
XX transformation with the mutated virus were not resistant to STYLCV.
XX In contrast, plants transformed with a virus in which Lys227 had been
XX replaced by Ala were found to be resistant.
XX XX
XX Sequence 1080 BP; 356 A; 248 C; 208 G; 268 T; 0 other:
XX
XX
XX alignment_scores:
XX Quality: 215.00 Length: 69
XX Ratio: 3.772 Gaps: 0
XX Percent Similarity: 82.609 Percent Identity: 55.072
XX
XX alignment_block:
XX us-09-289-346a-2 x AAT12905 ..
XX
XX Align seg 1/1 to: AAT12905 from: 1 to: 1080
XX
XX 2 LeuValTrpGlyGluPheGlnValAspGlyAlaAlaAlaAlaGlyGlyC 18
XX ||| ||||| |||||:::||||| ::||| |||||
XX 331 CTGGAATGGGGTACTTCCAGATCGACGACGATCTCGTACGCGAGACA 380
XX |||||:::||||||| |||||:::|||||:::|||||
XX 18 sGlnThrSerAsnAspAlaAlaAlaGluAlaLeuAsnAlaSerSerlysg 35
XX |||||:::||||||| |||||:::|||||:::|||||
XX 381 ACAGACGACGACGCTTACGCAAGCAATTACCGAGCAAGTAAGT 430
XX
XX 35 lUGlAAlaGlnAlaIleIleArgGluLysIleProGluLysTyrLeuPhe 51

```

```

seq_name: /cgnl_8/gcdata/geneseq/geneseqn/NA1996.DAT:AAT12906
seq_documentation_block:
ID AAT12906 standard; DNA; 1080 BP.
XX
XX AAT12906:
XX
XX 07-NOV-1996 (first entry)
XX
XX Sardinian tomato yellow leaf curl virus mutated C1 gene (K227R).
XX
XX Nucleotide triphosphate binding site; DNA helicase; RNA helicase;
XX modification; mutation; viral replication; deficient; inhibition;
XX viral resistance; geminivirus; tomato yellow leaf curl virus;
XX Sardinian isolate; STYLCV; transgenic plant; P-loop; C1 gene;
XX All gene; ss.
XX
XX Sardinian tomato yellow leaf curl virus.
XX
XX
XX Key Location/Qualifiers
FH CDS 1..1080
FT /*tag= a
FT /product= Rep_(K227R)
FT /note= "encodes Rep protein in which wild-type Lys
FT at position 227, i.e. within the NTP-
FT binding site, is replaced by Arg"
XX
XX
XX WO9608573-A1.
XX
XX 21-MAR-1996.
XX
XX 15-SEP-1995; 95WO-FR01192.
XX
XX 15-SEP-1994; 94FR-0011040.
XX
XX (CNRS ) CENT NAT RECH SCI.
XX
XX Gronenborn B;
XX
XX WPI: 1996-179947/18.
XX
XX P-PSDB; AAR88872.
XX
XX Prod. of virus-resistant transgenic plants - using mutated genomic
XX sequence from phytopathogenic DNA virus
XX
XX Disclosure: Fig 13; 93pp; French.
XX
XX Mutation of consensus amino acids in the NTP-binding site of
XX geminivirus Rep protein is used to produce replication deficient
XX viruses. The mutated viral nucleic acid is used for producing
XX transgenic plants that are resistant to, or tolerant of, the native
XX virus. The present sequence encodes a mutant form of the Rep (or C1)
XX protein from the Sardinian isolate of tomato yellow leaf curl virus
XX (STYLCV) in which the wild-type Lys227 residue has been changed to an
XX Arg residue; transgenic Nicotiana benthamiana plants generated by
XX transformation with the mutated virus were not resistant to STYLCV.
XX In contrast, plants transformed with a virus in which Lys227 had been
XX replaced by Ala were found to be resistant.
XX
XX Sequence 1080 BP; 356 A; 247 C; 210 G; 267 T; 0 other:
XX
XX
XX

```

alignment_scores: Quality: 215.00 Length: 69
 Ratio: 3.772 Gaps: 0
 Percent Similarity: 82.609 Percent Identity: 55.072

alignment_block:
 US-09-289-346A-2 x AAT93290 ..

Align seg 1/1 to: AAT93290 from: 1 to: 1080

```

2  LeuValITTPGlyGluPheGlnValAspGlyAlaAlaAlaGlyGlyC 18
   ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
18  SGLThSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerLySG 35
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
381 ACAGACACCCACGACGCTTACGCAAGCAATTACCGAGGAAGTAAGT 430
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
431 CGCAGGCTCTGATGATTAATTAAGCAATTAGCGCTAGAGATTACGTCTA 480
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
52  GlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysThr 68
   ::||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
481 CATTTCTATATATAAATAGTAATTAGATTTCAGGTCGCC 530
   ||| |||
68  oGluPro 70
   |||
531 GGCACCT 537
```

seq_name: /cgn1_8/gcgdata/geneseq/geneseqn/NA1997.DAT: AAT93314

seq_documentation_block:
 ID AAT93314 standard; DNA: 1183 BP.

```

XX AC AAT93314;
XX DT 27-APR-1998 (first entry)
XX DE Bean golden mosaic geminivirus CI open reading frame.
XX KW Geminivirus; BGMV; CI gene; transdominant mutation;
XX KM transgenic plant; disease resistance; ss; cyclic; circular.
XX OS Bean golden mosaic virus type II isolate Guatemala.
XX FH key Location/Qualifiers
XX FT CDS 1..1062
XX FT /tag- a
XX PN MO9739110-A1.
XX PD 23-OCT-1997.
XX PE 15-APR-1997; 97WO-US06300.
XX PR 16-APR-1996; 96US-001517.
XX PA (SEMI-) SEMINIS VEGETABLE SEEDS INC.
XX PA (WISC) WISCONSIN ALUMNI RES FOUND.
XX PI Ahlquist PG, Hanson SF, Luu HT, Maxwell DP, Stout JT;
XX DR MPI: 1997-526447/48.
XX DR P-PSDB; AAM34338.
XX XX Transgenic plants expressing geminivirus AC1 and CI wild-type and
XX PT mutant genes - have increased resistance to geminivirus infection
XX PT e.g. tomato mottle virus, tomato yellow leaf curl virus or bean
XX PT golden mosaic geminivirus
XX PS Example 5; Page 100-102; 132pp; English.
XX XX
```

CC This genomic DNA sequence includes the open reading frame (ORF) of
 CC the wild-type CI gene of bean golden mosaic virus (BGMV), a
 CC geminivirus that has a monopartite genome. The CI protein (see
 CC AAM34338) is required for replication. The wild-type CI ORF was
 CC subjected to Kunze mutagenesis (see AAT93290-93). The invention
 CC involves production of transgenic plants containing DNA comprising
 CC CI or AC1 wild-type or mutant sequences that negatively interfere
 CC in trans with geminiviral replication during infection. Such
 CC transgenic plants are resistant to viral infection. The AC1/CI
 CC genes are especially from BGMV, tomato mottle virus or tomato
 CC yellow leaf curl virus (see AAT93282-93) and encode polypeptides
 CC (see AAM34324-35) that have mutations in the highly conserved
 CC DNA-nicking domain and/or the NTP-binding domains.

Sequence 1183 BP; 372 A; 276 C; 248 G; 287 T; 0 other;

alignment_scores: Quality: 215.00 Length: 70
 Ratio: 3.644 Gaps: 0
 Percent Similarity: 84.286 Percent Identity: 57.143

alignment_block:
 US-09-289-346A-2 x AAT93314 ..

Align seg 1/1 to: AAT93314 from: 1 to: 1183

```

1  ThrLeuValITTPGlyGluPheGlnValAspGlyAlaAlaAlaGlyC 17
   ||| ::||| ||||| ||||| ||||| ||||| ||||| |||||
328 ACAATCGAATGCGGACAAATTCAGTCAGCGAGATCTGCAAGAGGAGG 377
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
17  YCYsGlnThSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerL 34
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
378 TCACGAGCTGCGACGACTCATATGCAAGGCAATTACGACGATTCAA 427
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
34  YsGluAlaLeuGlnIleIleArgLysLysIleProGluLysTyrLeu 50
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
428 TTCAATCTCCCTGACATATTTGAAGAGACAGCAACGAAAGATTACGTC 477
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
51  PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLys 67
   ::||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
478 CTTCAACATATCAACAAATTCGTTCTAATCTCGAACGATCTTCGTAAGT 527
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
67  rProGluPro 70
   ||||| |||||
528 GCCGGAACCA 537
```

seq_name: /cgn1_8/gcgdata/geneseq/geneseqn/NA1997.DAT: AAT93290

seq_documentation_block:
 ID AAT93290 standard; DNA: 1183 BP.

```

XX AC AAT93290;
XX DT 27-APR-1998 (first entry)
XX DE Bean golden mosaic geminivirus CI mutant gene.
XX KW Geminivirus; BGMV; CI gene; transdominant mutation;
XX KM transgenic plant; disease resistance; ss; cyclic; circular.
XX OS Bean golden mosaic virus type II isolate Guatemala.
XX FH key Location/Qualifiers
XX FT CDS 1..1062
XX FT /tag- a
XX PN MO9739110-A1.
XX PD 23-OCT-1997.
XX PE 15-APR-1997; 97WO-US06300.
XX XX
```

DE	
XX	
XX	PWRG 2288 35S-rep gene cassette.
XX	
XX	Geminivirus; DNA-A; geminivirus replication inhibition; ac3 gene;
KW	transgenic plant; antiviral; gene therapy; bean golden mosaic virus;
KW	BGMV; alfalfa mosaic virus; AMV; cauliflower mosaic virus; CamV; ds.
XX	
XX	Bean golden mosaic virus.
OS	cauliflower mosaic virus.
OS	Alfalfa mosaic virus.
OS	Synthetic.
XX	
PN	US6118048-A.
XX	
PD	12-SEP-2000.
XX	
XX	24-APR-1998; 98US-0065999.
PF	
XX	
PR	25-APR-1997; 97US-0044925.
XX	
XX	
PA	(WISC) WISCONSIN ALDUMNI RES FOUND.
XX	
DR	WPI; 2000-610861/58.
XX	
XX	
PT	Genetic construct comprising a mutant geminiviral rep gene, useful for
XX	producing a plant resistant to geminiviral infection -
XX	
PS	Example; Column 15-16; 14pp: English.
XX	
XX	The present sequence is a 35S-rep gene cassette comprising the rep gene
CC	of bean golden mosaic virus (BGMV)-GA cloned downstream of the CamV
CC	35S promoter and an alfalfa mosaic virus (AMV) leader sequence. The
CC	sequence was integrated into pBSIT-KS+ to produce a rep gene expression
CC	vector.

CC or geminiviral replication. When expressed in a plant cell, this
CC inhibitor is able to dramatically reduce replication of geminivirus.
CC Genetic constructs that include sequences containing a portion of the
CC ac3 gene in addition to the trans-dominant inhibitor exhibit increased

replication. Geminiviruses are one of the greatest constraints on

by using the genetic construct.

896 TTGAATCTGCCCTTGACATATTGAAGGAAGACACACCGAAGATTACGTC 945

51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysThr 67

946 CTTCAACATCACAACATCGGTTCTAATCTGGAACGGATCTTGTCAAGT 995

67 rProGluPro 70
:|||||
996 GCCGGAACCA 1005

seq_name: /cgnl_8/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA94701

id_documentation_block:
ID AAA94701 standard; DNA: 1651 BP.

AC AAA94701:

DT 15-JAN-2001 (first entry)

DE PTrepN nucleotide sequence.

KW Geminivirus; DNA-A; geminivirus replication inhibition; ac3 gene;

KW transgenic plant; antiviral; gene therapy; bean golden mosaic virus;

KW BGW; alfalfa mosaic virus; AMV; cauliflower mosaic virus; CaMV; ds.

OS Bean golden mosaic virus.

OS Cauliflower mosaic virus.

OS Alfalfa mosaic virus.

OS Synthetic.

PN US6118048-A.

PD 12-SEP-2000.

PF 24-APR-1998: 98US-0065999.

PR 25-APR-1997: 97US-0044925.

PA (MISC) WISCONSIN ALUMNI RES FOUND.

DR WPI; 2000-610861/58.

XX Genetic construct comprising a mutant geminiviral rep gene, useful for

XX producing a plant resistant to geminiviral infection -

XX Example: Column 17-18: 14pp; English.

XX The present sequence is pTrepN, a vector containing a CaMV-35S

XX promoter-driven rep gene derived from bean golden mosaic virus (BGW)-GA.

XX Site-directed mutagenesis was used to engineer an NcoI site in the start

XX codon of the rep gene to facilitate cloning of DNA-nicking domain

XX mutants. The resulting genetic constructs act as trans-dominant

XX inhibitors of geminiviral replication. When expressed in a plant cell,

XX these inhibitors are able to dramatically reduce replication of

XX geminivirus. Genetic constructs that include sequences containing a

XX portion of the ac3 gene in addition to the trans-dominant inhibitor

XX exhibit increased efficiency and broadened specificity of inhibition of

XX geminiviral replication. Geminiviruses are one of the greatest

XX constraints on production of important crops, including cassava, beans,

XX cowpeas, peppers, tomatoes and cotton. The effects of the virus can be

XX overcome by using the genetic construct.

XX

sequence 1651 BP; 517 A; 392 C; 343 G; 399 T; 0 other;

alignment_scores:
Quality: 215.00 Length: 70
Ratio: 3.644 Gaps: 0
Percent Similarity: 84.286 Percent Identity: 57.143

alignment_block:

US-09-289-346A-2 x AAA94701 ..

Align seg 1/1 to: AAA94701 from: 1 to: 1651

1 ThrleuValTrpGlyGluPheGlnValAspGlyAlaAlaAlaGlyG1 17
||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
796 ACATTCGATCGGACAAATTCAGTCGACCGCAGATCTGCAAGAGGAGC 845

17 YCysGlnThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerL 34
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||
846 TCAGCAGTCTGCCACGACGCTCATATGCAAGCATTAAACCGACATTCA 895
34 YSGluGluAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeu 50
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||
896 TTGAATCTGCCTTGACATATTGAAAGGAAGCAACGCAAGATTACGTC 945
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAsnParGlyIlePheAspLysTh 67
:|||||:|||||:|||||:|||||:|||||:|||||:|||||
946 CTTCACATTCACAAACATTCGTTCTTAATCTCGAACGATCTTCGTAAGT 995
67 rProGluPro 70
:|||||
996 GCCGGAACCA 1005

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```

553 AACGGGCGCGAGTTCCTGTGCATCCAAAGAACAATAACTACATCCTCC 602
26 actua|aleuasnA|aserSerLySGluclalaleuin|leI|earyg 43
+ ||||||::: ||||| ||||| ::||| |||
603 C...GCCATTAGCATGCTTTCCAAAGAGAGCGCCCCGAGATCAACACGTG 649
43 l|ulyst|lePro..... 46
650 AAAAGGCCCAAANAATCCCGGCCGAATTTTGTCNAACCACAGTGGGAGAAC 699
47 ...glUlystYrLeuphegInPheHIsAsnLeAsnSerAsn 59
||| ::||| ::|||::: |||
700 CTCGAGCCCTCTCCTCAAGATTTCACACATTCATCCGAAT 741

seq_name: gb_est1:A1959235

seq_documentation_block:
LOCUS A1959235 560 bp mRNA EST 20-AUG-1999
DEFINITION fd59609.y1 zebrafish Mashu MPMG EST Danio rerio CDNA 5' similar to
gb:X6150 40S RIBOSOMAL PROTEIN S18 (HUMAN);, mRNA sequence.
ACCESSION A1959235
VERSION A1959235.1 GI:5751948
KEYWORDS EST.
SOURCE zebrafish.
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Rasborinae; Danio.
1 (bases 1 to 560)
Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy
,S., Hillier,L., Knuchak,T., Martin,J., Beck,C., Wyllie,T., Underwood
,R., Stepoe,M., Theising,B., Allen,M., Bowers,Y., Person,B.,
Swaller,T., Gibbons,M., Page,D., Harvey,N., Schurk,R., Ritter,E.,
Kohn,S., Shih,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R.
and Wilson,R.
Mashu zebrafish EST Project 1998
Unpublished (1998)
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrafsh@watson.wustl.edu
CDNA library Preparation: Matthew Clark, CDNA library Arrayed by:
Matthew Clark, DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
info@genomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@resgen.com) and
ResourcenCenter@mprimatdenbank, Berlin, Germany (web address:
www.rzp.d.de)
Seq primer: T3 ET from Amersham
High quality sequence stop: 491.
Location/Qualifiers
1..560
/organism="Danio rerio"
/db_xref="taxon:7935"
/cclone_id="Zebrafish Mashu MPMG EST"
/sex="mixed"
//issue_type="26 somite embryos, adult livers, shield
stage embryos"
/lab_host="XLI-blue MRF"
/note="vector: pSPORT1; site_1: NotI; site_2: SalI; 1st
strand cDNA was primed with a Not I - oligo(dT)15 primer
[5';GACCTAGTTCACATCCGAGCGCGCCGCTTTTTTTTTTTTTTTT];
double-stranded cDNA was ligated to Sal I adaptors (BRL),
digested with Not I and cloned into the Not I and Sal I
sites of the pSPORT1 vector (BRL). Library was constructed
by Matthew Clark (Lehrach lab; ICRR, London and Max Planck
Institut fuer Molekulare Genetik Berlin). cDNAs for EST
analysis were selected following oligonucleotide
hybridization fingerprinting of arrayed clones from
zebrafish late somitogenesis (26 ss), adult liver or

```

embryonic shield stage (5.6 h) libraries. Fingerprint data were used to computationally cluster cDNAs, and a single cDNA from each cluster was chosen for sequencing. In some cases multiple members of the same cluster were sequenced to assess clustering parameters or single clones were sequenced additional times to assess quality control."

BASE COUNT 141 a 130 c 161 g 128 t
ORIGIN

alignment_scores:
Quality: 72.00 Length: 61
Ratio: 1.946 Gaps: 2
Percent Similarity: 60.656 Percent Identity: 31.148

alignment_block:
US-09-289-346A-2 x AI959235 ..

Align seg 1/1 to: AI959235 from: 1 to: 560

1 ThrLeuValTrpGlyGluPheGlnValAspGlyAlaAlaAlaGlyc1 17
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22 ACCTTCTCGTGGGG.....GGGGGTGGCGG 50

17 yCySGlnThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerL 34
||||| :||||| :|||||
51 GGTGTGACCCCTCTCTCCACCGCTCCGCCACGGCTGCCAGCGATC 100

34 ysgJugLulAlaGlnIleIleArgGluLysIleProGluLysTryLeu 50
:||||| :|||||
101 AACATCTCTCTCT.....GTCAATGCCAGAGAGATTTCAG 135

51 PheGlnPheHisAsnLeuAsnSerAsnLeuAsp 61
:||||| :|||||
136 CACATCCTTCGTCTCTCTCAACAGACATTGAT 168

seq_name: gb_est1:BE401979

seq_documentation_block:
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DEFINITION CS8003B04990908 ITFC CSB Wheat Endosperm Library Triticum aestivum
ACCESSION CNA clone CSB003B09, mRNA sequence.
VERSION BE401979
KEYWORDS BE401979.1 GI:9361447
SOURCE EST.
ORGANISM bread wheat.
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidaeae
Triticeae; Triticum.
1 (bases 1 to 579)
REFERENCE
AUTHORS Anderson,O.A., Appels,R., Bailey,P., Blake,T., Close,T., Cloutier
S., Dubcovsky,J., Feuillet,C., Gale,M., Graner,A., Gustafson,P.,
Herrmann,R.G., Holton,T., Jacquemin,J.M., Jia,J., Joudrier,P.,
Langridge,P., Lazo,G.R., Lin,J.J., McGuire,P., Ogihara,T.,
Pechoni,I.N., Qalasei,C., Schuch,W., Selvaraj,G., Shariflu,M.,
Sorrells,M., Warburton,M. and Wezel,G.
International Triticeae EST Cooperative (ITEC): Production of
Expressed Sequence Tags for Species of the Triticeae
Unpublished (2000)
JOURNAL COMMENT
CONTACT Appels R
Div. of Plant Industry, CSIRO
Canberra ACT 2601 AUSTRALIA
Tel: 61 62 465496
Fax: 61 62 465000
Email: rudiepi@csiro.au
International Triticeae EST Cooperative (ITEC)
http://wheat.pw.usda.gov/genome.
LOCATION/Qualifiers
1..579
/organism="Triticum aestivum"
/cultivar="Wyuna"

```

/db_xref="taxon:4565"
/clone_lib="IRPC CSB Wheat Endosperm Library"
/tissue_type="endosperm"
/dev_stage="8-12 days post anthesis"
/lab_host="Escherichia coli SOLR"
/note="Vector: Lambda zap/Bluescript; Site_1: XhoI;
Site_2: EcoRI; Plants grown in Phytoion with 18C/13C
(day/night) 16 hour light. M13 Reverse sequencing primer
used. 1.0 kbp average insert size."
BASE COUNT      100 a      178 c      167 g      134 t
ORIGIN
alignment_scores:
  Quality: 71.00      Length: 49
  Ratio: 2.290      Gaps: 2
  Percent Similarity: 63.265      Percent Identity: 42.857
alignment_block:
US-09-289-346A-2 x BEA01979 ..
Align seg 1/1 to: BEA01979 from: 1 to: 579
9 ValAspGIAlaAlaAlaAlaGlyGlyCysGlnThrsSerAsnAspAlaI 25
::: |||:::|||||:::|||||:::|||||:::|||||
283 ATCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 332
25 aAlaGluAlaLeuAsnAlaSerSerlySGluAlaLeuGlnIleIleA 42
|||||:::|||||:::|||||:::|||||:::|||||
333 CGCTGAGCGCCCAAGCGCTGCTGAGAGAGAGAA..... 366
42 rGtGluysIleProGluLys.....TyrLeuPhe 51
|||||:::|||||:::|||||:::|||||:::|||||
367 ..GAGAGATTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 411
seq_name: gb_est1:AV736082
seq_documentation_block:
LOCUS      AV736082      616 bp      mRNA      EST      17-OCT-2000
DEFINITION AV736082 CB Homo sapiens cDNA clone CBMABH09 5', mRNA sequence.
ACCESSION  AV736082
VERSION     AV736082.1 GI:10853663
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 616)
REFERENCE   1 (bases 1 to 616)
  AUTHORS   Zhang,Q., Ye,M., Wu,X., Gu,J., Huang,Q., Zhou,Y., Shen,Y., Han,Z.,
  TITLE     Chen,S., Mao,M. and Chen,Z.
  JOURNAL   Homo sapiens CB library cDNA clones
  COMMENT   Unpublished (2000)
  CONTACT   Zhu Chen
  LOCATION  Shanghai Institute of Hematology, Rui-Jin Hospital
            197 Rui-Jin II Road, Shanghai 200025, P. R. China
            Tel: 86-21-64740490
            Fax: 86-21-64743206
            Email: mbshl@sh.sh.cn
  NOTE      This clone is available at Shanghai Hematology Institute in
            Shanghai.
            Chinese National Human Genome Center at Shanghai
            351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong.
FEATURES             Location/Qualifiers
     source          1..616
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="CBMABH09"
                     /clone_lib="CB"
                     /tissue_type="cord blood"
                     /cell_type="CD34+ hematopoietic stem/progenitor cell"
                     /lab_host="BM25.8"
                     /note="Vector: pBluescript; Site_1: EcoRI; The insert is

```

```

BASE COUNT      173 a      149 c      171 g      118 t      5 others
ORIGIN
alignment_scores:
  Quality: 71.00      Length: 51
  Ratio: 1.919      Gaps: 2
  Percent Similarity: 72.549      Percent Identity: 35.294
alignment_block:
US-09-289-346A-2 x AV736082 ..
Align seg 1/1 to: AV736082 from: 1 to: 616
12 AlAlaAlaAlaGlyGlyCysGln...ThsSerAsnAspAlaAlaAlaG 27
|||||:::|||||:::|||||:::|||||:::|||||
6 GCGCGCGCTGACCGCGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAG 55
27 uAlaLeuAsnAlaSerSerlySGluAlaLeuGlnIleIleArgGlu 44
:::|||||:::|||||:::|||||:::|||||:::|||||
56 AGCGCTACACCGCGCGCTGCTGCTGCAGCCATGCTCTATGTC..... 98
44 ySileProGluLysTyrLeuPheGlnPheHisAsnLeuAsnSerAsnLeu 60
|||||:::|||||:::|||||:::|||||:::|||||
99 ..ATCCCTGAAGAAGTTCACACATATTTTGGAGTACTCAACACCAACATC 146
61 Asp 61
|||
147 GAT 149
seq_name: gb_gss:AQ950848
seq_documentation_block:
LOCUS      AQ950848      572 bp      DNA      GSS      27-JAN-2000
DEFINITION Sheared DNA-51M3.TF Sheared DNA Trypanosoma brucei genomic clone
ACCESSION  AQ950848
VERSION     AQ950848.1 GI:6774113
KEYWORDS    GSS.
SOURCE      Trypanosoma brucei.
ORGANISM    Trypanosoma brucei.
Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 572)
REFERENCE   1 (bases 1 to 572)
  AUTHORS   El-Sayed,N., Zhao,S., Zhao,H., Gill,S., Suh,E., Malek,J., Fujii,C.,
  TITLE     Gerrard,C., Leech,V., de Jong,P., Ulliv,E., Melville,S., Donelson,J.,
  JOURNAL   Fraser,C. and Adams,M.
  COMMENT   Determination of clone end sequences from Trypanosoma brucei GUTat
            10.1 sheared DNA library
            Unpublished (1999)
            Other_GSSs: Sheared DNA-51M3.TF
            CONTACT: Najib M. El-Sayed
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            7712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: nelsayed@tigr.org
            Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared
            DNA library constructed at TIGR. Clones will be available for
            distribution through ATCC. Sheared DNA end sequences search page:
            http://www.tigr.org/cdb/mdb/cdbdb/.
            Seq primer: M13-Forward
            Class: Shotgun.
FEATURES             Location/Qualifiers
     source          1..572
                     /organism="Trypanosoma brucei"
                     /strain="TREU927/4 GUTat 10.1"
                     /db_xref="taxon:5691"
                     /clone_lib="Sheared DNA-51M3"
                     /clone_lib="Sheared DNA"
                     /note="Vector: pUC18; Site_1: SmaI; Constructed at The

```

```

INSTITUTE FOR GENOMIC RESEARCH (TIGR), ROCKVILLE, MD.
GENOMIC DNA ISOLATED FROM A CLONED POPULATION OF
Trypanosoma brucei (TREU927/4 GUTat 10.1) WAS MECHANICALLY
SHEARED TO GIVE A TIGHT SIZE DISTRIBUTION (APPROX 2 KB).
THE V + I METHOD USED FOR THE LIBRARY CONSTRUCTION IS
DESCRIBED IN DETAIL IN SMITH, H.O., AND VENTER, J.C.
(Making small insert libraries for whole genome shotgun
sequencing projects. In Genome Sequencing: A Practical
Approach, eds. M. Vaundin and B. Barrell, Oxford University
Press, 1999)."
BASE COUNT      115 a       118 c       180 g       159 t
ORIGIN

alignment_scores:
    Quality:      70.00          Length:      31
    Ratio:        2.500         Gaps:      0
    Percent Similarity: 90.323   Percent Identity: 38.710

alignment_block:
US-09-289-346A-2 x AQ950848 ..

Align seg 1/1 to: AQ950848 from: 1 to: 572

11 GLYALAALAAIAAGLYGCGINTHrSerAsnSPAlaIaaGI 27
|||||:::|||||:::|||||:::|||||:::|||||:::
291 GGCGCTCCGGCATTGGCGGTGCCAACACGACGATGACTGCATTGA 340

27 uAlaLeuAsnAlaSerLysGlInuAlaLeuGlnIleIe 41
|||||:::|||||:::|||||:::|||||:::|||||:::
341 AGCTTTGCTGTCGCGAGACTCTCCGACGCCAGTTCAAGTGATG 383

seq_name: gb_gss:AQ947513

seq_documentation_block:
LOCUS      AQ947513              587 bp           GSS               27-JAN-2000
DEFINITION Sheared DNA-49M17.TF Sheared DNA Trypanosoma brucei genomic clone
ACCESSION  AQ947513
VERSION    AQ947513.1 GI:6770778
KEYWORDS   GSS.
SOURCE     Trypanosoma brucei.
ORGANISM   Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1 (bases 1 to 587)
AUTHORS    El-Sayed,N., Zhao,S., Zhao,H., Gill,S., Suh,E., Malek,J., Fujii,C.,
            Gerrard,C., Isech,V., de Jong,P.P., Ulliu.E., Melville,S., Donelson,J.J.,
            Fraser,C. and Adams,M.
TITLE       Determination of clone end sequences from Trypanosoma brucei GUTat
            10.1 sheared DNA library
JOURNAL    Unpublished (1999)
COMMENT    Other_GSSs: Sheared DNA-49M17.TR
            Contact: Najib M. El-Sayed
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel.: 301 838 0200
            Fax: 301 838 0208
            Email: nelsayed@tigr.org
            Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared
            DNA library constructed at TIGR. Clones will be available for
            distribution through ATCC. Sheared DNA end sequences search page:
            http://www.tigr.org/tdb/mdb/cbdb/.
            Seq primer: M13-Forward
            Class: Shotgun

FEATURES             Location/Qualifiers
     source            1..587
                     /organism="Trypanosoma brucei"
                     /strain="TREU927/4 GUTat 10.1"
                     /db_xref="taxon:5691"
                     /clone="Sheared DNA-49M17"
                     /clone_id="Sheared DNA"

```

[illegible]

/clone="t40c19"
/clone.lib="Trypanosoma cruzi random genomic library"
/cell.type="epimastigote"
/note="Vector: pBS(-) (Stratagene); T. cruzi DNA was randomly sheared using a nebulizer and the 1 to 2 Kb range was gel purified and cloned into the dephosphorylated HincII site of the vector"

BASE COUNT 113 a 110 c 99 g 90 t

ORIGIN

alignment_scores:
Quality: 69.00 Length: 52
Ratio: 2.029 Gaps: 1
Percent Similarity: 65.385 Percent Identity: 36.538

alignment_block:
US-09-289-346a-2 x AQ906722 ..

Align seg 1/1 to: AQ906722 from: 1 to: 412

```

8 GlnValaspGlyAlaAlaAlaGlyCysGlnThrSerAsnAspAl 24
   :::::::::::::: :::: :::: :::: :::: ::::
218 AGACGGATGGCTACCGACAGACGCGCGCTATCTACAGTTACCGACGC 267
   :: :: :::: :::: :::: :::: :::: ::::
24 aAlaAlaGluAlaLeuAsnAsnSerLysGluGluAlaLeuGln 40
   :: :: :::: :::: :::: :::: :::: ::::
268 CCGACCGTGAAGCAGAAATGCAACGACAGAGACTCAATTTCTCTCTA 317
   :: :: :::: :::: :::: :::: :::: ::::
41 IleArgGluLysIleProGluLysTyrLeuPheGlnPheHisAsnLeu 57
   :::: :::: :::: :::: :::: :::: ::::
318 CTTCGAGAGCGCTTGGCGCAACAGCTATCTACGCTGCAATTACCAATTAA 367
   :::: :::: :::: :::: :::: :::: ::::
57 nser 58
   ::::
368 TTCA 371

```

seq_name: gb_gss:A0656777

seq_documentation_block: 570 bp DNA GSS 23-JUN-1999
LOCUS A0656777
DEFINITION Sheared DNA-27M23.TR Sheared DNA Trypanosoma brucei genomic clone
ACCESSION A0656777
KEYWORDS Sheared DNA-27M23, DNA sequence.
VERSION A0656777.1 GI:5164625
GSS.

SOURCE Trypanosoma brucei.
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

Trypanosoma.
1 (bases 1 to 570)

REFERENCE 1 (bases 1 to 570)
AUTHORS El-Sayed, N., Zhao, S., Zhao, H., Gill, S., Suh, E., Malek, J., Fujii, C., Gerrard, C., Leech, V., de Jong, P., Olu, E., Melville, S., Donelson, J., Fraser, C., and Adams, M.
TITLE Determination of clone end sequences from Trypanosoma brucei GUTat 10.1 sheared DNA library
JOURNAL Unpublished (1999)
COMMENT Other-GSSs: Sheared DNA-27M23.TF
Contact: Neijb M. El-Sayed
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208

FEATURES
source
1..570
Location/Qualifiers
Email: nelsayed@tigr.org
Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared DNA library constructed at TIGR. Clones will be available for distribution through ATCC. Sheared DNA end sequences search page: <http://www.tigr.org/tldb/mdb/tldb/>.
Seq primer: M13-Reverse
Class: Sholgun.

/organism="Trypanosoma brucei"
/strain="TREU927/4 GUTat 10.1"
/db_xref="taxon:5691"
/clone="Sheared DNA-27M23"
/clone.lib="Sheared DNA"
/note="Vector: pUC18; Site 1: SmaI; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (approx 2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999)."

BASE COUNT 84 a 132 c 151 g 203 t

ORIGIN

alignment_scores:
Quality: 68.50 Length: 62
Ratio: 1.756 Gaps: 4
Percent Similarity: 62.903 Percent Identity: 38.710

alignment_block:
US-09-289-346a-2 x A0656777/rev ..

Align seg 1/1 to reverse of: A0656777 from: 1 to: 570

```

8 GlnValaspGly.....AlaAlaAlaGlyGlyCysGlnThrSerAs 22
   :::: :::: :::: :::: :::: :::: ::::
228 CACTGGACGGTATCAAAATTACAGCCGACGCGCTGCAACGCAAA 179
   :::: :::: :::: :::: :::: :::: ::::
22 n..AspAlaAlaGluAlaLeuAsnAla.....SerSerLysG 35
   :::: :::: :::: :::: :::: :::: ::::
178 CAGCCAAAGCGCTAGCGGTGCATTAACGCAATGTCGTCAGCGCGCT 129
   :::: :::: :::: :::: :::: :::: ::::
35 lGluAlaLeuGlnIleIleArgGluLysIlePro...GlnLysTyrLeu 50
   :::: :::: :::: :::: :::: :::: ::::
128 CAGGTGCTGTGAAATTAACAAAGCCAAACCGCAGCATGACCTACAG 79
   :::: :::: :::: :::: :::: :::: ::::
51 PheGlnPheHisAsnLeuSerAsnLeuAspArg 62
   :::: :::: :::: :::: :::: :::: ::::
78 ACAGCAACCCACTTTTTCAGAGCAAGAGAGACAG 43
   :::: :::: :::: :::: :::: :::: ::::

```

seq_name: gb_est1:AM012852

seq_documentation_block: 598 bp mRNA EST 10-SEP-1999
LOCUS AM012852
DEFINITION LDT-0013 Winter flounder liver Pleuronectes americanus cDNA clone
IDT-0013 5' similar to vltronectin, mRNA sequence.
ACCESSION AM012852
VERSION AM012852.1 GI:5861630
KEYWORDS EST.
SOURCES Pleuronectes americanus.
ORGANISM Pleuronectes americanus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes; Pleuronectoidae; Pleuronectidae; Pleuronectes.

REFERENCE 1 (bases 1 to 598)

AUTHORS Douglas, S.E., Gallant, J.W., Bulterwell, C.E., Wolff, C., Munholland, J., and Reith, M.E.
TITLE Winter flounder expressed sequence tags: Establishment of an EST database and identification of novel fish genes
JOURNAL Marine Biotechnology (1999) In press
COMMENT Contact: Reith M
Marine Biology
NRC Institute for Marine Biosciences
1411 Oxford St., Halifax, Nova Scotia, B3H 3Z1, Canada
Tel: (902) 426-8276
Fax: (902) 426-9413

Email: michael.reith@ncr.ca
Seq primer: M13 Forward.
Location/Qualifiers

FEATURES
source 1..598 /organism="Pleuronectes americanus"
/db_xref="taxon:8263"
/clone_lib="JDT-0013"
/clone_lib="Winter flounder liver"
/sex="female"
/dev_stage="adult"
/note="Organ: liver"

BASE COUNT 123 a 180 c 158 g 136 t 1 others
ORIGIN

alignment_scores:
Quality: 68.50 Length: 67
Ratio: 1.593 Gaps: 2
Percent Similarity: 64.179 Percent Identity: 28.358

alignment_block:
US-09-289-346A-2 x AW012852 ..

Align seg 1/1 to: AW012852 from: 1 to: 598

```

11 GLYALAIAAIAAGLYGYSGLNThrSerAsnAspAlaAlaAGL 27
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
95 GGAATGGCAGTGCATCCATGTCGTCTGATGAGAGCTGCTGTGA 144
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
27 uAlaLeuAsnAlaSerSerLysGluGluAlaLeuGlnIle.....I 41
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
145 GACTTTGACTCGGTGTGCCCAAAAGACCGCTGGGTGACACCTTGA 194
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
41 leaTgGluLysIleProGluLys.....TyrLeuPheGlnPhe 53
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
195 TGCAGAGAGGACACACGAGAAACGTCACCCCGCTGCTACGACTGTG 244
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
54 HlAsnLeuAsnSerAsnLeuAsnParGilePheAspLysThrProGlu 70
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
245 CACCACTTTCACACATCTGACGGGTTGTCTCTCTCCGCCCATCCCC 294
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
70 o 70
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
295 A 295

```

seq_name: gb_gss:A2208697

seq_documentation_block:

LOCUS A2208697 910 bp DNA GSS 31-AUG-2000
DEFINITION SP_0150_A2.C02.SP66 Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library Strongylocentrotus purpuratus genomic clone Plate-150 Col-4 Row-E, DNA sequence.

ACCESSION A2208697
VERSION A2208697.1 GI:8421822

KEYWORDS GSS.
SOURCE Strongylocentrotus purpuratus.
ORGANISM Strongylocentrotus purpuratus.

REFERENCE
AUTHORS Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa; Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae; Strongylocentrotus.
1 (bases 1 to 910)
Cameron, R.A., Mahlras, G., Rast, J.P., Martinez, P., Biondi, T.R., Swartzell, S., Wallace, J.C., Pousetka, A.J., Livingston, B.T., Wray, G.A., Ertensohn, C.A., Lehrach, H., Britten, R.J., Davidson, E.H. and Hood, L.
A sea urchin genome project: Sequence scan, virtual map, and additional resources
Proc. Natl. Acad. Sci. U. S. A. 97 (17), 9514-9518 (2000)

TITLE

JOURNAL MEDLINE
COMMENT 20402566
Contact: Cameron, RA, Davidson, EH, Hood, L
Division of Biology 156-29
California Institute of Technology
Pasadena California 91125, USA

Tel: (626) 395-8421
Fax: (626) 793-3047
Email: acameron@caltech.edu
Plate: 150 row: E column: 4
Seq primer: SP6
Class: BAC ends
High quality sequence stop: 910.
Location/Qualifiers

FEATURES
source 1..910

/organism="Strongylocentrotus purpuratus"
/db_xref="taxon:7668"
/clone_lib="Plate=150 Col=4 Row=E"
/clone_lib="Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library"
/note="Organ: sperm; Vector: BAC63.6; BAC Clones in E-Coli DH10B"

BASE COUNT 248 a 255 c 170 g 237 t
ORIGIN

alignment_scores:
Quality: 68.50 Length: 56
Ratio: 1.957 Gaps: 3
Percent Similarity: 62.500 Percent Identity: 35.714

alignment_block:
US-09-289-346A-2 x A2208697 ..

Align seg 1/1 to: A2208697 from: 1 to: 910

```

18 CysGlnThrSerAsnAspAlaAlaGlu...AlaLeuAsnAlaSerSe 33
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
604 TGCAACCTGTCTTACGGGCGCATCCCGGAAATGTTTAAACAATCTAT 653
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
33 rLysGluGluAlaLeuGlnIleIle....ArgGluLysIleProGlu 48
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
654 CTTAGTCCACACAGACACTAGTGAATATGCAAACTACGCGGAAA 703
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
48 ySTYrLeuPheGlnPheHlAsnLeuAsnSerAsnLeuAsnParGile 64
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
704 AATGG.....CACACTATGTGAAATAATTACCGGAGATTGG 741
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
65 AspLysThrProGluPro 70
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
742 GGTAAACCCCTTCGCCG 759

```

seq_name: gb_est2:BG275828

seq_documentation_block:

LOCUS BG275828 503 bp mRNA EST 21-FEB-2001
DEFINITION NXSL_148_D05_P NXSL (nsf Xylem Side wood Inclined) Pinus taeda CDNA clone NXSL_148_D05_5', mRNA sequence.

ACCESSION BG275828
VERSION BG275828.1 GI:13069536

KEYWORDS EST.
SOURCE loblolly pine.
ORGANISM Pinus taeda.

REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
1 (bases 1 to 503)
Sederoff, R.
Molecular Basis of wood formation in the pine Megagenome
unpublished (2000)
Contact: Johnson, Arthur
North Carolina State University
Tel: 919 515 7800
Fax: 919 515 7801
Email: ajohnson@unity.ncsu.edu

TITLE

JOURNAL
COMMENT
Seq primer: T3.
Location/Qualifiers

FEATURES
source 1..503

/organism="Pinus taeda"
/strain="Coastal plain loblolly pine from North Carolina"

/db.xref="taxon:3352"
/clone="NXSI.148.D05"
/clone_lib="NXSI (NsF Xylem Side wood Inclined)"
/tissue_type="Xylem"
/cell_type="Side"
/dev_stage="Juvenile"
/lab_host="XLI-Blue"
/note="Vector: Bluescript SK; Site.1: Eco RI; Site.2: XhoI
; The library is from early (spring) wood, taken from
three six-year old trees (three different genotypes), in
the juvenile phase. These trees were induced to form side
wood by bending to a 45 degree angle and tying them to the
ground. Differentiating xylem was harvested from the sides
of the inclined stems, and a mixture of all three
genotypes was used for the library. oligo-dT primed cDNA
was directionally cloned into the EcoRI-XhoI Bluescript SK
vector arms. NOTE: The sequences contain a 'cDNA adapter'
between the EcoRI site and the start of the EST. The
adapter sequence is 'AATTCGACGACG'."

BASE COUNT 112 a 115 c 108 g 151 t 17 others
ORIGIN

alignment_scores:

Quality: 67.00 length: 52
Ratio: 2.094 Gaps: 2
Percent Similarity: 61.538 Percent Identity: 34.615

alignment_block:

US-09-289-346a-2 x BG275828/rev ..

Align seg 1/1 to reverse of: BG275828 from: 1 to: 503

18 CysglThSerAsnSPAlaAlaGluAlaLeuAsnAlaSerSeryl 34
||||| : : : : : ||||| : : : : :
498 TGTGGCTGACAGCACCGAGTTCTCAGAAAGCAATCGCTCAATCT 449
34 sglGluAlaLeuGlnIlelle.AirgGluLysIleProGluLysTyrLeu 50
||||| : : : : : ||||| : : : : :
448 GGCCTGCTTACACACCTCTTAAACACCACTCCGGACGATAT... 402
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
||||| : : : : : ||||| : : : : :
401CTGAATGGGATTATTAGACGACGATATTGACCAAAAT 367

67 rPro 68
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366 ACCC 363

seq_name: gb_est1:A1563120

seq_documentation_block:

LOCUS A1563120 314 bp mRNA EST 26-MAR-1999
DEFINITION EST00244 watermelon lambda zap library Citrullus lanatus cDNA clone
WMS446 5' similar to Photosystem I Accessory Protein E, mRNA
sequence.

ACCESSION A1563120
VERSION A1563120.1 GI:4521502

KEYWORDS

EST.

SOURCE

watermelon.

ORGANISM

Citrullus lanatus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eustosids I; Cucurbitales; Cucurbitaceae; Citrullus.

1 (bases 1 to 314)

Shin,J.S.

Watermelon Leaf cDNAs

Unpublished (1999)

Contact: Jeong Sheop Shin

Plant Molecular Genetics

Graduate School of Biotechnology, University of Korea

136-701 Anam-dong 5/1 Seoul, Korea

Tel: 00 82 2 3290 3430

Fax: 00 82 2 927 9028
Email: jshin@kuonx.korea.ac.kr
Seq primer: T3.

FEATURES

source

Location/Qualifiers

1..314

/organism="Citrullus lanatus"

/cultivar="lucky"

/db.xref="taxon:3654"

/clone="WMS446"

/clone_lib="watermelon lambda zap library"

/dev_stage="seedling"

/note="Organ: leaf; Citrullus lanatus ('Thunb.') Mansf."

BASE COUNT 69 a 105 c 59 g 81 t

ORIGIN

alignment_scores:

Quality: 66.50 length: 62
Ratio: 1.750 Gaps: 2
Percent Similarity: 61.290 Percent Identity: 32.258

alignment_block:

US-09-289-346a-2 x A1563120/rev ..

Align seg 1/1 to reverse of: A1563120 from: 1 to: 314

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||||| : : : : : ||||| : : : : :
212 GGAGCGCGACGCGAGGTGGGAGCGACGCTCTCGACGCGCGACCGC 163
27 AlaLeuAsnAlaSerSerylsgLglAlaLeuGlnIlelleArgLlu 44
||| : : : : : ||| : : : : :
162 GATACCAATCTAGATGATCTTGAACACAGATTGCAATCTTGGGAGAA 113
44 ysIleProGluLysTyrLeuPheGlnPheHisAsnLeuAsnSerAsnLeu 60
||| : : : : : ||| : : : : :
112 AGCGCAGAGAA.....GATACCTAGAGAGAGAAAT 81
61 AspArgIlePheAspLys.....ThrProGln 69
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80 GAGATGTGTGTTGAGAGGAGGATGACCACTCCAGAA 45

seq_name: gb_gss:TA231H070

seq_documentation_block:

LOCUS TA231H070 565 bp DNA GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 231H07, reverse sequence,
genomic survey sequence.

ACCESSION A1480948

VERSION A1480948.1 GI:11846717

KEYWORDS GSS.

SOURCE Trypanosoma brucei.

ORGANISM Trypanosoma brucei

Eukaryota; Euzoenozoa; Kinetoplastida; Trypanosomatidae;

Trypanosoma.

1 (bases 1 to 565)

Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,

Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,

MeiVillie,S.E., Rajandream,M.A. and Barrell,B.G.

Direct Submission

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing

project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,

Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and

nh@sanger.ac.uk

Constructured at the Institute for Genomic Research (TIGR),

Rockville, MD. Genomic DNA isolated from a cloned population of

Trypanosoma brucei (TREU927/4 Gynat 10.1) was mechanically sheared

to give a tight size distribution (

4 kb). The v+ i method used for the library construction is

described in detail in Smith, H. and Venter, J.C. (Making small

insert libraries for whole genome shotgun sequencing projects. In

Genome Sequencing: A Practical Approach, eds. M. Vaubin and B.

Barrell, Oxford University Press, 1999).

COMMENT


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FEATURES             POLYA-No.      Location/Qualifiers
Source               1. 618
                    /organism="Drosophila melanogaster"
                    /db_xref="taxon:7227"
                    /clone_lib="LD30829"
                    /clone_lib="LD Drosophila melanogaster embryo POT2"
                    /sex="male and female"
                    /dev_stage="0 to 24 hours mixed stage embryonic"
                    /lab_host="XLI Blue"
                    /note="Organ: embryo; Vector: POT2; Site_1: EcoRI; Site_2:
                    XhoI; Sized fractionated cDNAs were directly ligated into
                    POT2."
BASE COUNT          181 a      166 c      139 g      132 t
ORIGIN
alignment_scores:
  Quality:          66.50          Length:          54
  Ratio:            1.847          Gaps:          1
  Percent Similarity: 66.667      Percent Identity: 33.333
alignment_block:
US-09-289-346A-2 x AA950726      ..
Align seg 1/1 to: AA950726 from: 1 to: 618
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   |||||:::||||::: ||| ::::|||::: ||| ::::|||:::
150 TGTCTAGTCTCTGGAAGCCGGCTTCGTGGAATGTCCTGCCCTCTCCACTTC 199
   34 sGIuGlAla...LeuGlnIleIleArgGluLysIleProGluLysTyrL 50
      ::|||:::||||::: ::::|||::: ||| ::::|||:::
200 GGAAGAAAGTCCCGTCTGCTGCTGCAAGAACCTTTCGACAAACGAGC 249
   50 eupheGlnPheHisAsnLeuAsnSerAsnLeuAsnParGilePheAspLys 66
      || ::::|||::: ||| ::::|||::: ||| ::::|||:::
250 TTCAGCGCAATATGATGATGATGAATAAAGCTCTGAGAAAGAGAGAGCGCT 299
   67 ThrProGluPro 70
      |||||:::||||
300 ACTCCGCGAGCGCT 311

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2216 AGTAATGATGCTCCGACGAGCCCTTAAATGACGTTTACGTCGACGAG 2167
37 lalaugnllelllearglulysileproglulyslyrleupheglnphe 53
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
2166 CTTAGCAATTAATTAGGAAAAACTCCCTAAAGATTTTATTATTTCATAT 2117
54 HisanleuasnSerAsnleuaspargllepheasplysthrp 68
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
2116 CATATTTAAATGTATTTAGATGATTTT.....ACACCT 2078

seq_name: /cgn1_7/ptodata/1/lna/6B_COMB.seq:US-08-838-151A-48

seq_documentation_block:
; Sequence 48, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Gemnivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1062 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORGANISM: Bean Golden Mosaic Gemnivirus
; STRAIN: Type II
; INDIVIDUAL ISOLATE: Guatemala
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1059
; US-08-838-151A-48

alignment_scores:
Quality: 215.00 Length: 70
Ratio: 3.644 Gaps: 0
Percent Similarity: 84.286 Percent Identity: 57.143

alignment_block:
US-09-289-346A-2 x US-08-838-151A-48

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Align seq 1/1 to: US-08-838-151A-48 from: 1 to: 1062

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328 ACATCGAATGGGACCAATTCCAAGTCGACGCAAGATCTCCACAGAGAG 377
17 yCysGlnThrSerAsnAspAlaAlaGlnAlaLeuAsnAlaSerSerL 34
| ||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
378 TCAGCACTGCGCCACGACTCATATGCAAGGCAATTTAAACGCAATTCAA 427
34 ysglgluaAlaLeuGlnlelllearglulysileproglulyslyrleu 50
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
428 TTGAATCTGCCCTTGACAATATTTGACGAGACAGAACCGAAGATTCGTC 477
51 pheGlnPheHisanleuasnSerAsnleuaspargllepheasplysth 67
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
478 CTTCAACATCAACAACATCCGTTCTAATCTGAAACGATCTTCGTCAAAGT 527
67 rProGluPro 70
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528 GCCGGAACCA 537

seq_name: /cgn1_7/ptodata/1/lna/6B_COMB.seq:US-08-838-151A-51

seq_documentation_block:
; Sequence 51, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Gemnivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1062 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORGANISM: Bean Golden Mosaic Gemnivirus
; STRAIN: Type II
; INDIVIDUAL ISOLATE: Guatemala

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FEATURE:
NAME/KEY: CDS
LOCATION: 1..1059
US-08-838-151A-51
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Quality: 215.00      length: 70
Ratio: 3.644         Gaps: 0
Percent Similarity: 84.286   Percent Identity: 57.143
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US-09-289-346A-2 x US-08-838-151A-51
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328 ACAATCGAATGGGACAAATCCAAAGTCGACGCGCAGATCTGCAGAGAGG 377
```

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17 yCysGlnThrSerAsnAspAlaAlaIaGlyAlaLeuAsnAlaSerSert 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
378 TCAGCAGTCGCCAACGATCATATGCAAGGCAATTAACGCGAGATTCAA 427
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```
34 ysgIugIuaIaIeugIuIleIleArgIuIuSIIeProGluIuIuSITyrl 50
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```

```
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIIePheAspIySth 67
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478 CTTCACATCATCAACAATCCGCTCTAATCTCGAACGCGATCTTCGCAAGT 527
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67 rProGluPro 70
:|||||:
528 GCCGGAACCA 537
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; Sequence 54, Application US/08838151A
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; Patent No. 6291743
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; GENERAL INFORMATION:
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; APPLICANT: Stout, John T
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; APPLICANT: Luu, Hang T
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; APPLICANT: Maxwell, Douglas
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; APPLICANT: Ahlquist, Paul
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; TITLE OF INVENTION: Transgenic Plants Expressing GeminiVirus
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; NUMBER OF SEQUENCES: 63
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; CORRESPONDENCE ADDRESS:
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; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
```

```
; STREET: Two Prudential Plaza, Suite 4700
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; CITY: Chicago
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; STATE: Illinois
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; COUNTRY: U.S.A.
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; ZIP: 60601
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; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: Patent Release #1.0, Version #1.30
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; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/08/838.151A
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; FILING DATE:
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; CLASSIFICATION: 800
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; ATTORNEY/AGENT INFORMATION:
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; NAME: Mueller, Lisa V
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; REGISTRATION NUMBER: 38,978
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; TELECOMMUNICATION INFORMATION:
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; TELEPHONE: 312-616-5400
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; TELEFAX: 312-616-5460
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INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 1062 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bean Golden Mosaic GeminiVirus
STRAIN: Type II
INDIVIDUAL ISOLATE: Guatemala
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1059
US-08-838-151A-54
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Quality: 215.00      length: 70
Ratio: 3.644         Gaps: 0
Percent Similarity: 84.286   Percent Identity: 57.143
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US-09-289-346A-2 x US-08-838-151A-54
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328 ACAATCGAATGGGACAAATCCAAAGTCGACGCGCAGATCTGCAGAGAGG 377
```

```
17 yCysGlnThrSerAsnAspAlaAlaIaGlyAlaLeuAsnAlaSerSert 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
378 TCAGCAGTCGCCAACGATCATATGCAAGGCAATTAACGCGAGATTCAA 427
```

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34 ysgIugIuaIaIeugIuIleIleArgIuIuSIIeProGluIuIuSITyrl 50
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428 TTGAATCTGCTTGACAAATTTGAAGAGAACACCGAAGATTACGTC 477
```

```
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIIePheAspIySth 67
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478 CTTCACATCATCAACAATCCGCTCTAATCTCGAACGCGATCTTCGCAAGT 527
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67 rProGluPro 70
:|||||:
528 GCCGGAACCA 537
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; Sequence 7, Application US/08809103B
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; Patent No. 6133505
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; GENERAL INFORMATION:
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; APPLICANT: GROENENBORN, Bruno
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; TITLE OF INVENTION: PHYTOANTHROGENIC DNA VIRUS RESISTANT
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; NUMBER OF SEQUENCES: 17
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; CORRESPONDENCE ADDRESS:
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; ADDRESSEE: YOUNG & THOMPSON
```

```
; STREET: 745 South 23rd Street
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; CITY: Arlington
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; STATE: Virginia
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; COUNTRY: U.S.A.
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; ZIP: 22202
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; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
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; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: Patent Release #1.0, Version #1.30
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; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/08/809,103B
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FILING DATE: 17-MAR-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94.11040
FILING DATE: 15-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR95/01192
FILING DATE: 15-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: PATCH, Andrew J.
REGISTRATION NUMBER: 32,925
REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 521-2297
TELEFAX: (703) 685-0573
TELEX: 248425 EMBON
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1145 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1077
US-08-809-103B-7

alignment_scores:
Quality: 215.00 Length: 69
Ratio: 3.772 Gaps: 0
Percent Similarity: 82.609 Percent Identity: 55.072

alignment_block:

US-09-289-346A-2 x US-08-809-103B-7 ..

Align seg 1/1 to: US-08-809-103B-7 from: 1 to: 1145

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331 CTGAATGGGCTTGCATCTTCCAGATCGACGACGATCTGCTAGGGGAGACA 380
18 sGlnThrSerAsnAspAlaAlaAlaGluAlaLeuAsnAlaSerSerLysG 35
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
381 ACAGACAGCCACGACGCTTACGCAAGCAATTACGCAAGAGTAAGT 430
35 IuGluAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeuPhe 51
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431 CGCAGGCTCTTGATGTAATTAAAGATTAGCGCTACAGATTACGTTCTA 480
52 GlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysThrPr 68
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481 CATTTTCATATATAATAGTAATTAGATAAGGTTTCCAGGTGCTCC 530
68 oGluPro 70
| |||
531 GGCACCT 537

seq_name: /cgn1_7/ptodata/1/lna/6A_COMB.seq:US-08-809-103B-1
seq_documentation_block:
; Sequence 1, Application US/08809103B
; Patent No. 613505
; GENERAL INFORMATION:
; APPLICANT: GRONENBORN, Bruno
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
```

STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,103B
FILING DATE: 17-MAR-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94.11040
FILING DATE: 15-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR95/01192
FILING DATE: 15-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: PATCH, Andrew J.
REGISTRATION NUMBER: 32,925
REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 521-2297
TELEFAX: (703) 685-0573
TELEX: 248425 EMBON
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1148 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1077
US-08-809-103B-1

alignment_scores:
Quality: 215.00 Length: 69
Ratio: 3.772 Gaps: 0
Percent Similarity: 82.609 Percent Identity: 55.072

alignment_block:

US-09-289-346A-2 x US-08-809-103B-1 ..

Align seg 1/1 to: US-08-809-103B-1 from: 1 to: 1148

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331 CTGAATGGGCTTGCATCTTCCAGATCGACGACGATCTGCTAGGGGAGACA 380
18 sGlnThrSerAsnAspAlaAlaAlaGluAlaLeuAsnAlaSerSerLysG 35
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
381 ACAGACAGCCACGACGCTTACGCAAGCAATTACGCAAGAGTAAGT 430
35 IuGluAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeuPhe 51
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
431 CGCAGGCTCTTGATGTAATTAAAGATTAGCGCTACAGATTACGTTCTA 480
52 GlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysThrPr 68
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
481 CATTTTCATATATAATAGTAATTAGATAAGGTTTCCAGGTGCTCC 530
68 oGluPro 70
| |||
531 GGCACCT 537

seq_name: /cgn1_7/ptodata/1/lna/6A_COMB.seq:US-08-809-103B-3
seq_documentation_block:
; Sequence 3, Application US/08809103B
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18  sGlnThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerLysG 35
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
381 ACAGACACGACGACGCTTACGCAAGCAATTACGACGAGTAAGT 430
35  LuGluAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeuPhe 51
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:
431 CGACGCGCTTGATGATTAATTAAGAAATTAGCGCTAGAGATTACGTTCTA 480
52  GlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysThrPr 68
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:
481 CATTTCTATATATATATGTAATTAGATAAGGTTTCCAGGTGCTCC 530
68  oGluPro 70
   |||
531 GGCACCT 537

seq_name: /cgn1_7/ptodata/1/lna/5B.COMB.seq:US-08-838-151A-43
seq_documentation_block:
: Sequence 43, Application US/08838151A
: Patent No. 6291743
: GENERAL INFORMATION:
: APPLICANT: Stout, John T
: APPLICANT: Lau, Hang T
: APPLICANT: Maxwell, Douglas
: APPLICANT: Ahlquist, Paul
: APPLICANT: Hanson, Steve
: TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
: TITLE OF INVENTION: Genes
: NUMBER OF SEQUENCES: 63
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Dressler, Rocky, Milnamow & Katz
: STREET: Two Prudential Plaza, Suite 4700
: CITY: Chicago
: STATE: Illinois
: COUNTRY: U.S.A.
: ZIP: 60601
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/838,151A
: FILING DATE:
: CLASSIFICATION: . 800
: ATTORNEY/AGENT INFORMATION:
: NAME: Mueller, Lisa V
: REGISTRATION NUMBER: 38,978
: REFERENCE/DOCKET NUMBER: SVS3801P0260
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312-616-5400
: TELEFAX: 312-616-5460
: INFORMATION FOR SEQ ID NO: 43:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1183 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: circular
: MOLECULE TYPE: DNA (genomic)
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: ORIGINAL SOURCE:
: ORGANISM: Bean Golden Mosaic Geminivirus
: STRAIN: Type II Isolates
: INDIVIDUAL ISOLATE: Guatemala
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..1059
: PUBLICATION INFORMATION:
: AUTHORS: Faria, JC
: AUTHORS: Gilbertson, RL
: AUTHORS: Hanson, SP

```

```

: AUTHORS: Morales, FJ
: AUTHORS: Ahlquist, P
: AUTHORS: Loniello, AO
: AUTHORS: Maxwell, D
: TITLE: Bean Golden Mosaic Geminivirus Type II
: TITLE: Isolates from the Dominican Republic and
: TITLE: Guatemala: Nucleotide Sequences, Infectious
: TITLE: Pseudorecombinants, and Phylogenetic Relationships
: JOURNAL: Phytopathology
: VOLUME: 84
: ISSUE: 3
: PAGES: 321-329
: DATE: 1994
: US-08-838-151A-43

alignment_scores:
  Quality: 215.00      Length: 70
  Ratio: 3.644        Gaps: 0
  Percent Similarity: 84.286  Percent Identity: 57.143

alignment_block:
  US-09-289-346A-2 x US-08-838-151A-43  ..
Align seg 1/1 to: US-08-838-151A-43 from: 1 to: 1183

1  ThrLeuValTrpGlyGluPheGlnValAspGlyAlaAlaAlaIleGyl 17
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
328 ACAATCGAATGGGACAAATTCACAGTCGACGCGCATCTGCAAGAGAG 377
17  yCySGlnThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerL 34
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
378 TCACAGCTGCGCCACAGCATCATATGCAAGCGCTTAACGACGATTCAA 427
34  ysgGluAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeu 50
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
428 TTGAATCTCGCTTACAAATTAATGAAGACAGACCAAGAAATTAAGTC 477
51  PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLys 67
   :||||:|||||:|||||:|||||:|||||:|||||:|||||:
478 CTTCACATCATCAACATCGCTTCTAATCTGCAAGCATCTTGTCAAGT 527
67  rProGluPro 70
   :|||||
528 GCGCGAACCA 537

seq_name: /cgn1_7/ptodata/1/lna/6B.COMB.seq:US-08-838-151A-45
seq_documentation_block:
: Sequence 45, Application US/08838151A
: Patent No. 6291743
: GENERAL INFORMATION:
: APPLICANT: Stout, John T
: APPLICANT: Lau, Hang T
: APPLICANT: Maxwell, Douglas
: APPLICANT: Ahlquist, Paul
: APPLICANT: Hanson, Steve
: TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
: TITLE OF INVENTION: Genes
: NUMBER OF SEQUENCES: 63
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Dressler, Rocky, Milnamow & Katz
: STREET: Two Prudential Plaza, Suite 4700
: CITY: Chicago
: STATE: Illinois
: COUNTRY: U.S.A.
: ZIP: 60601
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:

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```
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 1183 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bean Golden Mosaic Geminiivirus
STRAIN: Type II
INDIVIDUAL ISOLATE: Guatemala
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1059
US-08-838-151A-45
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```
alignment_scores:
Quality: 215.00 Length: 70
Ratio: 3.644 Gaps: 0
Percent Similarity: 84.286 Percent Identity: 57.143
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alignment_block:
US-09-289-346A-2 x US-08-838-151A-45 ..

Align seg 1/1 to: US-08-838-151A-45 from: 1 to: 1183

```
1 ThleuValTrpGlyGluPheGlnValAspGlyAlaAlaAlaIaGlyI 17
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
328 ACATCGAATGGGGACATTCGAAAGCGATGCAAGATTCAAGAGAGG 377
17 yCysGlnThrSerAsnAspAlaAlaIaGluAlaLeuAsnAlaSerI 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
378 TCAGCAGCTGCCACAGCATTATGCAAGGCAATTAAACGACGATCAA 427
34 ysgIuGluAlaLeuGlnIleIleArgGluIysIleProGluIysTyrl 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
428 TTGAATCTGCTTGACATATTTGAGAGAACACACCGAAGATTACGTC 477
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspIys 67
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
478 CTTCACATATCAACAACATCGCTTAATCTGCAACGATCTTCGTAAGT 527
67 rProGluPro 70
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
528 GCCGGAACCA 537

seq_name: /cgnl_7/ptodata/1/lna/6A_COMB.seq:us-09-065-999-5

seq_documentation_block:
; Sequence 5, Application US/09065999
; Patent No. 6118048
; GENERAL INFORMATION:
; APPLICANT: Hanson, Stephen F.
; APPLICANT: Maxwell, Douglas P.
; TITLE OF INVENTION: TRANS-DOMINANT INHIBITION OF GEMINIVIRAL
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: One South Plinckney Street
```

```
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/09/065,999
APPLICATION NUMBER: US/09/065,999
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 960296,94754
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1651 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-065-999-5
```

```
alignment_scores:
Quality: 215.00 Length: 70
Ratio: 3.644 Gaps: 0
Percent Similarity: 84.286 Percent Identity: 57.143
```

alignment_block:
US-09-289-346A-2 x US-09-065-999-5 ..

Align seg 1/1 to: US-09-065-999-5 from: 1 to: 1651

```
1 ThleuValTrpGlyGluPheGlnValAspGlyAlaAlaAlaIaGlyI 17
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
796 ACAATCGAATGGGGACATTCGAAAGCGATGCAAGATTCAAGAGAGG 845
17 yCysGlnThrSerAsnAspAlaAlaIaGluAlaLeuAsnAlaSerI 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
846 TCAGCAGCTGCCACAGCATTATGCAAGGCAATTAAACGACGATTCAA 895
34 ysgIuGluAlaLeuGlnIleIleArgGluIysIleProGluIysTyrl 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
896 TTGAATCTGCTTGACATATTTGAGAGAACACACCGAAGATTACGTC 945
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspIys 67
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
946 CTTCACATATCAACAACATCGCTTAATCTGCAACGATCTTCGTAAGT 995
67 rProGluPro 70
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
996 GCCGGAACCA 1005

seq_name: /cgnl_7/ptodata/1/lna/6A_COMB.seq:us-09-065-999-6

seq_documentation_block:
; Sequence 6, Application US/09065999
; Patent No. 6118048
; GENERAL INFORMATION:
; APPLICANT: Hanson, Stephen F.
; APPLICANT: Maxwell, Douglas P.
; TITLE OF INVENTION: TRANS-DOMINANT INHIBITION OF GEMINIVIRAL
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
```

```
STREET: One South Pinckney Street
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/065,999
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 960296.94754
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1651 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-065-999-6
```

```
alignment_scores:
Quality: 215.00      Length: 70
Ratio: 3.644         Gaps: 0
Percent Similarity: 84.286   Percent Identity: 57.143
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alignment_block:
US-09-289-346A-2 x US-09-065-999-6 ..

Align seg 1/1 to: US-09-065-999-6 from: 1 to: 1651

```
1 ThrleuValTPGlyGluPheGlnValAspGlyAlaAlaAlaIaGly1 17
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
796 ACAATCGAATGGGACATTCCTCAAGTCGACGCGAGATCTGCAAGAGG 845
17 yCysGlnThrSerAsnAspAlaAlaIaGluAlaLeuAsnAlaSer1 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
846 TCAGCAGCTCTGCCAAGCATCATATGCAAGCATTAACGCGAGATTCAA 895
34 ySGluGluAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeu 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
896 TTGAATCTGCTTGACATATTGAAGGAAGAACAACGAAAGATTACGTC 945
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLys7 67
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
946 CTTCAACATCACAACATCGTTCTAATCTCGAAGCATCTTCGTCAAAGT 995
67 rProGluPro 70
:|||||:|||||
996 GCCGGAACCA 1005
```

seq_name: /cgn1_7/ptodata/1/lna/6A_COMB.seq:US-09-065-999-8

```
seq_documentation_block:
; Sequence 8, Application US/09065999
; Patent No. 6118048
; GENERAL INFORMATION:
; APPLICANT: Hanson, Stephen F.
; APPLICANT: Maxwell, Douglas P.
; TITLE OF INVENTION: TRANS-DOMINANT INHIBITION OF GEMINIVIRAL
; TITLE OF INVENTION: DNA REPLICATION BY GEMINIVIRUS REP GENE MUTANTS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
```

```
ADDRESSEE: Quarles & Brady
STREET: One South Pinckney Street
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/065,999
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 960296.94754
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1894 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-065-999-8
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alignment_scores:
Quality: 215.00      Length: 70
Ratio: 3.644         Gaps: 0
Percent Similarity: 84.286   Percent Identity: 57.143
```

alignment_block:
US-09-289-346A-2 x US-09-065-999-8 ..

Align seg 1/1 to: US-09-065-999-8 from: 1 to: 1894

```
1 ThrleuValTPGlyGluPheGlnValAspGlyAlaAlaAlaIaGly1 17
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
796 ACAATCGAATGGGACATTCCTCAAGTCGACGCGAGATCTGCAAGAGG 845
17 yCysGlnThrSerAsnAspAlaAlaIaGluAlaLeuAsnAlaSer1 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
846 TCAGCAGCTCTGCCAAGCATCATATGCAAGCATTAACGCGAGATTCAA 895
34 ySGluGluAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeu 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
896 TTGAATCTGCTTGACATATTGAAGGAAGAACAACGAAAGATTACGTC 945
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLys7 67
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
946 CTTCAACATCACAACATCGTTCTAATCTCGAAGCATCTTCGTCAAAGT 995
67 rProGluPro 70
:|||||:|||||
996 GCCGGAACCA 1005
```

seq_name: /cgn1_7/ptodata/1/lna/6A_COMB.seq:US-09-065-999-7

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seq_documentation_block:
; Sequence 7, Application US/09065999
; Patent No. 6118048
; GENERAL INFORMATION:
; APPLICANT: Hanson, Stephen F.
; APPLICANT: Maxwell, Douglas P.
; TITLE OF INVENTION: TRANS-DOMINANT INHIBITION OF GEMINIVIRAL
; TITLE OF INVENTION: DNA REPLICATION BY GEMINIVIRUS REP GENE MUTANTS
; NUMBER OF SEQUENCES: 8
```

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: One South Pinckney Street
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/065,999
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 960296, 94754
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2072 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-065-999-7

```

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alignment_scores:  
    Quality: 215.00  
      Ratio: 3.644  
Percent Similarity: 84.286  
Percent Identity: 57.143
```

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alignment_block:
US-09-289-346A-2 x US-09-065-999-7
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Align seg 1/1 to: US-09-065-999-7 from: 1 to: 2072

[illegible]

```

67 rProgiUpPro 70
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996 GCCGGAACCA 1005
seq_name: /cgm1_7/prodata/1/ina/5b_COMB.seq:US-08-838-151A-1

```

```
seq documentation block:
: Sequence 1, Application US/08838151A
: Patent No. 6291743
:
: GENERAL INFORMATION:
:
: APPLICANT: Scout, John T
: APPLICANT: Iuu, Hang T
: APPLICANT: Maxwell, Douglas
: APPLICANT: Ahlquist, Paul
:
```

1 APPLICANT: Hanson, Steve
2 TITLE OF INVENTION: Transgenic Plants Expressing Gemlinivirus
3 TITLE OF INVENTION: Genes
4 NUMBER OF SEQUENCES: 63
5 CORRESPONDENCE ADDRESS:
6 ADDRESSEE: Dressler, Rockey, Milnamow & Katz
7 STREET: Two Prudential Plaza, Suite 4700
8 CITY: Chicago
9 STATE: Illinois
10 COUNTRY: U.S.A.
11 ZIP: 60601
12
13 COMPUTER READABLE FORM:
14 MEDIUM TYPE: Floppy disk
15 COMPUTER: IBM PC compatible
16 OPERATING SYSTEM: PC-DOS/MS-DOS
17 SOFTWARE: Patentin Release #1.0, Version #1.30
18 CURRENT APPLICATION DATA:
19 APPLICATION NUMBER: US/08/838,151A
20 FILING DATE:
21

1 CLASSIFICATION: 800
2 ATTORNEY/AGENT INFORMATION:
3 NAME: Mueller, Lisa V
4 REGISTRATION NUMBER: 38,978
5 REFERENCE/DOCKET NUMBER: SVS38010266
6 TELECOMMUNICATION INFORMATION:
7 TELEPHONE: 312-616-5400

TELEFAX: 312-616-3460
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:

```

; LENGTH: 1162 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
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```

```

;      TOPOLOGY: circular
;      MOLECULE TYPE: DNA (genomic)
;      HYPOTHETICAL: NO
;      NEXT FEATURE: NO

```

```

; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Tomato Mottle Gemini Virus
;

```

```

; INDIVIDUAL ISOLATE:
;
; FEATURE:
; NAME/KEY: CDS
;

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; LOCATION: 44..1127
; PUBLICATION INFORMATION:
; AUTHORS: Gilbertson,
;

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```
;; AUTHORS: Hidayat, ;  
;; AUTHORS: Papiomatari;  
;; AUTHORS: Rojas, MR  
;
```

```

;
;   AUTHORS:  Hou, YM
;   AUTHORS:  Maxwell
;   TITLE:    Pseudoreg
;
```

```

; TITLE:  cloned DNA components of tomato mottle and bean
; TITLE:  dwarf mosaic geminiviruses.
; JOURNAL: Jour. General Virol.

```

VOLUME: 74
PAGES: 23-31
DATE: 1993

US-08-838-151A-1

alignment_scores:	213.00	Length:	70
Quality:		Gaps:	0
Ratio:	3.610		
Percent Similarity:	84.286	Percent Identity:	54.286

US-09-289-346A-2 x US-08-838-151A-1 ..
Align seg 1/1 to: US-08-838-151A-1 from: 1 to: 1162

```

1  TnrluValITrpglygluphegnValaspGlyAlaalaAlaIaglyG 17
   |||::: |||||:::|||||:::|||||:::|||||:::|||||
371 ACAATCGAATCGGAGACATTCCAGATCGACGCGCAGATCTCGCAGAGAGG 420

```

```
17 yCysGlnThrSerAsnSPALAAlaGluAlaLeuAsnAlaSerSerL 34
   |  |||:::|||||::: |||:::|||||:::|||||
421 CCAGCAGTCTGCTAATGATCATATGCCAAGCGTTAAATCAAGTTCCG 470
   |||:::|||||::: |||:::|||||:::|||||
34 ySGluGluAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeu 50
   |||:::|||||::: |||:::|||||:::|||||
471 TTCAATCTGCTTAGCAGTTCTTAAGGAGAACCAACCAAAAGATTGTGTA 520
   |||:::|||||::: |||:::|||||:::|||||
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
   |||:::|||||::: |||:::|||||:::|||||
521 TTACAAATCATTAACATCCGCTTAACCTAGAACCAATATTCCCAAGGC 570
   |||:::|||||::: |||:::|||||:::|||||
67 rProGluPro 70
   |||:::|||||::: |||:::|||||:::|||||
571 TCCGGAACCG 580
```

OM of: US-09-289-346a-3 to: GenEmbl:* out_format: pfs

Date: Jan 3, 2002 8:17 PM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

-MODEL=framed_p2n_model -DEY=xlp
-O=/cgn1_1/USPFO.spool/US09289346/rnat_03012002_153304_15362/app_query.fasta.1.1163
-DB=GenEmbl -OFMT=fastap -SUFFIX=p2n.rge -GAPOP=12.000
-GAPEXT=4.500 -MINMATCH=0.100 -LOOPEL=0.000 -LOOPEXT=0.000
-GAPOP=4.500 -OGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blonsum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
-NOR=ext -MINLEN=0 -MAXLEN=200000000
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-NO_XLPHY -WAIT -THREADS=1

Search information block:

Query: US-09-289-346a-3
Query length: 70
Database: GenEmbl:*
Database sequences: 1472140
Database length: 341344837
Search time (sec): 7316.720000

Score list:

Seqence	Strd Orig	ZScore	EScore	Len	Documentation
gb_v1:MTGA	-	332.00	7.4e-32	2588	K02029 Tomato golden mosaic vi
gb_v1:AY029750	-	293.00	6.33.08	2588	AY029750 Tomato severe rugose
gb_v1:AF291705	-	291.00	6.28.48	2622	AF291705 Tomato rugose mosaic
gb_v1:LM092532	-	276.00	6.01.65	1193	U92532 Leonurus mosaic virus R
gb_v1:AF288227	-	271.00	5.89.16	1383	AF288227 Sweet potato leaf cur
gb_v1:AF104036	-	271.00	5.82.99	2878	AF104036 Sweet potato leaf cur
gb_v1:TY132548	-	267.00	5.74.22	2763	AJ132548 Ipomoea yellow vein v
gb_v1:AF131071	-	264.00	5.73.73	1345	AF131071 Tomato mild mottle ge
gb_v1:AF350330	-	263.00	5.65.24	2767	AF350330 Tobacco leaf curl vir
gb_v1:MG8686	-	262.00	5.63.43	2617	MG8686 Bean golden mosaic gemi
gb_v1:MG875278	-	260.00	5.74.25	447	U75278 Macroptilium golden mosa
gb_v1:AF188708	-	260.00	5.64.62	1365	AF188708 Cowpea golden mosaic
gb_v1:AF098840	-	259.00	5.64.37	1405	AF098840 Macroptilium golden m
gb_v1:SG067926	-	259.00	5.70.16	554	U67926 Sida golden mosaic gemi
gb_v1:AB001315	-	251.00	5.51.97	570	AB001315 Tobacco leaf curl viru
gb_v1:AB001318	-	251.00	5.51.97	570	AB001318 Tobacco leaf curl viru
gb_v1:AB001303	-	250.00	5.49.73	570	AB001303 Tobacco leaf curl viru
gb_v1:AB001294	-	250.00	5.48.94	625	AB001294 Tobacco leaf curl viru
gb_v1:AB001296	-	250.00	5.48.94	625	AB001296 Tobacco leaf curl viru
gb_v1:AB001297	-	250.00	5.48.94	625	AB001297 Tobacco leaf curl viru
gb_v1:AB001308	-	249.00	5.46.70	625	AB001308 Tobacco leaf curl viru
gb_v1:AB001293	-	248.00	5.44.45	625	AB001293 Tobacco leaf curl viru
gb_v1:CMVAJ3191	-	247.00	5.29.31	2787	AJ223191 Chayote mosaic virus
gb_v1:AB001298	-	246.00	5.39.97	625	AB001298 Tobacco leaf curl viru
gb_v1:AB001319	-	245.00	5.37.92	611	AB001319 Tobacco leaf curl viru
gb_v1:CLCVNA452	-	245.00	5.24.96	2744	AJ002452 cotton leaf curl viru
gb_v1:CLCVNA455	-	245.00	5.24.96	2744	AJ002455 cotton leaf curl viru
gb_v1:AF155064	-	244.00	5.22.65	1165	AF155064 Okra enation virus DN
gb_v1:AF026553	-	243.00	5.27.87	1165	AF026553 Potato yellow mosaic
gb_v1:PPYVA	-	243.00	5.20.96	2553	D00940 Potato yellow mosaic vi
gb_v1:AT073498	-	242.00	5.23.31	1533	U73498 African tomato leaf cur
gb_v1:AB014346	-	242.00	5.18.10	2787	AB014346 Tomato yellow leaf cu
gb_v1:AB014347	-	242.00	5.18.09	2791	AB014347 Tomato yellow leaf cu
gb_v1:AF071228	-	242.00	5.18.08	2793	AF071228 Tomato yellow leaf cu
gb_v1:AF105975	-	242.00	5.17.69	2923	AF105975 Tomato yellow leaf cu
gb_v1:BCYVCONTF	-	242.00	5.17.67	2927	X97203 Beet curly top virus cu
gb_v1:BCU02311	-	241.00	5.17.85	2927	U02311 Beet curly top virus CF
gb_v1:TYLCV12	-	241.00	5.15.85	2930	X76319 Tomato yellow leaf cur
gb_v1:BCU56975	-	241.00	5.15.42	2930	U56975 Beet curly top virus WC
gb_v1:AF307861	-	240.00	5.13.78	2734	AF307861 Ageratum yellow vein

seq_name: gb_v1:MTGA
seq_documentation_block: 2588 bp ss-DNA circular VRL 02-AUG-1993
LOCUS MTGA
DEFINITION Tomato golden mosaic virus, component A of complete genome.
ACCESSION K02029
VERSION K02029.1 GI:332213
KEYWORDS coat protein: complete genome: unidentified reading frame.
SOURCE TGMV cloned ds-DNA, clone PBH404.
ORGANISM Tomato golden mosaic virus
VIRUSES: ssDNA viruses; Geminiviridae; Begomovirus.
REFERENCE 1 (bases 1 to 2588)
Hamilton, W.D. O., Stein, V.E., Coutts, R.H.A. and Buck, K.W.
Complete nucleotide sequence of the infectious cloned DNA
components of tomato golden mosaic virus: Potential coding regions
and regulatory sequences
EMBO J. 3, 2197-2205 (1984)
Geminiviruses are characterised by twin isometric virions, major
capsid polypeptides of about 28 kD, and ss-DNA genomes. The genomes
of cassava latent virus (CLV) and tomato golden mosaic virus (TGMV)
consist of two circular components, while that of maize streak
virus (MSV) consists of a single circle.
[1] Identifies the following additional open reading frames on the
complementary strand that would code for proteins with >10 kD:
A11 -- 13-1543 (passing through origin)
A12 -- 1601-1212
A13 -- 1465-1067

FEATURES
source
The sequence at 1-235 is highly homologous to an equivalent region
on component B; it doesn't appear to code for protein and has the
potential to form a stable hairpin [1]. An analogous region is
found in CSV.
The virion-sense (+) strand is shown below.

Location/Qualifiers

1..2588
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/db_xref="taxon:10831"
327..1070
/note="coat protein (AR1)"
/codon_start=1
/protein_id="AAA46582.1"
/db_xref="GI:332214"

BASE COUNT 672 a 513 c 605 g 798 t
ORIGIN 140 bp upstream of HpaI site; beginning of A-B homology region.
alignment_scores:
Quality: 332.00 Length: 70
Ratio: 5.108 Gaps: 0
Percent Similarity: 92.857 Percent Identity: 92.857

alignment_block:
US-09-289-346a-3 x MTGA/rev ..
Align seg 1/1 to reverse of: MTGA from: 1 to: 2588

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|||||
2271 ACTCTTTATGAGGAGAAATTCACGCTGCAGCGTGAAGTGTGAAGAGG 2272
|||||
17 YCYSGlThrSerAsnAspAlaAlaAlaAlaLeuAlaAlaSerSera 34
|||||
2221 TTGCAACAACATCTACGACCGCTGACGAGCGCTTAAATGCTTCTTCCA 2172
|||||

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34 laaiaaalaaleuGlnlleleargluuylsileprogluylstyrlou 50
|||||
2171 AAGAGAGAGCCCTGCAGATATTTAGAGAGAAATCCAGAAAATATTTA 2122
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
|||||
2121 TTTCAGTTCCACAAATCTAAATAGCAATTTAGATATTTGATTAAGAC 2072
67 rProGluPro 70
|||||
2071 TCCTGAACCA 2062

seq_name: gb_v1:AY029750

seq_documentation_block: 2588 bp DNA circular VRL 08-MAY-2001
LOCUS AY029750
DEFINITION Tomato severe rugose virus DNA-A, complete sequence.
ACCESSION AY029750
VERSION AY029750.1 GI:14009278
KEYWORDS
SOURCE Tomato severe rugose virus.
ORGANISM
Virus; ssDNA viruses; Geminiviridae; Begomovirus.
REFERENCE
1 (bases 1 to 2588)
Rezende,W.L., Goulart,L.R., Parreira,K.S. and Figueiredo,J.E.F.
The full-length DNA-A nucleotide sequence of a novel
tomato-infecting begomovirus, 'Tomato severe rugose virus', in Brazil
JOURNAL Unpublished
2 (bases 1 to 2588)
Rezende,W.L., Goulart,L.R., Parreira,K.S. and Figueiredo,J.E.F.
Direct Submision
TITLE Submitted (03-APR-2001) Instituto de Genetica e Biologica,
JOURNAL Universidade Federal de Uberlandia, Av. Amazonas s/n, Bloco 2E,
Sala 24, Campus Umuarama, Uberlandia, Minas Gerais 38.400-000,
Brazil

FEATURES
source
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Location/Qualifiers
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/strain="Minas Gerais"
/db_xref="taxon:158463"
/country="Brazil"
/note="segment: DNA-A"
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/gene="AV1"
305..1060
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/db_xref="GI:14009282"
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YRKPRITRLRGPDVPRGCEGCKVOSYESRDVSVGVCITVSDVTRNGITRRVGK
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EVALLLYMACIASNPVYATLKIRIFYDSITN"
complement(1057..1455)
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complement(1057..1455)
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/codon_start=1
/product="enhancer protein"
/protein_id="AAK50358.1"
/db_xref="GI:14009280"
/translation="MDSRTGGLITARQANGVYIETSNPLFKINRVEDPMYTTSRV
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/protein_id="AAK50361.1"
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/translation="MRNSSLTLPSPKXVOHRAAKRGIFRRRIDIEGCSYVHTICR
GHGFTIRGTHHCTSGREMRLYIGDIKSPFLDKKSGGSNVNHEQSLPRNTVQPOPE
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/codon_start=1
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/db_xref="GI:14009279"
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IKVREIHENGEPRHLVHLLQPCNYCROQRNREFDVSPTSRSTHPRNTIORAKSSDYK
STVYDKDGTIENGEEFOIDGRSARGGCOTANDAAELNAPSVDVALQITREKUPERFL
FQGHNNLSNLDRTFARAPPMVAPTPPLSSFTVNPREDMDADYFCRGAAAREPISI
IIECHDSRTKTMARAFGAHNYLSGLIDNPVYVSNHVEYVNIIDIAPIYLRKHWKE
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KVFPLNTPLYOGTOS"
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join(2583..2588,1..304)
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BASE COUNT 660 a 525 c 598 g 805 t
ORIGIN

alignment_scores:
Ratio: 293.00 Length: 70
Percent Similarity: 90.000 Percent Identity: 78.571

alignment_block:
US-09-289-346a-3 x AY029750/rev ..

Align seg 1/1 to reverse of: AY029750 from: 1 to: 2588

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2258 ACTATCGAATGGGCGGAATTCCAATCGACGCGAAGTCTAGACGCGG 2209
17 YCysGlnThrSerAsnAspAlaAlaAlaAlaLeuAlaAlaSerSerA 34
|||||
2208 TTGGCAGACACACTAAGCATGCTGCCGACAGACCTTCAACCCACCTTCA 2159
34 laaiaaalaaleuGlnlleleargluuylsileprogluylstyrlou 50
|||||
2158 AAGAGAGAGCCCTGCAGATATTTAGAGAGAAATCCAGAAAATATTTA 2109
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
|||||
2108 TTTCAGTTCCACAAATCTAAATAGCAATTTAGATATTTGATTAAGAC 2059
67 rProGluPro 70
|||||
2058 TCCTGAACCA 2049

seq_name: gb_v1:AF291705

seq_documentation_block: 2622 bp DNA circular VRL 25-SEP-2000
LOCUS AF291705
DEFINITION Tomato rugose mosaic virus DNA-A, complete sequence.
ACCESSION AF291705
VERSION AF291705.1 GI:10281644

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852 CCAGCAGACTGCTAACGACGACGCCGAGGCTCTAAACGACGTTCTA 803
34 laaalaalaaleuGlnlleargGluTylleProGluTylleu 50
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802 AACAGAGTGGCTGCATATATCAGAGAAACCTCGTGAATAATTTA 753
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTrh 67
|||||
752 TTTCATTTTCATATATTAGTTAGTAATTAGATTTTCTCTCTCC 703
67 rpro 68
|||
702 ACCCT 699

seq_name: gb_vf:AF104036

seq_documentation_block:
LOCUS AF104036 2828 bp DNA circular VR1 05-AUG-1999
DEFINITION Sweet potato leaf curl virus DNA A, complete sequence.
ACCESSION AF104036
VERSION AF104036.1 GI:5702158
KEYWORDS
SOURCE Sweet potato leaf curl virus.
ORGANISM Sweet potato leaf curl virus.
VIRUSES: ssDNA viruses; Geminiviridae; Begomovirus.
REFERENCE 1 (bases 1 to 2828)
AUTHORS Lotrakul, P., Valverde, R.A., Clark, C.A., Sim, J. and De la Torre, R.
TITLE Detection of a geminivirus infecting sweet potato in the United States
JOURNAL Plant Dis. 82, 1253-1257 (1998)
REFERENCE 2 (bases 1 to 2828)
AUTHORS Lotrakul, P. and Valverde, R.A.
TITLE Cloning of a DNA-A-like genomic component of sweet potato leaf curl virus: nucleotide sequence and phylogenetic relationships
JOURNAL Molecular Plant Pathology On-line (1999)
REMARK http://www.bspg.org.uk/mpool/1999/0422lotrakul/
AUTHORS 3 (bases 1 to 2828)
TITLE Lotrakul, P. and Valverde, R.A.
JOURNAL Direct Submission
SUBMITTED (02-NOV-1998) Plant Pathology and Crop Physiology, Louisiana State University, 302 Life Sciences Bldg., LSU, Baton Rouge, LA 70803, USA
FEATURES
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location/Qualifiers
/organism="Sweet potato leaf curl virus"
/db_xref="taxon:100755"
/chromosome="DNA A"
/country="USA"
132..476
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132..476
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/db_xref="GI:5702159"
/translation="MAELMDPLONPLPDTLVGFRCLMSVKYLQSLIKKYEPTGLFEL
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/db_xref="GI:5702162"
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/note="AL1: REP gene"
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/translation="MAPPKRKTKOAKNFITYPRCSLSKEDCLAOLNIOTPSNKKYI
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OFHNLYSNLDRIFSPSPSYSSPSSSSFNAPDIIISMAANVMSAARPRPISIV
TEGPRIGKTVAARSIGPHNYLCGHILDSPKAYSNSAMYNIDVDVNPQYLKFKFEPG
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/note="AL4"
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/protein_id="AAD47174.1"
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BASE COUNT 741 a 606 c 675 g 806 t
ORIGIN

alignment_scores:
Quality: 271.00 Length: 68
Ratio: 4.517 Gaps: 0
Percent Similarity: 88.235 Percent Identity: 79.412

alignment_block:
US-09-289-346A-3 x AF104036/rev ..
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|||||
2354 ACCATCACCTGGGCTGAATTCAGAGTGCAGCGCATCTGCTAAGAGAGG 2305

17 yCysGlnThrSerAsnAspAlaAlaAlaAlaAlaAlaAlaSerSera 34
|||||
2304 CCAGCAGACTGCTAACGACGACGCCGAGAGGCTCTAAACGACGTTCTA 2255

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/isolate="HN96-H5KW"
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/clone="PHNH5akw"
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/note="Obtained from a tomato plant collected in Dec. 1996
by M.K. Nakhla and D.P. Maxwell"
complement(<1. .678)
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IKIARELHDEYHLVLIQFEGKRTONCRFDVVSSTRSTHHPNVQAKSSIDVK
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FOYHNLSSNLRIFAKAPEPMIPPEPLSSFTNVDEMOWETDYGKGVAAKPERPIS
IIIEGDSR"
rep_origin 676. .832
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1001. >1345
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BASE COUNT 329 a 289 c 313 g 414 t
ORIGIN
alignment_scores:
Quality: 264.00 Length: 70
Ratio: 4.258 Gaps: 0
Percent Similarity: 88.571 Percent Identity: 70.000
alignment_block:
US-09-289-346a-3 x AF131071/rev ..
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||||: ||||||||||||||:|||||||||||||||||||||||||
348 ACAATCGAATGGGAGAGATTCCAGATGACGCGCAGATCTCTACAGSAGG 299
17 YCysgInThSerAsnAspAlaAlaAlaAlaLeuAlaAlaSerSera 34
||||: ||||||||||||||:|||||||||||||||||||||||||
298 TCAGCAACGACGTAACGACCGCTGCCGAGCCCTTAATGCCCTCTCGA 249
34 laAlaAlaAlaLeuGlnlleleargGluysTleProGluysTyrleu 50
||||: ||||||||||||||:|||||||||||||||||||||||||
248 AAGAGAGAGCCATGCGAATTATTAAGAGAAAGCCCAAGAGATTTCTT 199
51 PheGlnPhehisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
||||: ||||||||||||||:|||||||||||||||||||||||||
198 TTTCATATATACAAACCTGTCTAGTAACCTAGACAGATATTTCGTAAGGC 149
67 rProGluPro 70
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148 TCCGGAACCG 139

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seq_name: gb_vl:AF350330
seq_documentation_block: 2767 bp DNA circular VRL 02-JUL-2001
LOCUS AF350330
DEFINITION Tobacco leaf curl virus from zimbabwe, complete genome.
ACCESSION AF350330
VERSION AF350330.1 GI:14582850
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
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141. .491
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LICVIRADYVATRRYRNFHARLEGSSEKALROPIYOPCCPHCRKQTTVDLPA
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301. .1077
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301. .1077
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EDNEPSTAVQNDKRDROYLRFRQVTVYGSGCKEAIYKRRFRLNHHVYNNQOEA
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/db_xref="GI:14582855"
/translation="MDLRIGEDITAHQANQVFWETNPPLYEKTKHHIRPFKNYD
IITHIQIRFNYNLRKALGIHKCFLNQVWTTLOPLIGHPLRFRTOYLVLYDLNLSVITL
NNVIRAVAHVNLVDVLDGTIDVHEVHIIRFKLY"
complement(1219. .1626)
/gene="C2"
complement(1219. .1626)
/gene="C2"
/codon_start=1
/product="C2"
/protein_id="AAK69689.1"
/db_xref="GI:14582854"
/translation="MQHSSPSFGHSTQIPIKVLHKKAKTKAIRRKRIDLACGCSYIHH

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gene
CDS
    1GCRNHGFTNCRHHCASSSEWRFYLGDNKSALFODNQTPHKTVLQELRHHTPSNTIO
    LQPEGIDDSQWSELPGIDLTASDMSFLKSI"
    complement(1535..2614)
    /gene="C1"
    /product="C1"
    /codon_start=1
    /protein_id="AAK69688.1"
    /db_xref="GI:14582853"
    /translation="MAPKRRRINSKNFVITYPKCSLTKEETLSQLLEPTNKKYI
    KICRELHENGEPHLVLIOPECKENCKNHRFDVSPTRSAHFHNIGCASSSDVKS
    YIDKGDIDLEWCEQVDCRSAGCGCONANDADLINGSASAFHAIIRKLPKDFIF
    QYHNLTNLDRIFOAPPEPIYSPFSSSDQVPELECGWSENCCGAARPMRPISIV
    IEGDSRTKTTIWARSLGPHNYLGHLDLSPKYSNDAWNYIDVDYHLYLKWKKEFG
    AQRDMSNTKKCKPIOVKGCITPILCNPGPISSTREFLEAKNALMSWLKNTFI
    TLDRPLYSIDTNSPPPOSDESHSP"
    complement(2200..2457)
    /gene="C4"
    complement(2200..2457)
    /gene="C4"
    /codon_start=1
    /product="C4"
    /protein_id="AAK69691.1"
    /db_xref="GI:14582856"
    /translation="MGNLISTCLFSSRENSSTARITDSSTWYPOGCHISIOFRELNO
    APTSSPTSTRMETHINGENSRSTDEVLEEAAMLTHNPTL"

BASE COUNT      720 a      551 c      649 g      847 t
ORIGIN

alignment_scores:
    Quality: 263.00      Length: 70
    Ratio: 4.242      Gaps: 0
    Percent Similarity: 88.571      Percent Identity: 70.000

alignment_block:
US-09-289-346a-3 x AF350330/rev ...

Align seg 1/1 to reverse of: AF350330 from: 1 to: 2767

1  ThleuValTrrpglyglupheglnValaSpQlyArSerAlaargGlyc1 17
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
2287 ACACCTGAATGCGGAGAAATTCAGGTGCGACGAGAGAGTGTACAGAGG 2238
17 yCyseGlnThSerAsnAspAlaAlaAlaAlaAlaAlaAlaSerSera 34
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
2237 CTGCCAAGATGCTAACGACGATCGCGGACGCTTTAAACGACAGCTCCG 2188
34 laAlaAlaAlaLeuGlnlleleargGluLysIleProGluLysTyrLeu 50
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2187 CTGAAGACGCTATGCTATTATTAGGAAAACCTCCCTAAAGATTATTAT 2138
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
2137 TTTCAGTATCATATATTAAAGACTAATTTAGATGATTTTCCAGGCTCC 2088
67 rProGluPro 70
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2087 CCCAGAGCCT 2078

seq_name: gb_vi:MBGARAL

seq_documentation_block:
LOCUS      MBGARAL      2617 bp ss-DNA      circular      VRL      02-AUG-1993
DEFINITION      Bean golden mosaic geminivirus viral coat protein (ARI) gene,
complete cds; putative replicative protein (AL1) gene, putative
cds; AL2 gene, complete cds; and AL3 gene, complete cds.
ACCESSION      M88686
VERSION      M88686.1 GI:331462
KEYWORDS      coat protein; replicative protein.
SOURCE      Bean golden mosaic virus (individual isolate Brazil, strain Type 1)
REPLICAIVE form DNA.

```

```

ORGANISM      bean golden mosaic virus
REFERENCE
AUTHORS      Gilbertson,R.L., Faria,J.C., Hanson,S.F., Morales,F.J.,
Abuqist,P.G., Maxwell,D.P. and Russell,D.R.
TITLE      Cloning of the Complete DNA Genomes of Four Bean-Infecting
Geminiviruses and Determining Their Infectivity by Electric
Discharge Particle Acceleratio
Phytopathology 81, 980-985 (1991)
REFERENCE
AUTHORS      Gilbertson,R.L., Hidayat,S.H., Martinez,R.T., Leong,S.A., Faria,J.C.,
Morales,F.J. and Maxwell,D.P.
TITLE      Differentiation of bean-infecting geminiviruses by nucleic acid
hybridization probes and aspects of bean golden mosaic in Brazil
Plant Dis. 75, 336-342 (1991)
REFERENCE
AUTHORS      Gilbertson,R.L., Faria,J.C., Abuqist,P.G. and Maxwell,D.P.
TITLE      Genetic diversity in geminiviruses causing bean golden mosaic
disease: The nucleotide sequence of the infectious cloned DNA
components of a Brazilian isolate of bean golden mosaic geminivirus
Unpublished (1992)
JOURNAL
FEATURES
SOURCE      location/Qualifiers
1..2617
/organism="bean golden mosaic virus"
/proviral
/isolate="Brazil"
/strain="Type 1"
/db_xref="Taxon:10839"
/dev_stage="Replicative form"
/gemline
1..181
/standard_name="Common Region"
/note="putative"
/function="putative origin of replication"
358..1113
/gene="ARI"
358..1113
/gene="ARI"
/note="putative"
/codon_start=1
/function="coat protein"
/product="coat protein"
/protein_id="AAA46313.1"
/db_xref="GI:331464"
/translation="MPKRDAAQRHMGCTSKTSRSANSPRCNGPKYKAAERVRPM
IRKPRITRLKRPDPRGCEGCKVQSTIEQRHDVSHVKVNCVSDVTGNGITTHRVGK
RRCVKSYYILKIMDENIKLNHTNSVFWLVDRDRPYGPMDGQVFNMFNDNEPST
ATVKNDLDRDREQVHKRFYGVKYGQYASNEQALVRFWKVNNVYVYVNHQEGKYEENHT
ENALLVMACHTASMPVYATLIRIFYFDSITN"
complement(1110..1508)
/gene="AL3"
complement(1110..1508)
/gene="AL3"
complement(1110..1508)
/note="putative"
/codon_start=1
/db_xref="GI:331465"
/translation="MDSRTGERITRQAEKNGYITWEISNPLEYFKMYNVEDIYYTTRV
YHLQIRFNHNLKRLGLHKAFLNFQWNTISLQASGTYLNNRKYVLVLLDRIGVLSL
NNVIRAVRFATDKSYVNVVLENNHKEYK"
complement(1255..1644)
/gene="AL2"
complement(1255..1644)
/gene="AL2"
complement(1255..1644)
/note="putative"
/codon_start=1
/protein_id="AAA46315.1"
/db_xref="GI:331466"
/translation="MRNSSSTPPSIKYOHRAAKKRAIRRRRVDECGCTIYVHNGS
GHGFTIRGTHICTSSGEMRVYIGDKSLFDQVQRGSTIRHDSITPPPNVYQPPQZ
GTGSGQFPPEPSPIDISSFEWDIEK"
complement(101n(1556..2617,1..241)
/gene="AL1"

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CDS
complement(join(1556..2617,1..24))
/gene="All"
/note="putative"
/codon_start=1
/function="viral replication"
/product="replicative protein"
/protein_id="AAA46312.1"
/db_xref="GI:331463"
/translation="MPPKRRIRANKNYFLYTPQSTIKESNIELOLNIQTPVNNKRI
IKERFIHNGEPHHLALIOPEKFOCTNCRVFDLKHPTTSSVSHANTOSAKSSDVKS
YIEKGDYIEWGHFQVDSRARGQOOLANDASKEAMQIIEKIPKELF
QYHNLSSNIDRIETKAPDPWSEPYHLSSFTNVPRMOEWADYFGRGAARPERISI
IEEDSRFTGKTMMARALGTNHYLSGHLDFNSVVFNSHAENVYIDIDIAPIYLTKHKE
LMGAQDMOSNCKGKGPVQIKGIRSYICNGDEASYSKCFIDKEENNAIKNWTIHNA
KFIFNSPLXOSSQSCETSNQTSR"

BASE COUNT      677 a      491 c      592 g      857 t
ORIGIN

alignment_scores:
  Quality: 262.00      Length: 67
  Ratio: 4.367      Gaps: 0
  Percent Similarity: 89.552      Percent Identity: 73.134

alignment_block:
US-09-289-346a-3 x MBGARAL/rev ...

Align seg 1/1 to reverse of: MBGARAL from: 1 to: 2617

4 TTPQYGLUPHegInValaAspGlyArgSerAlaArgGlyGlyGlnTh 20
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
2305 TGGGGTCATTTCAGTCAGCGAAGATGCTGCTAGAGAGGTCACAGAC 2256
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
20 rSerAsnSPAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 37
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
2255 AGCTAAAGATGCGCGCATCGCAAGCATTCCTTCAAGAGAGAGAG 2206
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
37 lAleuGlnIleIleArgGlyLysIleProGlyLysTyrLeuPheGlnPhe 53
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
2205 CCATGCAATTAATCAAGAGAACTACCGGAAAGTTCTCTCCAAATAT 2156
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
54 HisAsnLeuAsnSerAsnLeuAsnParGlyIlePheAspLysThrProGluPr 70
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
2155 CACAATTATTCAGTACCTGATAGATGATATTCACAAAGCTCGGATCC 2106
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
70 o 70
2105 G 2105
seq_name: gb_vi:MGU75278

seq_documentation_block:
LOCUS      MGU75278      447 bp      DNA      27-NOV-1996
DEFINITION  Macropitllium golden mosaic geminivirus replication-associated
protein (AC1) gene, partial cds.
ACCESSION  U75278
VERSION    U75278.1 GI:1688188
KEYWORDS
SOURCE
ORGANISM   Macropitllium golden mosaic geminivirus.
            Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
REFERENCE  1 (bases 1 to 447)
            Roye,M.E.
            Diversity and phylogeny of whitefly-transmitted geminiviruses from
            Jamaica
JOURNAL    Thesis (1996)
AUTHORS    2 (bases 1 to 447)
            Roye,M.E., McLaughlin,W.A. and Maxwell,D.P.
TITLE      Three distinct geminiviruses infecting M. jathyroides from Jamaica
            but not BGWV
JOURNAL    Unpublished (1996)
REFERENCE  3 (bases 1 to 447)
            Roye,M.E., McLaughlin,W.A. and Maxwell,D.P.

```

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TITLE      Direct Submission
JOURNAL    Submitted (17-OCT-1996) Biochemistry, University of the West
            Indies, Mona, Kingston 7, Jamaica
FEATURES
source
1..447
/organism="Macropitllium golden mosaic geminivirus"
/strain="Jamaican"
/isolate="2"
/db_xref="taxon:51676"
/clone="PMGA2"
/complement(1..447)
/gene="AC1"
complement(<1..>447)
/gene="AC1"
CDS
/gene="AC1"
/codon_start=1
/product="replication-associated protein"
/protein_id="AAB36919.1"
/db_xref="GI:168189"
/translation="HVLIQFOGKFNCTNRLFDLYSPSRSAHFHPNIOGAKSSDVKS
YVEKGDPTIEMGVFOIDGRSARGQOOLANDASKEAMQIIEKIPKELF
QYHNLSSNIDRIETKAPDPWSEPYHLSSFTNVPRMOEWADYFGRGAARPERISI
IEEDSRFTGKTMMARALGTNHYLSGHLDFNSVVFNSHAENVYIDIDIAPIYLTKHKE
LMGAQDMOSNCKGKGPVQIKGIRSYICNGDEASYSKCFIDKEENNAIKNWTIHNA
KFIFNSPLXOSSQSCETSNQTSR"

BASE COUNT      97 a      112 c      110 g      128 t
ORIGIN

alignment_scores:
  Quality: 260.00      Length: 70
  Ratio: 4.262      Gaps: 0
  Percent Similarity: 87.143      Percent Identity: 68.571

alignment_block:
US-09-289-346a-3 x MGU75278/rev ...

Align seg 1/1 to reverse of: MGU75278 from: 1 to: 447

1 ThreuValaTTPQYGLUPHegInValaAspGlyArgSerAlaArgGlyGln 17
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
294 ACCATCGAATGGGAGGTGTTCCAGATCGACGAGAAAGTGTCTGACGGCG 245
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
17 YCysGlnThSerAsnSPAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
244 TCAGCAAAATCATCTACAGTCAGCGCGCGCAAGCATTAATTCGTGACAAA 195
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
34 lAlaAlaAlaAlaLeuGlnIleIleArgGlyLysIleProGlyLysTyrLeu 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
194 AGGAGCGCGCCATGATAGATAGTCAAGAGAGTTCGCCGAAAGATTCTC 145
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAsnParGlyIlePheAspLysTh 67
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
144 TTTCATATATCCACACCTATCCAGTACCTGATAGATTTTCATGAAGCA 95
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
67 rProGluPro 70
94 TCCGGAACCA 85
seq_name: gb_vi:AF188708

seq_documentation_block:
LOCUS      AF188708      1365 bp      DNA      07-NOV-1999
DEFINITION  Cowpea golden mosaic geminivirus replication associated protein
(rep) and coat protein (cp) genes, partial cds.
ACCESSION  AF188708
VERSION    AF188708.1 GI:6273115
KEYWORDS
SOURCE
ORGANISM   cowpea golden mosaic geminivirus.
            Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
REFERENCE  1 (bases 1 to 1365)
            Faria,J.C.
            Partial nucleotide sequence of cowpea golden mosaic geminivirus
            from Brazil
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 1365)

```

AUTHORS Faria, J.C.
 TITLE Direct Submission
 JOURNAL Submitted (21-SEP-1999) Biotechnology Laboratory, EMBRAPA, Caixa Postal 179, Goiania, GO 75375, Brazil

FEATURES
 source 1..1365
 /organism="cowpea golden mosaic geminivirus"
 /strain="CGMV-BR"
 /specific_host="cowpea"
 /db_xref="taxon:69263"
 complement(<1..676)
 /gene="rep"
 complement(<1..676)
 /gene="rep"
 /note="AC1"
 /codon_start=1
 /product="replication associated protein"
 /protein_id="AA06318.1"
 /db_xref="GI:6273117"
 /translation="MPPKRFKIMAKNFFLYPQCSIGKESAI EQLQTLQTPVKKYI
 RVCRELHENGEPHLALIQEGKFCQCTNRLFDLKHPTSSVSHPIQAKSSDVKS
 YIEKDDYENGHPFQIDGRSARGCOITNDASALNASSKEAMQIIEKLPKFLF
 OYHNLSSNLDRIFFMKRPEPWPFPPLSFTNVPKQMDADYFGRDAARERPVSI
 IYEGDSR"
 674..820
 1021..>1365
 /gene="cp"
 1021..>1365
 /gene="cp"
 /note="AV1"
 /codon_start=1
 /product="coat protein"
 /protein_id="AA06317.1"
 /db_xref="GI:6273116"
 /translation="MYKRDAPWRHMSGTSKVSTNPFSPRSGGPKYNKAEMNRP
 YKPRTRYMRSDRPGRGCEGPKQVSFQKNDVSHIGVICTLSDVTGGGITHRYGK
 RCVKSVYLKAV"
 BASE COUNT 339 a 259 c 332 g 435 t
 ORIGIN

alignment_scores:
 Quality: 260.00 Length: 67
 Ratio: 4.483 Gaps: 0
 Percent Similarity: 86.567 Percent Identity: 73.134

alignment_block:
 US-09-289-346a-3 x AF188708/rev ..

Align seg 1/1 to reverse of: AF188708 from: 1 to: 1365

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4  TTPGlyGluPhgInValaSPglVArGSeRAlaArGlyGlyCysGlnTh 20
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
340 TGGGGTCATTTTCAAATCGACGAGAAATCTGCTAGAGAGCTCAGCAGAC 291
20 rSerAsnAspAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 37
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||
290 AATTAAAGATGTCAGCATCGAGCGCTTAAATGCTTCAAGAGCAAGAC 241
37 lalaGlnIleIleArGluLysTlleProGluLysTyrLlePhgGlnPhe 53
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
240 CCAATGCAAAATTATCAAGAGAACTACCGGAGAGTTCTTCCAGATAT 191
54 HisAsnLeuAsnSerAsnLeuAsnParGlyIlePheAspLysThrProGluP 70
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
190 CACAACCTATATCACTAACTGATAGATATTCAAAAGCCTCCGGAACC 141
70 o 70
140 A 140
seq_name: gb_vi:AF098940
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seq_documentation_block:
 LOCUS AF098940 1405 bp DNA VRL 04-MAR-1999
 DEFINITION Macropitillium golden mosaic geminivirus strain Jamaica 1
 partial cds.
 ACCESSION AF098940
 VERSION AF098940.1 GI:4336584
 KEYWORDS
 SOURCE
 ORGANISM
 Macropitillium golden mosaic geminivirus.
 Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 1 (bases 1 to 1405)
 Roye, M.E.
 genetic diversity and phylogeny of whitefly-transmitted
 geminiviruses from Jamaica
 Unpublished
 2 (bases 1 to 1405)
 Roye, M.E., McLaughlin, W.A. and Maxwell, D.P.
 Molecular characterization of two distinct geminiviruses infecting
 M. lathyroides from Jamaica
 Unpublished
 3 (bases 1 to 1405)
 Roye, M.E., McLaughlin, W.A. and Maxwell, D.P.
 Direct Submission
 Submitted (14-Oct-1998) Biotechnology Centre, University of the
 West Indies, Mona, Kingston 7, Jamaica
 Location/Qualifiers
 1..1405
 /organism="Macropitillium golden mosaic geminivirus"
 /strain="Jamaica strain 1"
 /specific_host="Macropitillium lathyroides"
 /db_xref="taxon:51676"
 /country="Jamaica"
 /clone="PMGJA2; PMGJA3"
 complement(<1..701)
 /gene="rep"
 complement(<1..701)
 /gene="rep"
 /codon_start=1
 /product="replication associated protein"
 /protein_id="AAD17850.1"
 /db_xref="GI:4336586"
 /translation="MPKRSFESIKAKNFFLYPQCSLTKREALSQTINLTPVKKFI
 KICREHEDGPHLHVLIQFOGKFNCTNRLFDLVPKSAHFHNPICAKSSDVKS
 YVEKGGDITLMEVFOIDGRSARGCOITNDAAEALNSGTKEAMRIYKLPKFLF
 OYHNLSSNLDRIFFMKDPEPWPFPPLSFTNVPKQMDADYFGRSAAARERPMSI
 IYEGDSRCKGTWAC"
 702..1030
 /note="intergenic region"
 1031..>1405
 /gene="cp"
 1031..>1405
 /gene="cp"
 /codon_start=1
 /product="coat protein"
 /protein_id="AAD17849.1"
 /db_xref="GI:4336585"
 /translation="MPKRDGSRRTTPGVAKVSRRLNYSPPRGYGPSSNKAQEMVNRPM
 YKPRTRYMRSDRPGRGCEGPKQVSFQKNDVSHIGVICTLSDVTGGGITHRYGK
 RCVKSVYLKAVTMDENINCSC"
 BASE COUNT 328 a 333 c 357 g 386 t 1 others
 ORIGIN

alignment_scores:
 Quality: 260.00 Length: 70
 Ratio: 4.262 Gaps: 0
 Percent Similarity: 87.143 Percent Identity: 68.571

alignment_block:
 US-09-289-346a-3 x AF098940/rev ..

Align seg 1/1 to reverse of: AF098940 from: 1 to: 1405


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1  ThrLeuValTrpGlyGluPheGlnValAspGlyArgSerAlaArgIyl 17
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
374  ACCATGAATGGGAGTGTTCAGATCGACGGAAGAGTCTCGAGGCG 325
17  yCysGlnThrSerAsnAspAlaIaIaIaIaIaLeuAlaIaIaSerSera 34
1  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
324  TCGCAACATCTACGATCCAGCCGCCGAGCATTAATTTCTGGAACAA 275
34  IaIaIaIaIaLeuGlnIleIleArgGlnIlyStIleProGlnIlyTyrlau 50
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
274  AGGAGCGCGCCATGACAGATAGTCAGAGAGAAAGTTGCCGAAAGTTCTC 225
51  PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspIlyst 67
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
224  TTTCAATATCATCAACCTATCCAGTAACCTGATGATTTTCATGAAGGA 175
67  rProGluPro 70
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
174  TCCGGAACCA 165

seq_name: gb_v1:SGU67926

seq_documentation_block:
LOCUS      SGU67926      554 bp      DNA      VRL      28-JAN-1998
DEFINITION Sida golden mosaic geminivirus Rep protein (AC1) gene, partial cds.
ACCESSION  U67926
VERSION    U67926.1  GI:1546801
KEYWORDS
SOURCE     sida golden mosaic virus.
            sida golden mosaic virus
            Viruses: ssDNA viruses; Geminiviridae; Begomovirus.
REFERENCE  1 (bases 1 to 554)
            Roye,M.E., McLaughlin,W.A., Nakhla,N.K. and Maxwell,D.P.
            Genetic Diversity among geminiviruses associated with the weed
            species Sida spp, Macroptilium lathyroides, and Missadula
            amplissima from Jamaica
            Plant Dis. 81, 1251-1256 (1997)
2 (bases 1 to 554)
            Roye,M.E., McLaughlin,W.A. and Maxwell,D.P.
            Direct Submission
            Submitted (23-AUG-1996) Plant pathology, University of Wisconsin,
            1630 Linden Drive, Madison, WI 53706-1598, USA
JOURNAL
FEATURES
            source
            1..554
            /organism="sida golden mosaic virus"
            /strain="Jamaica"
            /isolate="Jamaica, May 1993"
            /db_xref="taxon:51034"
            /note="DNA A component"
            complement(1..554)
            /gene="AC1"
            /complement(<1..>554)
            /note="replication-associated protein"
            /codon_start=1
            /product="Rep protein"
            /protein_id="AAB97865.1"
            /db_xref="GI:1546802"
            /translation="SISKEAISQLOTLKTPVNNKKFIKICRELHNGEPHLVLLTOFE
            GKYNNTNRFDIVSPTRSAHFHPNIOGAKSSDVSKVEKGDGTIEGKVGQIDGRSA
            RGGCOTANDAALAEALNSCTKEDALKIIEKLPERYLFOYHNLSNIDNIFSKPEPWS
            HPELPSTFAVPGQMDEWADGFCGR"
gene
CDS
BASE COUNT  121 a 127 c 139 g 167 t
ORIGIN
alignment_scores:
Quality: 259.00      Length: 70
Ratio: 4.246      Gaps: 0
Percent Similarity: 87.143      Percent Identity: 68.571
alignment_block:

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US-09-289-346A-3 x SGU67926/rev
Align seg 1/1 to reverse of: SGU67926 from: 1 to: 554

1  ThrLeuValTrpGlyGluPheGlnValAspGlyArgSerAlaArgIyl 17
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
290  ACCATGAATGGGAGTGTTCAGATCGACGGAAGAGTCTCGTGTGAGC 241
17  yCysGlnThrSerAsnAspAlaIaIaIaIaIaLeuAlaIaIaSerSera 34
1  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
240  TCGCAACACGCTACGACCGCCGCCGAGCATTAATTTCTGGAACAA 191
34  IaIaIaIaIaLeuGlnIleIleArgGlnIlyStIleProGlnIlyTyrlau 50
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
190  AGGAGCATGCACTGAAATATCATCAGAGAGAGTTACCGAAGATATCTC 141
51  PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspIlyst 67
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
140  TTTCAATATCATCAACCTATCCAGTAACCTGATGATTTTCAGTAAGCC 91
67  rProGluPro 70
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
90  TCCGGAACCG 81

seq_name: gb_v1:AB001315

seq_documentation_block:
LOCUS      AB001315      570 bp      DNA      VRL      13-FEB-1999
DEFINITION Tobacco leaf curl virus CI and C4 genes, clone YOKOHAMA3-1, partial
            and complete cds.
ACCESSION  AB001315
VERSION    AB001315.1  GI:3798714
KEYWORDS
SOURCE     tobacco leaf curl virus (isolate:YOKOHAMA3,
            specific host:Eupatorium makinoi) DNA, clone:YOKOHAMA3-1.
            tobacco leaf curl virus
            Viruses: ssDNA viruses; Geminiviridae; Begomovirus.
REFERENCE  1 (bases 1 to 570)
            Ooi,K.
            Direct Submission
            Submitted (19-FEB-1997) to the DDBJ/EMBL/GenBank databases.
            Kazuyuki Ooi, Kyushu University, Department of Biology, 6-10-1
            Hakozaki Higashi-ku, Fukuoka, Fukuoka 812, Japan
            (E-mail:koois@embbox.nc.kyushu-u.ac.jp, Tel:+81-92-642-2624,
            Fax:+81-92-642-2645)
2 (bases 1 to 570)
            Ooi,K., Ohshita,S., Ishii,I. and Yahara,T.
            Molecular phylogeny of geminivirus infecting wild plants in Japan
            J. Plant Res. 110, 247-257 (1997)
JOURNAL
FEATURES
            source
            1..570
            /organism="tobacco leaf curl virus"
            /isolate="YOKOHAMA3"
            /specific_host="Eupatorium makinoi"
            /db_xref="taxon:67762"
            /clone="YOKOHAMA3-1"
            complement(1..570)
            /gene="C1"
            /complement(<1..>570)
            /gene="C1"
            /codon_start=1
            /protein_id="BAA34033.1"
            /db_xref="GI:4426541"
            /translation="EVALSQLONTPTPNKLYIKICRELHEDGSPHLVLLQFEKRYK
            CONRRFPDIVSPTRSAHFHPNIOGAKSSDVSKYIDKGDLTLEMGTFQIDGSSARGC
            ONANDACAALNAASSKAELALATIREKLRDPTFOYHNLSNIDRIEAPLEVEVCPFT
            ASSPDVPEELLEMASSEWSSAARPM"
            complement(231..488)
            /gene="C4"
            /complement(231..488)
            /gene="C4"
            /codon_start=1
            /protein_id="BAA34034.1"

```

```
/db_xref="GI:3798715"  
/translation="MEALISMCESSKANTNAKINDDSTWYPOPOHISIRTRRELNP  
APTSSPTSTRTEIRSGEHSRSTEEVLEEARMLTHVORR"  
BASE COUNT      141 a      121 c      126 g      182 t  
ORIGIN
```

```
alignment_scores:      Quality: 251.00      Length: 85  
                        Ratio: 4.115      Gaps: 1  
Percent Similarity: 71.765      Percent Identity: 58.824
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```
alignment_block:  
US-09-289-346A-3 x AB001315/rev ..
```

```
Align seg 1/1 to reverse of: AB001315 from: 1 to: 570
```

```
1 ThrleuValTTrpGlyGluPheGlnValAspGlyArgSerAlaArgGlyG1 17  
||||| ||||| |||||:||||| ||||| ||||| ||||| |||||  
318 ACCCTCGAATGGGACATTCACAGATCGACGAGAAAGTCTAGAGAGAG 269  
17 YCysGlnThrSerAspAspAlaAlaAlaAlaLeuAlaLeuAlaSerSera 34  
|||||:||||| ||||| ||||| ||||| ||||| ||||| |||||  
268 CTGCCAGATCTACGACGCGATGTGACAGAGCGCTTAATGCAAGTCTA 219  
34 laAlaAlaAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeu 50  
||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
218 AGGACAGAAAGCTTAGCAATATTAGGAGAAAGCTCCCTAAAGATTATA 169  
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIle..... 63  
|||||:||||| ||||| ||||| ||||| ||||| ||||| |||||  
168 TTTCATATATCATATTAATTAATAGATTAGATTGATTTTTCCTCTCC 119  
64 ..... PheAspLysThrP 68  
118 GTTGGAGGTTTGTGTGCTCTTCACAGCCCTCATCCTTGATCAAGTTC 69  
68 roGlu 69  
|||||  
68 CAGAA 64
```



```

2216 AGCTAATGATGCTCCGACAGAGCCCTTAATGACGTTACGTCAGACAG 2167
37  lalauglnllelaarglulysilleeproglulysylrlephcglpPhe 53
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
2166 CTTTAGCAATATTAGGAAAGAACTCCCTTAAGCTTTATTATTTCAATAT 2117
54  HlSaSnLeuAsnSerAsnLeuAspArgllePheAspLysThrPro 68
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
2116 CATATATTAAATGTAATTAGATAGGATTTT.....ACACCT 2078

seq_name: /cgnl_8/gcgdata/geneseq/geneseqn/NA1995.DAT:AAQ84371

seq_documentation_block:
ID   AAQ84371 standard; DNA; 434 BP.
XX
AC   AAQ84371;
XX
DT   19-AUG-1995 (first entry)
XX
DE   Gemini1 virus-specific polyribozyme-E target sequence.
XX
KW   ribozyme target sequence; polyribozyme-E;
KM   tomato leaf curl virus; RNA cleavage; tomato transgenic plant;
XX   virus disease-resistance; ss.
XX   Tomato leaf curl virus.
OS
FH   Key      Location/Qualifiers
FT   misc-feature 13..43
      /tag= a
      /note= "ribozyme R1 target sequence"
FT   misc-feature 26..28
      /tag= b
      /note= "ribozyme R1 cleavage site"
FT   misc-feature 312..342
      /tag= c
      /note= "ribozyme R2 target sequence"
FT   misc-feature 325..327
      /tag= d
      /note= "ribozyme R2 cleavage site"
FT   misc-feature 384..414
      /tag= e
      /note= "ribozyme R3 target sequence"
FT   misc-feature 397..399
      /tag= c
      /note= "ribozyme R3 cleavage site"
XX
PN   WO9503404-A.
XX
PD   02-FEB-1995.
XX
PF   22-JUL-1993; 93WO-EP01946.
XX
PR   22-JUL-1993; 93AU-0047014.
PR   22-JUL-1993; 93WO-EP01946.
XX
PA   (BIOC-) BIOCEM SA.
XX   (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX
PI   Baudino S, Comeau D, Dry IB, Gruber V, Lenee P;
PI   Mason J, Rezaiian MA, Ridgen JE, Rezaiian MA;
XX
DR   MPI; 1995-075232/10.
XX
PT   Synthetic DNA virus ribozyme(s) - reduce replication, infection
PT   and/or assembly of viruses by cleaving target virus sequence,
PT   useful for preparing resistant plants; esp tomatoes.
XX
PS   Example 10; Fig 11b; 90pp; English.
XX
CC   The sequence is a tomato leaf curl virus target sequence for
CC   polyribozyme-E, which hybridizes to and cleaves the sequence and
CC   thereby reduces replication, infection and/or assembly of the virus

```

```

CC   substantially. The ribozyme may be expressed in a transgenic plant,
CC   e.g. tomato, to confer virus disease-resistance.
XX
SQ   Sequence 434 BP; 126 A; 86 C; 91 G; 131 T; 0 other:

alignment_scores:
      Quality: 222.00      Length: 85
      Ratio: 3.763
Percent Similarity: 69.412      Percent Identity: 52.941

alignment_block:
US-09-289-346a-3 x AAQ84371 ..

Align seg 1/1 to: AAQ84371 from: 1 to: 434

1  ThrLeuValTrpGlyGluPheGlnValAspGlyArgSerAlaArgGlyCl 17
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
95  ACCCTCGAATGGGAGAGATTTCAGATCGATGACGATCTGCAGAGGGCG 144
17  YCysGlnThrSerAsnAspAlaAlaAlaAlaAlaLeuAlaAlaSerAsp 34
| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
145  ACACCAATTCACCCATAGACGCTTACGCCGACGCCCTTACACTGAGACTA 194
34  lalaialaaleuglnllelaarglulysilleeproglulysylrleu 50
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
195  AGTCAGAGGCTCTTACGCTCTTAGGGAATTAGCCCTTAAGCATTAAGTGT 244
51  PheGlnPheHlSaSnLeuAsnSerAsnLeuAspArglle..... 63
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
245  TTAACAATTTCATTAATTAAATGTAATTAGATAGATTTTACACCTCC 294
64  .....PheAspLysThrP 68
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
295  GTTGACGCTTATGCTTCTCCTTTTATCTTCTTTCATGATGAGTTC 344
68  roglu 69
|||||
345  CAGAA 349

seq_name: /cgnl_8/gcgdata/geneseq/geneseqn/NA1995.DAT:AAQ84372

seq_documentation_block:
ID   AAQ84372 standard; DNA; 479 BP.
XX
AC   AAQ84372;
XX
DT   19-AUG-1995 (first entry)
XX
DE   Gemini1 virus-specific polyribozyme-F target sequence.
XX
KW   ribozyme target sequence; polyribozyme-F;
KM   tomato leaf curl virus; RNA cleavage; tomato transgenic plant;
XX   virus disease-resistance; ss.
XX   Tomato leaf curl virus.
OS
FH   Key      Location/Qualifiers
FT   misc-feature 46..96
      /tag= a
      /note= "ribozyme R4-R5 target sequence"
FT   misc-feature 58..60
      /tag= b
      /note= "ribozyme R4 cleavage site"
FT   misc-feature 81..83
      /tag= c
      /note= "ribozyme R5 cleavage site"
FT   misc-feature 356..386
      /tag= d
      /note= "ribozyme R2 target sequence"
FT   misc-feature 370..372
      /tag= c
      /note= "ribozyme R2 cleavage site"
XX

```

FT	misc_feature	429..459	/*tag= e
FT		/note= "ribozyme R3 target sequence"	
FT	misc_feature	442..444	/*tag= d
FT		/note= "ribozyme R3 cleavage site"	
XX			
PN	W09503404-A.		
XX			
PD	02-FEB-1995.		
XX			
PF	22-JUL-1993:	93WO-EP01946.	
XX			
PR	22-JUL-1993:	93AU-0047014.	
PR	22-JUL-1993:	93WO-EP01946.	
XX			
PA	(BIOC-) BIOCEM SA.		
PA	(CSIR) COMMONWEALTH SCI & IND RES ORG.		
PI			
PI	Baudino S, Comeau D, Dry IB, Gruber V, Lenee P;		
PI	Mason J, Rezaiian MA, Rigiden JF, Rezanan MA;		
XX			
DR	WPI: 1995-075232/10.		
XX			
PF	Synthetic DNA virus ribozyme(s) - reduce replication, infection		
PT	and/or assembly of viruses by cleaving target virus sequence,		
PT	useful for preparing resistant plants, esp tomatoes.		
XX			
PS	Example 10; Fig 11c; 90pp; English.		
XX			
CC	The sequence is a tomato leaf curl virus target sequence for		
CC	polyribozyme-F, which hybridizes to and cleaves the sequence and		
CC	thereby reduces replication, infection and/or assembly of the virus		
CC	substantially. The ribozyme may be expressed in a transgenic plant,		
CC	e.g. tomato, to confer virus disease-resistance.		
XX			
Sequence	479 BP; 145 A; 95 C; 97 G; 142 T; 0 other;		

alignment_scores:	Quality: 222.00	Length: 85
	Ratio: 3.763	Gaps: 1
Percent Similarity:	69.412	Percent Identity: 52.941
alignment_block:		
US-09-289-346A-3 x AA084372	..	

Align seg 1/1 to: AAQ84372 from: 1 to: 479

1 TheLeuValThrPgiVLuphediValAspGlyArgSerAlaIaArgLysI 17
140 ACCCTGCATGGGAGAGTTTCAGATGCATGGACCATCTGCAGAGGGG 1639
17 yCysGlnThrSerAsnAspAlaIaIaIaIaLeuAlaIaIaSerSera 34
190 ACAACATATAGCCCATAGCCCTTACGCCACCGCCCTTAACTCTGAAGTA 2399
34 IaIaIaIaIaLeuGlnIleIaArgLysIlePgiLysTyrLeu 50
240 AGTCAGAGCCCTCTTAAAGCTTCCTTAGGAAATTAGCCCTTAACGATTATGTT 2899
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgLle..... 63
290 TTACAACTTTCATPAAATTAAATAGTAAATAGATAGGATTTTTCACCTCC 3399
64PheAspLysThrP 68
340 GTTGGAGGTTTATGTTTCCTTTTTCATCTCTCTTTTCATGCAGCTC 3899
68 roGlu lu 69
|||||
290 CAGAA 394

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seq_name: /cgm1_8/gcgcdatr/geneseq/geneseqn/NA1995.DAT:AAQ84375
seq_documentation_block:
ID   AAQ84375 standard; DNA; 550 BP.
```

XX 19-AUG-1995 (first entry)
DE Tomato leaf curl virus Australian strain DNA sequence.
XX
XX Tomato leaf curl virus; Australia strain; plant disease; ds.
XX
OS Tomato leaf curl virus (Australia).
XX
FN W09503404-A.
XX
PD 02-FEB-1995.
XX
PF 22-JUL-1993; 93WO-EP01946.
XX
PR 22-JUL-1993; 93AU-0047014.
XX 22-JUL-1993; 93WO-EP01946.
XX
PA (BIOC-) BIOCEM SA.
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX
PI Baudino S, Comeau D, Dry IB, Gruber V, Lenee P,
PI Mason J, Rezanan MA, Rigden JE, Rezanan MA;
XX
DR WPI; 1995-075232/10.
XX
PT Synthetic DNA virus ribozyme(s) - reduce replication, infection
PT and/or assembly of viruses by cleaving target virus sequence,
PT useful for preparing resistant plants, esp tomatoes.
XX
PS Disclosure; Fig 1; 90pp; English.
XX
CC The sequence represents the complementary sense DNA strand of an
CC Australian strain of tomato leaf curl virus. Ribozymes specific
CC for this sequence may be used in generation of transgenic plants
CC with disease-resistance.
XX
XX Sequence 550 BP; 148 A; 120 C; 134 G; 142 T; 6 other;

[illegible]

```
alignment_block:
```

Align seg 1/1 to: AAQ84375 from: 1 to: 550

34 laalaalaleuglnllelleargluylleprogluylstyrlau 50
::: |||||:::||||| ||::: |:::
240 AGTCAGAGGCTTTAACGCCTTAGCGGAATTAGCCCTTAACGATTTATGTT 289

51 PheglnPheHisAsnLeuAsnSerAsnLeuAspArgIle..... 63
:::|||:::|||:::|||:::|||:::|||:::|||:::|||
290 TTCACATTTTCATAATTAAATAAGTAAATTAGATAGCATTTTTACACCTCC 339

64 PheAspLysThr 68
340 GTTGAGAGGTTTATGTCTTCCTTTTATTCCTCTCTTTGGATCGAGTTC 389

68 roglu 69
|||||
390 CAGAA 394

1 ThrLeuValTrpGlyAluPheGlnValAspGlyArgSerAlaArgLys 17
||||| ||||| ||||| ||||| ::::: ||||| ||||| ||||| |||||
201 ACCCTCGAATGGGAGACTTTCAATGATGATGAGACGATCTCGAAGGGGG 250

17 yCysGlnThrSerAsnAspAlaAlaAlaAlaAlaAlaSerSera 34
||:::||||| ||| ||||| ::::: |||
251 ACAACAAATCACCCAAATGACGCTTAGCGGCCAGCCTTAACAGTAGGA 300

34 laalaalaleuglnllelleargluylleprogluylstyrlau 50
::: |||||:::||||| ||||| ||::: |:::
301 AGTCAGAGGCTTTAACGCCTTAGGGAATTAGCCCTTAAGATTATGTT 350

51 PheglnPheHisAsnLeuAsnSerAsnLeuAspArgIle..... 63
:::|||:::|||:::|||:::|||:::|||:::|||:::|||
351 TTACATTTCAAAATTAAATAGTAATTTAGATAGCATTTTTNNNTACACC 4000

64 PheAspLysT 67

```

401 TCCGTTGAGGTTATGTTCTCCCTTTTATGCTCTCTTTGTGATCGAG 450
67 hrpProGlu 69
:::|||||
451 TTCGAGAA 458

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seq_name: /cgnl_8/gcgdata/geneseq/geneseqn/NA1997.DAT: AAT93294

seq_documentation_block:

ID AAT93294 standard; DNA; 1160 BP.

AC AAT93294;

DT 27-APR-1998 (first entry)

DE Tomato mottle virus AC1 open reading frame.

XX Geminivirus; TOMOV; AC1 gene; transdominant mutation;

KW transgenic plant; disease resistance; ss; cyclic; circular.

OS Tomato mottle virus isolate Florida.

XX Key Location/Qualifiers

FH CDS 44..1129

FT /*tag- a

XX WO9739110-A1.

PD 23-OCT-1997.

PF 15-APR-1997; 97WO-US06300.

PR 16-APR-1996; 96US-0015517.

XX (SEMI-) SEMINIS VEGETABLE SEEDS INC.

PA (WISC) WISCONSIN ALUMNI RES FOUND.

XX Ahlquist PG, Hanson SF, Luu HT, Maxwell DP, Stout JT;

XX WPI; 1997-526447/48.

DR P-PSDB; AAW34332.

XX Transgenic plants expressing geminivirus AC1 and CI wild-type and

PT mutant genes - have increased resistance to geminivirus infection

PT e.g. tomato mottle virus, tomato yellow leaf curl virus or bean

XX golden mosaic geminivirus

XX Example 3.3; Page 57-58; 132pp; English.

XX This genomic DNA sequence includes the open reading frame of the

CC wild-type AC1 gene of tomato mottle virus (TOMOV), a geminivirus

CC that has a bipartite genome. The AC1 gene must be expressed for

CC efficient replication of the two genomic components, DNA-A and

CC DNA-B. It encodes a protein (see AAW34336) having a DNA binding

CC site specific to the DNA-A common region, a DNA nicking activity,

CC and an ATP binding activity. The invention involves production of

CC transgenic plants containing DNA comprising AC1 or CI wild-type or

CC mutant sequences that negatively interfere in trans with

CC geminiviral replication during infection. Such transgenic plants

CC are resistant to viral infection. The AC1/CI genes are especially

CC from TOMOV, tomato yellow leaf curl virus or bean golden mosaic

CC geminivirus (see AAT93282-93) and encode polypeptides (see AAW34324-35)

CC that have mutations in the highly conserved DNA-nicking domain

CC and/or the ATP-binding domain.

XX Sequence 1160 BP; 360 A; 276 C; 257 G; 267 T; 0 other;

XX alignment_scores:

XX Quality: 218.00

XX Ratio: 3.695

XX Percent Similarity: 84.286

XX Length: 70

XX Gaps: 0

XX Percent Identity: 57.143

alignment_block:

US-09-289-346A-3 x AAT93294

Align seg 1/1 to: AAT93294 from: 1 to: 1160

```

1 ThrLeuValTrpGlyGluPheGlnValAspGlyArgSerAlaArgGly1 17
||||| ||||||| ||||||| ||||||| ||||||| |||||||
371 ACATCGATCGCGAGATTCTCCAGATCGACGCGAGATCTGCCAGAGAG 420
17 yCysGlnThSerAsnAspAlaAlaAlaAlaAlaAlaSerSera 34
||||| ||||||| ||||||| ||||||| ||||||| |||||||
421 CCACGAGCTGCTAATGATGATGCGAAAGCGTTAAATGCAAGTTCCG 470
34 laAlaAlaAlaLeuGlnIleLeuArgGluIleProGluLysTyrLeu 50
::: ||||| ::||| ||||| ::||| ||||| ::||| |||||
471 TTCATCTGCTTACGAGTTCTAAGGGAAGCAACCAAGCAATTTGTA 520
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLys 67
::||| ||||| ::||| ||||| ::||| ||||| ::||| |||||
521 TTACAAATCATTAACATCCGCTTAACCTAGACGATATTTCGAAAGGC 570
67 rProGluPro 70
::||| |||||
571 TCCGGAACCG 580

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seq_name: /cgnl_8/gcgdata/geneseq/geneseqn/NA1997.DAT: AAT93282

seq_documentation_block:

ID AAT93282 standard; DNA; 1169 BP.

AC AAT93282;

DT 27-APR-1998 (first entry)

DE Tomato mottle virus AC1 mutant TOMOV-AC1dlm gene.

XX Geminivirus; TOMOV-AC1dlm; AC1 gene; transdominant mutation;

KW transgenic plant; disease resistance; ss; cyclic; circular.

OS Tomato mottle virus isolate Florida.

XX Synthetic.

XX Key Location/Qualifiers

FH CDS 44..1129

FT /*tag- a

XX WO9739110-A1.

PD 23-OCT-1997.

PF 15-APR-1997; 97WO-US06300.

PR 16-APR-1996; 96US-0015517.

XX (SEMI-) SEMINIS VEGETABLE SEEDS INC.

PA (WISC) WISCONSIN ALUMNI RES FOUND.

XX Ahlquist PG, Hanson SF, Luu HT, Maxwell DP, Stout JT;

XX WPI; 1997-526447/48.

DR P-PSDB; AAW34324.

XX Transgenic plants expressing geminivirus AC1 and CI wild-type and

PT mutant genes - have increased resistance to geminivirus infection

PT e.g. tomato mottle virus, tomato yellow leaf curl virus or bean

XX golden mosaic geminivirus

XX Claim 11; Page 60-62; 132pp; English.

XX This DNA sequence comprises a transdominant lethal mutant,
 CC designated TOMOV-AC1dlm, of the AC1 gene of tomato mottle virus
 CC (TOMOV). It encodes an AC1 protein (see AAW34324) that carries

PE 15-APR-1997; 9/WO-US06300.
YY

AC	AA193284;
XX	

```

DT 27-APR-1998 (first entry)
XX
XX Tomato mottle virus AC1 mutant TOMOV-AC1d1m23 gene.
DE
XX
XX Geminivirus: TOMOV-AC1d1m23; AC1 gene; transdominant mutation;
KM transgenic plant; disease resistance; ss; cyclic; circular.
XX
XX Tomato mottle virus isolate Florida.
OS Synthetic.
XX
XX Key Location/Qualifiers
FT CDS 44..1129
FT /tag= a
XX
XX MO9739110-A1.
XX
XX 23-OCT-1997.
XX
XX 15-APR-1997; 97MO-US06300.
XX
XX 16-APR-1996; 96US-0015517.
XX
XX (SEMI-) SEMINIS VEGETABLE SEEDS INC.
XX (WISC-) WISCONSIN ALUMNI RES FOUND.
XX
XX Ahlquist PG, Hanson SF, Luu HT, Maxwell DP, Stout JT;
XX
XX MPI; 1997-526447/48.
XX P-PDB; AAW34326.
XX
XX Transgenic plants expressing geminivirus AC1 and CI wild-type and
XX mutant genes - have increased resistance to geminivirus infection
XX e.g. tomato mottle virus, tomato yellow leaf curl virus or bean
XX golden mosaic geminivirus
XX
XX Claim 11: Page 67-69; 132pp; English.
XX
XX This DNA sequence comprises a transdominant lethal mutant,
XX designated TOMOV-AC1d1m23, of the AC1 gene of tomato mottle virus
XX (TOMOV). It encodes an AC1 protein (see AAW34326) that carries
XX 2 mutations in an NTP-binding domain. The AC1 gene (see also
XX AAT93294) must be expressed for efficient replication of the two
XX genomic components, DNA-A and DNA-B, of the bipartite TOMOV genome.
XX The invention involves production of transgenic plants containing
XX DNA comprising geminivirus AC1 or CI wild-type or mutant sequences
XX that negatively interfere in trans with geminiviral replication
XX during infection. Such transgenic plants are resistant to viral
XX infection. The AC1/CI genes are especially from TOMOV, tomato
XX yellow leaf curl virus or bean golden mosaic geminivirus (see
XX AAT93282-93) and encode polypeptides (see AAW34324-35) that have
XX mutations in the highly conserved DNA-nicking and/or the NTP-binding
XX domains.
XX
XX Sequence 1169 BP; 364 A; 278 C; 257 G; 270 T; 0 other:
SQ

```

```

alignment_scores:
  Quality: 218.00      Length: 70
  Ratio: 3.695        Gaps: 0
  Percent Similarity: 84.286      Percent Identity: 57.143

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alignment_block:

US-09-289-346a-3 x AAT93284 ..

Align seg 1/1 to: AAT93284 from: 1 to: 1169

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1 ThrLeuValTrpGlyGluPheGlnValAspGlyArgSerAlaArgGlyG1 17
||||: |||||:|||||:|||||:|||||:|||||:|||||:|||||:
371 ACAATGCAATGCGAGATTCACAGATCGACGCGCATCTGCGACAGAGGG 420
17 yCyGlnThSerAsnAspAlaAlaAlaAlaLeuAlaAlaSerSerA 34
||||: |||||:|||||:|||||:|||||:|||||:|||||:
421 CCACGACTGCTAATGATTCATATGCGAAAGCGCTTAATGCAAGTTGCG 470

```

```

34 IaAlaAlaLeuGlnIleIleArgGlyLysIleProGlyLysTyrLeu 50
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:
471 TTCAATCTGCTTAGCGATTTCTAAGGAGAAACAACAAAGATTGTGA 520
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:
521 TTACAAATGATCATGATCCGCTTACCTGAGACGATATTCGCAAGGC 570
67 rProGluPro 70
:::|||||:
571 TCCGGAACCG 580

```

seq_name: /cgnl_8/gcdata/geneseq/geneseqn/NA1997.DAT:AAT93309

seq_documentation_block:

ID AAT93309 standard; DNA; 2602 BP.

AC AAT93309;

DT 27-APR-1998 (first entry)

XX Tomato mottle virus full-length A-component clone.

XX Geminivirus: TOMOV; AC1 gene; transdominant mutation;

XX transgenic plant; disease resistance; ss; cyclic; circular.

XX Tomato mottle virus isolate Florida.

XX MO9739110-A1.

XX 23-OCT-1997.

XX 15-APR-1997; 97MO-US06300.

XX 16-APR-1996; 96US-0015517.

XX (SEMI-) SEMINIS VEGETABLE SEEDS INC.

XX (WISC-) WISCONSIN ALUMNI RES FOUND.

XX Ahlquist PG, Hanson SF, Luu HT, Maxwell DP, Stout JT;

XX MPI; 1997-526447/48.

XX Transgenic plants expressing geminivirus AC1 and CI wild-type and

XX mutant genes - have increased resistance to geminivirus infection

XX e.g. tomato mottle virus, tomato yellow leaf curl virus or bean

XX golden mosaic geminivirus

XX Example 3.1: Page 76-77; 132pp; English.

XX This genomic DNA sequence comprises a full-length A-component clone

XX of tomato mottle virus (TOMOV), a geminivirus that has a bipartite

XX genome comprising DNA-A and DNA-B. It was isolated from TOMOV

XX infected Nicotiana benthamiana and tomato plant DNA by restriction

XX digestion. The DNA-B component (see AAT93310) was also isolated.

XX TOMOV DNA-A contains the AC1 gene (see AAT93294) that must be

XX expressed for efficient replication of DNA-A and DNA-B. The

XX invention involves production of transgenic plants containing DNA

XX comprising AC1 or CI wild-type or mutant sequences that negatively

XX interfere in trans with geminiviral replication during infection.

XX

SQ Sequence 2602 BP; 671 A; 561 C; 586 G; 784 T; 0 other:

alignment_scores:

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  Quality: 218.00      Length: 70
  Ratio: 3.695        Gaps: 0
  Percent Similarity: 84.286      Percent Identity: 57.143

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alignment_block:

US-09-289-346a-3 x AAT93309/rev ..

PS Claim 13: Page 111-112; 132pp; English.

XX This DNA sequence comprises construct BGAC228 that codes for a
 CC transdominant lethal mutant (see AAW34334) of the CI protein (see
 CC AAW34338) of bean golden mosaic virus (BGMV). It was obtained by
 CC Kunkel mutagenesis of the wild-type CI gene (see AAT93314). CI is
 CC required for replication. The invention involves production of
 CC transgenic plants containing DNA comprising geminivirus CI or AC1
 CC wild-type or mutant sequences that negatively interfere in trans
 CC with geminiviral replication during infection. Such transgenic
 CC plants are resistant to viral infection. The AC1/CI genes are
 CC especially from BGMV, tomato mottle virus or tomato yellow leaf
 CC curl virus (see AAT93282-93) and encode polypeptides (see AAW34324-35)
 CC that have mutations in the highly conserved DNA-nicking and/or the
 CC NTP-binding domains.

SQ Sequence 1062 BP; 338 A; 247 C; 218 G; 259 T; 0 other;

XX
 XX

alignment_scores:
 Quality: 217.00 Length: 70
 Ratio: 3.741 Gaps: 0
 Percent Similarity: 82.857 Percent Identity: 58.571

alignment_block:
 US-09-289-346A-3 x AAT93292 ..

Align seg 1/1 to: AAT93292 from: 1 to: 1062

```

1 ThrLeuValTrpGlyGluPheGlnValAspGlyArgSerAlaArgGlyG1 17
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
328 ACAATCGAATGGGCAATTCGAATCTCCACGCGCATCTCGAAGAGGAG 377
17 yCysGlnThrSerAsnAspAlaAlaAlaAlaLeuAlaAspSerA 34
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
378 TCAGCAGTCTGCCAAGCATATATGCAAGCAATTAACCCAGATTCAA 427
34 laAlaAlaLeuGlnIleIleArgGluIuysIleProGluIuysTyrLeu 50
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
428 TTGAATCTGCCTTGACATATTGAAGAGAAACAACCGAAGATTACGTC 477
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
478 CTTCAACATCACAACATCCGTTCTAATCTCGAAGCATCTTCGTCAAAGT 527
67 rProGluPro 70
   ||||| |||||
528 GCCCGAACA 537
seq_name: /cgnl_8/gcgdata/geneseq/geneseqn/NA1997.DAT:AAT93293
seq_documentation_block:
ID AAT93293 standard; DNA: 1062 BP.
XX
XX AAT93293:
AC
XX
XX DT
XX 27-APR-1998 (first entry)
XX
DE Bean golden mosaic geminivirus CI mutant ORF BGAC262.
XX
XX Geminivirus: BGMV; CI gene; transdominant mutation;
XX transgenic plant; disease resistance; ss: cyclic; circular.
XX
XX OS Bean golden mosaic virus type II isolate Guatemala.
XX
XX PN
XX WO9739110-A1.
XX
XX PD
XX 23-OCT-1997.
XX
XX PF
XX 15-APR-1997: 97MO-US06300.
XX
XX PR
XX 16-APR-1996: 96DS-0015517.
XX
XX

```

PA (SEMI-) SEMINIS VEGETABLE SEEDS INC.
 PA (WISC.) WISCONSIN ALUMNI RES FOUND.

XX
 XX PI Ahlquist PG, Hanson SE, Lou HT, Maxwell DP, Stout JT;
 XX
 XX DR WPI: 1997-526447/48.
 XX P-PDB: AAW34335.

PT Transgenic plants expressing geminivirus AC1 and CI wild-type and
 PT mutant genes - have increased resistance to geminivirus infection
 PT e.g. tomato mottle virus, tomato yellow leaf curl virus or bean
 PT golden mosaic geminivirus

PS Claim 13: Page 115-116; 132pp; English.

XX
 XX
 XX This DNA sequence comprises construct BGAC262 that codes for a
 CC transdominant lethal mutant (see AAW34335) of the CI protein (see
 CC AAW34338) of bean golden mosaic virus (BGMV). It was obtained by
 CC Kunkel mutagenesis of the wild-type CI gene (see AAT93314). CI is
 CC required for replication. The invention involves production of
 CC transgenic plants containing DNA comprising geminivirus CI or AC1
 CC wild-type or mutant sequences that negatively interfere in trans
 CC with geminiviral replication during infection. Such transgenic
 CC plants are resistant to viral infection. The AC1/CI genes are
 CC especially from BGMV, tomato mottle virus or tomato yellow leaf
 CC curl virus (see AAT93282-93) and encode polypeptides (see AAW34324-35)
 CC that have mutations in the highly conserved DNA-nicking and/or the
 CC NTP-binding domains.

SQ Sequence 1062 BP; 340 A; 245 C; 219 G; 258 T; 0 other;

XX
 XX

alignment_scores:
 Quality: 217.00 Length: 70
 Ratio: 3.741 Gaps: 0
 Percent Similarity: 82.857 Percent Identity: 58.571

alignment_block:
 US-09-289-346A-3 x AAT93293 ..

Align seg 1/1 to: AAT93293 from: 1 to: 1062

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1 ThrLeuValTrpGlyGluPheGlnValAspGlyArgSerAlaArgGlyG1 17
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
328 ACAATCGAATGGGCAATTCGAATCTCCACGCGCATCTCGAAGAGGAG 377
17 yCysGlnThrSerAsnAspAlaAlaAlaAlaLeuAlaAspSerA 34
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
378 TCAGCAGTCTGCCAAGCATATATGCAAGCAATTAACCCAGATTCAA 427
34 laAlaAlaLeuGlnIleIleArgGluIuysIleProGluIuysTyrLeu 50
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
428 TTGAATCTGCCTTGACATATTGAAGAGAAACAACCGAAGATTACGTC 477
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
478 CTTCAACATCACAACATCCGTTCTAATCTCGAAGCATCTTCGTCAAAGT 527
67 rProGluPro 70
   ||||| |||||
528 GCCCGAACA 537
seq_name: /cgnl_8/gcgdata/geneseq/geneseqn/NA1997.DAT:AAT93314
seq_documentation_block:
ID AAT93314 standard; DNA: 1183 BP.
XX
XX AAT93314:
AC
XX
XX DT
XX 27-APR-1998 (first entry)
XX
XX DE Bean golden mosaic geminivirus CI open reading frame.
XX
XX

```

```

KM  Geminiivirus; BGWV; C1 gene; transdominant mutation;
KM  transgenic plant; disease resistance; ss; cyclic; circular.
XX
OS  Bean golden mosaic virus type II isolate Guatemala.
XX
FH  Key          Location/Qualifiers
FT  CDS          1..1062
FT              /*tag= a
XX
PN  W09739110-A1.
XX
PD  23-OCT-1997.
XX
PF  15-APR-1997; 97WO-US06300.
XX
PR  16-APR-1996; 96US-0015517.
XX
PA  (SEMI-) SEMINIS VEGETABLE SEEDS INC.
XX  (WISC ) WISCONSIN ALUMNI RES FOUND.
XX
PI  Ahlquist PG, Hanson SF, Lou HT, Maxwell DP, Scout JT;
XX  WPI: 1997-526447/48.
XX  P-PSDB: AAW34338.
XX
PT  Transgenic plants expressing geminivirus AC1 and C1 wild-type and
PT  mutant genes - have increased resistance to geminivirus infection
PT  e.g. tomato mottle virus, tomato yellow leaf curl virus or bean
PT  golden mosaic geminivirus
XX
PS  Example 5; Page 100-102; 132pp; English.
XX
CC  This genomic DNA sequence includes the open reading frame (ORF) of
CC  the wild-type C1 gene of bean golden mosaic virus (BGWV), a
CC  geminivirus that has a monopartite genome. The C1 protein (see
CC  AAW34338) is required for replication. The wild-type C1 ORF was
CC  subjected to Kunkel mutagenesis (see AAT93290-93). The invention
CC  involves production of transgenic plants containing DNA comprising
CC  C1 or AC1 wild-type or mutant sequences that negatively interfere
CC  in trans with geminiviral replication during infection. Such
CC  transgenic plants are resistant to viral infection. The AC1/C1
CC  genes are especially from BGWV, tomato mottle virus or tomato
CC  yellow leaf curl virus (see AAT93282-93) and encode polypeptides
CC  (see AAW34324-35) that have mutations in the highly conserved
CC  DNA-nicking domain and/or the NTP-binding domains.
XX
SQ  Sequence 1183 BP; 372 A; 276 C; 248 G; 287 T; 0 other;

```

```

478  CTTCAACATCAACATCCGTTCTAATCTGACAGCATCTTCGCAAGT 527
67  rProglupro 70
   :|||||||
528  GCCGGAACCA 537
seq_name: /cgn1_8/gcgdata/geneseq/geneseqn/NA1997.DAT: AAT93290
seq_documentation_block:
ID  AAT93290 standard; DNA; 1183 BP.
XX
AC  AAT93290;
XX
DT  27-APR-1998 (first entry)
XX
DE  Bean golden mosaic geminivirus C1 mutant gene.
XX
KM  Geminiivirus; BGWV; C1 gene; transdominant mutation;
KM  transgenic plant; disease resistance; ss; cyclic; circular.
XX
OS  Bean golden mosaic virus type II isolate Guatemala.
XX
FH  Key          Location/Qualifiers
FT  CDS          1..1062
FT              /*tag= a
XX
PN  W09739110-A1.
XX
PD  23-OCT-1997.
XX
PF  15-APR-1997; 97WO-US06300.
XX
PR  16-APR-1996; 96US-0015517.
XX
PA  (SEMI-) SEMINIS VEGETABLE SEEDS INC.
XX  (WISC ) WISCONSIN ALUMNI RES FOUND.
XX
PI  Ahlquist PG, Hanson SF, Lou HT, Maxwell DP, Scout JT;
XX  WPI: 1997-526447/48.
XX  P-PSDB: AAW34332.
XX
PT  Transgenic plants expressing geminivirus AC1 and C1 wild-type and
PT  mutant genes - have increased resistance to geminivirus infection
PT  e.g. tomato mottle virus, tomato yellow leaf curl virus or bean
PT  golden mosaic geminivirus
XX
PS  Claim 13; Page 103-105; 132pp; English.
XX
CC  This DNA sequence comprises construct BGAC190 that codes for a
CC  control mutant (see AAW34332) of the C1 protein (see AAW34338) of bean
CC  golden mosaic virus (BGWV). It was obtained by Kunkel mutagenesis
CC  of the wild-type C1 gene (see AAT93314). C1 is required for
CC  replication. The invention involves production of transgenic
CC  plants containing DNA comprising geminivirus C1 or AC1 wild-type or
CC  mutant sequences that negatively interfere in trans with
CC  geminiviral replication during infection. Such transgenic plants
CC  are resistant to viral infection. The AC1/C1 genes are especially
CC  from BGWV, tomato mottle virus or tomato yellow leaf curl virus (see
CC  AAT93282-93) and encode polypeptides (see AAW34324-35) that have
CC  mutations in the highly conserved DNA-nicking and/or the NTP-binding
CC  domains.
XX
SQ  Sequence 1183 BP; 371 A; 277 C; 249 G; 286 T; 0 other;

```

```

alignment_scores:
  Quality: 217.00      Length: 70
  Ratio: 3.741        Gaps: 0
Percent Similarity: 82.857  Percent Identity: 58.571

```

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alignment_block:
  US-09-289-346A-3 x AAT93290  ..

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Align seg 1/1 to: AAT93290 from: 1 to: 1183

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1   ThrLeuValITrpgIygluphegInValAspGLyArSerAlaArgI 17
2   ::::::::::::::::::::::::::::::::::::::::::::::
328  ACMAATGCAGATGGGACAAATTCCAAGTCGACGCGAGATCTCGCAAGAGAGG 377
17  yCysGIInThrSerAsnAspAlaIaIaIaIaIaIaIaIaIaIaSerSera 34
18  :::::::::::::::::::::: 111  ::::::::::::::::::::::
378  TCAGACGCTCTCCACACGACATCATATATCCAAAGCGATTAAACGACAGATCCA 427
34  IaIaIaIaIaLeuGInIleIleArgGlnIlySLeProGlnIlySyrIleu 50
428  TTGAATCTGCCTTGACAAATATTGANAAGAGAAACACCGAAGATTACGTG 477
51  pheGInPheHisAsnLeuAsnSerAsnSerAsnLeuAspArgIlePheAspIlySTh 67
52  ::::111  :::::::::::::::::::::::::::::::::::::: 111::
478  CTTCAACATCGACACACATCGCTTCAATATCTCGAAGCGATCTCTGTAAGT 527
67  rProGluPro 70
68  ::::::::::::::
528  GCCGGAAACCA 537

seq_name: /cognl_8/gcgdata/geneseq/geneseqn/NA2000.DAT.NAA94700

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ID  _AAA94700 standard; DNA; 1651 BP.
XX
AC  _AAA94700:
XX
DT  _15-JAN-2001 (first entry)
XX
DE  _PMRG 2288 35S-rep gene cassette.
XX
KW  _Geminiviruses; DNA-A; geminivirus replication inhibition; ac3 gene;
KM  _transgenic plant; antiviral; gene therapy; bean golden mosaic virus;
KW  _BGMY; alfalfa mosaic virus; AMV; cauliflower mosaic virus; CaMV; ds.
XX
XX  _Bean golden mosaic virus.
OS  _Cauliflower mosaic virus.
OS  _Alfalfa mosaic virus.
OS  _Synthetic.
XX
PN  _US6118048-A.
XX
PD  _12-SEP-2000.
XX
XX  _12-SEP-2000.
XX
PF  _24-APR-1998; 98US-0065999.
XX
PR  _25-APR-1997; 97US-0044925.
XX
PA  _ (MISC ) WISCONSIN ALUMNI RES FOUND.
XX
DR  _WPI; 2000-610661/58.
XX
PT  _Genetic construct comprising a mutant geminiviral rep gene, useful for
PT  _producing a plant resistant to geminiviral infection -
XX
XX  _Example; Column 15-16; 14pp; English.
XX
XX  _The present sequence is a 35S-rep gene cassette comprising the rep gene
XX  _of bean golden mosaic virus (BGMY)-GA cloned downstream of the CamV
XX  _35S promoter and an alfalfa mosaic virus (AMV) leader sequence. The
XX  _sequence was integrated into PBSII-KS+ to produce a rep gene expression
XX  _vector. DNA-nicking domain mutations may be incorporated into rep gene
XX  _to produce a genetic construct that acts as a trans-dominant inhibitor
XX  _of geminiviral replication. When expressed in a plant cell, this
XX  _inhibitor is able to dramatically reduce replication of geminiviruses.
XX  _Genetic constructs that include sequences containing a portion of the
XX  _ac3 gene in addition to the trans-dominant inhibitor exhibit increased
XX  _efficiency and broadened specificity of inhibition of geminiviral
XX  _replication. Geminiviruses are one of the greatest constraints on
XX  _production of important crops, including cassava, beans, cowpeas,
XX

```

CC peppers, tomatoes and cotton. The effects of the virus can be overcome
CC by using the genetic construct.

50 Sequence 1651 BP; 517 A; 393 C; 342 G; 399 T; 0 other;

alignment_scores

Quality:	217.00	Length:	70
Partic:	3.741	Count:	0

Ratio:	5.741	Gaps:	0
Percent Similarity:	82.857	Percent Identity:	58.571

alignment_block:

US-09-289-346A-3.X AAA94700

Align seg 1/1 to: AAA94700 from: 1 to: 1651

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::: :::
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17 YcYgInThrSerAsnAspAlaIleAlaIleAlaIleuAlaIleSerSera 34
::: :::
846 TCAGCGAGTGCCCAACGACTCATATGCAAGAAGCATTAACCCGCAATTCAA 895

34 IalIalIalIaleugInIleIleArgLysLysIleProGluTyTleu 50
::: :::
896 TTGAATCTGCCITGGACAAATATTGAAAGAGAACCAACCAGAAAGATTACGTC 945

51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgLileAspLysTh 67
::: :::
946 CTTCACAGCATCACAACTCGTTCTAATCTCGAAACGATCTCGTCAAAAT 995

67 rProGluPro 70
::: :::
996 GCCGGAACCA 1005

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OM of: US-09-289-346A-3 to: EST:★ out_format : pls
Date: Jan 3, 2002 6:15 PM
About: Results were produced by the GenCore software, version 4.5.
Copyright (c) 1993-2000 Comphen Ltd.

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Search information block:
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Query length: 70
Database: EST:*
Database sequences: 11351937
Database length: 1077921985
Search time (sec): 8697.120000
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gb_esc12:BG593614	-	71.50 151.48 28.36 603 ! BG593614 EST492292 CSTS Solara
gb_esc12:BG599652	-	71.50 149.89 34.80 721 ! BG599652 EST504547 CSTS Solara
gb_esc12:BI1006561	-	71.50 149.89 35.69 737 ! BI1006561 I71B01 Mature tuber
gb_esc12:BG561297	-	71.00 154.56 19.10 376 ! BG561297 ETE58d3c09.y1 Rim

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/db_xref="taxon:9606"
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/clone_1b="CB"
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/cell_type="CD34+ hematopoietic stem/progenitor cell"
/lab_host="BM25.8"
/note="Vector: pBluescript; Site_1: EcoRI; The insert is
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[illegible]

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59 AsnIeuasp 61
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142 AACATCGAT 150

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DEFINITION  AV744255 CB Homo sapiens CDNA clone CBMAJD03 5', mRNA sequence.
ACCESSION   AV744255
VERSION     AV744255.1
KEYWORDS    GI:10861836
SOURCE      human.
ORGANISM    Homo sapiens
REFERENCE   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS     Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE       1 (bases 1 to 514)
JOURNAL     Zhang,Q., Ye,M., Wu,X., Gu,J., Huang,Q., Zhou,J., Shen,Y., Han,Z.
COMMENT     Chen,S., Mao,M. and Chen,Z.
            Homo sapiens CB library CDNA clones
            Unpublished (2000)
            Contact: Zhu Chen
            Shanghai Institute of Hematology, Rui-Jin Hospital
            197 Rui-Jin II Road, Shanghai 200025, P. R. China
            Tel: 86-21-64740490
            Fax: 86-21-64743206
            Email: mbs@shims.sh.cn
            This clone is available at Shanghai Hematology Institute in
            Shanghai.
FEATURES
     source             Chinese National Human Genome Center at Shanghai
                        351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong.
                        Location/Qualifiers
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                                /lab_host="BM25.8"
                                /note="Vector: pBluescript; Site_1: EcoRI. The insert is
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    Ratio:        1.975      Gaps:      2
    Percent Similarity: 75.472      Percent Identity: 35.849
alignment_block:
US-09-289-346A-3 x AV744255 ..
Align seg 1/1 to: AV744255 from: 1 to: 514
10 AspGlyArgSerAlaArgGlyGlyCysGln..ThrSerAsnAspAlaA 25
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1 AATTTCGGCGCCCGCTGCACACGCGCTGCACAGAAGCAGCAGAGGGCTTC 50
   1 AATAAATAAATAAATAAAserSerAlaAlaAlaAlaAlaAlaAla 42
   ::::::::::| ::::::::::| ::::::::::| ::::::::::| ::::
51 CACAGAGAGCGCTACACAGCGCCGCCGCTTGCTGCAGCAGCATGCTCTACTG. 99
   42 rGGLuLysIleProGluLysTyrIleuPheGlnIlePheHisAsnLeuAsnSer 58
   100 .....ATCCCTGAAAAAGTTCCAGCATATTGTCGAGTACTCAACACC 141
   59 AsnLeuAsp 61
   ||| ::::::::::|
142 AACATCGAT 150
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seq_documentation_block:
LOCUS       AV737185          585 bp      mRNA          EST          17-OCT-2000
DEFINITION  AV737185 CB Homo sapiens CDNA clone CBMAJG03 5', mRNA sequence.

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ACCESSION      AV737185
VERSION        AV737185.1  GI:10854766
KEYWORDS
SOURCE
ORGANISM       human.
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Euthioria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS        Zhang,O., Ye,M., Wu,X., Gu,Y., Huang,Q., Zhou,Y., Shen,Y., Han,Z.,
                Chen,S., Mao,M., and Chen,Z.
                Homo sapiens CB library cDNA clones
                Unpublished (2000)
TITLE           Contact: Zhu Chen
                Shanghai Institute of Hematology, Rui-Jin Hospital
                197 Rui-Jin II Road, Shanghai 200025, P. R. China
                Tel: 86-21-64740490
                Fax: 86-21-64743206
                Email: mbs@shs.sh.cn
                This clone is available at Shanghai Hematology Institute in
                Shanghai.
                Chinese National Human Genome Center at Shanghai
                351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong.
                Location/Qualifiers
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                /cell_type="CD34+ hematopoietic stem/progenitor cell"
                /lab_host="BM25.8"
                /note="Vector: pBluescript; Site 1: EcoRI. The insert is
                cloned randomly with the EcoRI digestion"
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    Ratio:         1.975      Gaps:         2
Percent Similarity: 75.472      Percent Identity: 35.849
alignment_block:
US-09-289-346A-3 x AV737185 ..
Align seg 1/1 to: AV737185 from: 1 to: 585
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   ::::::::::: ||| |||||::: ||::: ||:::
1  AATTGCGCGCCGCCGTCGACACGCCGTCGACGAAGACGACGAAGGCGCTTC 50
25 aaIaIaIaIaIeuaIaIaIaSerSerAlaAlaIaIaIaIeudIaIeIa 42
   ::::::::::: ||| |||||::: ||::: ||:::
51 CACAGAGAGCCCTACACAGCCGCCGCTGTGCTGCACACCATGCTCTTAATG. 99
42 rggIuIuysIleProGluIuysTyrIleuPheGlnIphEhIAsnIeuaSnsr 58
100 .....ATCCCTGCAAAAGTTTCACGATATTATTTCGAGTACGCAACACC 141
   |||||::: |||::: ||::: ||:::
142 AACATCGAT 150
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seq_documentation_block:
LOCUS          AV736552      586 bp      mRNA      EST      17-Oct-2000
DEFINITION     AV736552 CB Homo sapiens cDNA clone CBNAUE10 5', mRNA sequence.
ACCESSION      AV736552
VERSION        AV736552.1  GI:10854133
KEYWORDS
EST.
SOURCE         human.
ORGANISM       Homo sapiens

```


TITLE Homo sapiens CB library cDNA clones
JOURNAL Unpublished (2000)
COMMENT Contact: Zhu Chen
 Shanghai Institute of Hematology, Rui-jin Hospital
 197 Rui-jin II Road, Shanghai 200025, P. R. China
 Tel: 86-21-64740490
 Fax: 86-21-64743206
 Email: mshisms.scn.sh.cn
 This clone is available at Shanghai Hematology Institute in
 Shanghai.
 Chinese National Human Genome Center at Shanghai
 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong.
FEATURES
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 1..596
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 /clone="CBPBC02"
 /clone_lib="CB"
 /cissue_type="cord blood"
 /cell_type="CD34+ hematopoietic stem/progenitor cell"
 /lab_host="BM25.8"
 /note="Vector: pBluescript; Site1: EcoRI; The insert is
 cloned randomly with the EcoRI digestion"
BASE COUNT 165 a 142 c 170 g 117 t 2 others
ORIGIN
 alignment_scores:
 Quality: 79.00 Length: 53
 Ratio: 1.975 Gaps: 2
 Percent Similarity: 75.472 Percent Identity: 35.849
 alignment_block:
 US-09-289-346A-3 x AV741448 ..
 Align seg 1/1 to: AV741448 from: 1 to: 596
 10 AspGlyArgSerAlaArgGlyGlyCysGln...ThrSerAsnAspAlaAl 25
 1 AATTGCGCGCCGCGTCGACACGCGCTGGAGAGACGACAGAGGGCGCTTC 50
 25 aAlaAlaAlaLeuAlaAlaSerSerAlaAlaAlaAlaLeuGlnIleLeu 42
 51 CACAGGAGGCGCTACACGCCGCCGCTGTGTGTCGACGCGCATGCTCTAGTG. 99
 42 rGgLUlySlleProGlnUlySTyrLeuPheGlnPheHisAsnLeuAsnSer 58
 100ATCCCTGAAAGATTCCAGCATATTTTGGCAGTACTCACAACC 141
 59 AsnLeuAsp 61
 142 AACATCGAT 150
 seq_name: gb_est1:AV738839
 seq_documentation_block:
 LOCUS AV738839 615 bp mRNA EST 17-OCT-2000
 DEFINITION AV738839 CB Homo sapiens cDNA clone CBM4HD06 5', mRNA sequence.
 ACCESSION AV738839
 VERSION AV738839.1 GI:10856420
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
 1 (bases 1 to 615)
 Zhang,Q., Ye,M., Wu,X., Gu,J., Huang,Q., Zhou,J., Shen,Y., Han,Z.,
 Chen,S., Mao,M. and Chen,Z.
 Homo sapiens CB library cDNA clones
 Unpublished (2000)
TITLE Contact: Zhu Chen
JOURNAL Shanghai Institute of Hematology, Rui-jin Hospital
COMMENT 197 Rui-jin II Road, Shanghai 200025, P. R. China


```

/db_xref="taxon:9606"
/clone_lib="CBFRTG04"
/clone_lib="CB"
/tissue_type="cord blood"
/cell_type="CD34+ hematopoietic stem/progenitor cell"
/lab_host="BM25.8"
/notes="Vector: pBluescript; Site 1: EcoRI. The insert is
cloned randomly with the EcoRI digestion"
BASE COUNT      135 a      135 c      157 g      96 t
ORIGIN

alignment_scores:
  Quality:      75.50      Length:      64
  Ratio:        1.866      Gaps:        2
  Percent Similarity: 64.062      Percent Identity: 31.250

alignment_block:
US-09-289-346A-3 x AV739224 ...

Align seg 1/1 to: AV739224 from: 1 to: 525

8 GlnValAspGlyArgSerAlaArgGlyGlyCysGln..... 19
:::|||||
9 CCGGTCCAGCGCGCGCGCTTCGACAGCGCTCCGAGAGACAGACAGAG 58
CGCGCTTCGCTGCTGCAGCCATGCTCTAGT.....ATCCCTGAA 149
20 .....ThisSerAsnAspAlaAlaAlaAlaAlaAlaAla 31
|||||
59 GTACGGCTGCAGAGACAGACAGAGAGGCTTCACAGAGGCTTCACAG 108
1aserSerAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 47
|||||
109 CCGCGCTTCGCTGCTGCAGCCATGCTCTAGT.....ATCCCTGAA 149
48 LysTyrLeuPheGlnPheHisAsnLeuAsnSerAsnLeuAsp 61
|||||
150 AAGTTCACGATATTTCGCGAGTACTCACACACACATCGAT 191

seq_name: gb_est1:AV744285

seq_documentation_block:
LOCUS      AV744285      559 bp      mRNA      EST      17-OCT-2000
DEFINITION AV744285 CB Homo sapiens cDNA clone CBNAYA06 5', mRNA sequence.
ACCESSION  AV744285
VERSION     AV744285.1 GI:10861866
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 559)
  Zhang, Q., Ye, M., Wu, X., Gu, J., Huang, Q., Zhou, J., Shen, Y., Han, Z.,
  Chen, S., Mo, M. and Chen, Z.
  Homo sapiens CB library cDNA clones
  Unpublished (2000)
  Contact: Zhu Chen
  Shanghai Institute of Hematology, Rui-Jin Hospital
  197 Rui-Jin II Road, Shanghai 200025, P. R. China
  Tel: 86-21-64740490
  Fax: 86-21-64743206
  Email: mshlms.stn.sh.cn
  This clone is available at Shanghai Hematology Institute in
  Shanghai.
  Chinese National Human Genome Center at Shanghai
  351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong.
  location/Qualifiers
FEATURES             1..559
  source
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /clone_lib="CBNAYA06"
    /clone_lib="CB"
    /tissue_type="cord blood"
    /cell_type="CD34+ hematopoietic stem/progenitor cell"

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```

/lab_host="BM25.8"
/notes="Vector: pBluescript; Site 1: EcoRI. The insert is
cloned randomly with the EcoRI digestion"
BASE COUNT      136 a      143 c      167 g      109 t
ORIGIN

alignment_scores:
  Quality:      75.50      Length:      55
  Ratio:        1.887      Gaps:        1
  Percent Similarity: 72.727      Percent Identity: 32.727

alignment_block:
US-09-289-346A-3 x AV744285 ..

Align seg 1/1 to: AV744285 from: 1 to: 559

7 PheGlnValAspGlyArgSerAlaArgGlyGlyCysGlnThrSerAsnAs 23
:::|||||
45 TATCGAATTCGCGCGCGCGCTACGCTACGCTCGCAGAGACAGACAGAG 94
23 palAlaAlaAlaAlaAlaAlaAlaSerSerAlaAlaAlaAlaAla 40
|||||
95 GCGTTCACAGAGAGAGCTACACGCGCGCTTCGTCGACAGCCATGCTC 144
40 lelleArgGlyLysIleProGlyLysTyrLeuPheGlnPheHisAsnLeu 56
|||||
145 TAGTG.....ATCCCTGAAAAGTTCCAGCATATTTCGAGTACTC 185
57 AsnSerAsnLeuAsp 61
|||||
186 AACACCAACATCGAT 200

seq_name: gb_est2:BF493366

seq_documentation_block:
LOCUS      BF493366      288 bp      mRNA      EST      19-APR-2001
DEFINITION AT01702.3prime AT Drosophila melanogaster adult testes potB7
ACCESSION  BF493366
VERSION     BF493366.1 GI:11576667
KEYWORDS    EST.
SOURCE      fruit fly.
ORGANISM    Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1 (bases 1 to 288)
  Stapleton, M., Brockstein, P., Hong, L., Agbayani, A., Baxter, E., Berman
  B., Carlson, J., Champe, M., Chavez, C., Chew, M., Dorsett, V., Farfan
  D., Frise, E., George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P.,
  Liao, G., Miranda, A., Mista, S., Mungall, C. J., Nuno, J., Pacleb, J.,
  Paragas, V., Park, S., Phouanavong, S., Wan, K., Yu, C., Lewis, S. E.,
  Celinker, S. and Rubin, G. M.
  BDGP/HMT AT Drosophila EST project
  Unpublished (2000)
  Other ESTs: AT01702.5prime
  Contact: Stapleton, M.
  BDGP
  Lawrence Berkeley National Lab
  One Cyclotron Rd, Berkeley, CA 94720, USA
  Fax: 510 486 6798
  Email: http://www.fruitfly.org/EST_est@fruitfly.berkeley.edu
  hit genomic AB003586; arm:2L [121407,1518758]
  estimated-cyto:21F2-22A4; 04/07/2001
  plate: AT 17 row: A column: 2
  High quality sequence stop: 155.
  location/Qualifiers
FEATURES             1..288
  source
    /organism="Drosophila melanogaster"
    /db_xref="taxon:7227"
    /clone="AT01702"
    /clone_lib="AT Drosophila melanogaster adult testes potB7"

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```

/sex="male"
/dev stage="0-3 day old Ore-R males"
/lab host="plates Ap 10-AF.120: DH5-alpha. plates
AT.121-AT.319: DH5-alpha Tona"
/Note="Organ: ADULT testes; Vector: pOTB7; Site_1: EcoRI;
Site_2: XhoI; The mRNA for the testis library was made
from testes and seminal vesicles hand dissected from 0-3
day old Ore-R males. RNA kindly provided by the lab of
Margaret Fuller. Sized fractionated cDNAs were directly
ligated into pOTB7. Plasmid cDNA library."

BASE COUNT      62 a      65 c      63 g      98 t
ORIGIN

alignment_scores:
    Quality: 75.00      Length: 60
    Ratio: 1.744      Gaps: 1
    Percent Similarity: 71.667      Percent Identity: 33.333

alignment_block:
US-09-289-346A-3 x BF493366 ..

Align seg 1/1 to: BF493366 from: 1 to: 288.

6  GtupheglnValAspGlyArgSerAlaArgGlyGlyCysGlnThrSerAs 22
   ::::::::::::::::::::| | | | | ::::::::::::::::::::
80  AATTTAAATGATGATGAGGCGGCTGCTGTGTGTGTGTGTGTGTGTG 129
   ::::::::::::::::::::| | | | | ::::::::::::::::::::
22  nAspAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 39
   ::::::::::::::::::::| | | | | ::::::::::::::::::::
130  CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 179
   ::::::::::::::::::::| | | | | ::::::::::::::::::::
39  InileleArgGluLysIleProGluLysTyrllePheGlnPheHisAsn 55
   || | | | | | | | | | | | | | | | | | | | | | | | | |
180  CCCGGATTACGTCATCTT.....TGACTGATCTC 211

56  LeuAsnSerAsnLeuAspArgIlePheAsp 65
   || | | | | | | | | | | | | | | | | | | | | | | | | |
212  TTGGCGCCGACTGCTGATCGCGCTCTGTGAGC 241

seq_name: gb_estl:AV738283

seq_documentation_block:
LOCUS      AV738283      463 bp      mRNA      EST      17-OCT-2000
DEFINITION AV738283 CB Homo sapiens cDNA clone CBNBDE03 5', mRNA sequence.
ACCESSION  AV738283
VERSION     AV738283.1 GI:10855664
KEYWORDS   EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 463)
REFERENCE   1 (bases 1 to 463)
AUTHORS    Zhang,Q., Ye,M., Wu,X., Gu,J., Huang,Q., Zhou,J., Shen,Y., Han,Z.,
            Chen,S., Mao,M. and Chen,Z.
            Homo sapiens CB library cDNA clones
            Unpublished (2000)
            Contact: Zhu Chen
            Shanghai Institute of Hematology, Rui-Jin Hospital
            197 Rui-Jin II Road, Shanghai 200025, P. R. China
            Tel: 86-21-64740490
            Fax: 86-21-64743206
            Email: mshlms.stn.sh.cn
            This clone is available at Shanghai Hematology Institute in
            Shanghai.
            Chinese National Human Genome Center at Shanghai
            351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong.
            Location/Qualifiers
                source
                    1. 463
                        /organism="Homo sapiens"
                        /db_xref="taxon:9606"
                        /clone="CBNDE03"
                        /clone_lib="CB"

/sex="male"
/dev stage="cord blood"
/lab host="BM25.8"
/Note="Vector: pBluescript; Site_1: EcoRI; The insert is
cloned randomly with the EcoRI digestion"

BASE COUNT      120 a      111 c      141 g      88 t
ORIGIN

alignment_scores:
    Quality: 75.00      Length: 53
    Ratio: 1.875      Gaps: 2
    Percent Similarity: 75.472      Percent Identity: 33.962

alignment_block:
US-09-289-346A-3 x AV738283 ..

Align seg 1/1 to: AV738283 from: 1 to: 463

10  AspGlyArgSerAlaArgGlyGlyCysGln...ThrsAsnAspAlaAl 25
   ::::::::::| | | | | | | | | | | | | | | | | | | | |
1  AATTCGCGCGCGCGCTCGACACGCGCTGCGAGACGACGACGAGGCGCTTC 50
   ::::::::::| | | | | | | | | | | | | | | | | | | | |
25  aAlaAlaAlaAlaAlaAlaSerSerAlaAlaAlaAlaAlaAlaAla 42
   ::::::::::| | | | | | | | | | | | | | | | | | | | |
51  CACAGAGGCGCTACACGCTGCGCGCTGTGTGTGTGTGTGTGTGTGTG 99
   ::::::::::| | | | | | | | | | | | | | | | | | | | |
42  rGluLysIleProGluLysTyrllePheGlnPheHisAsnLeuAsnSer 58
   || | | | | | | | | | | | | | | | | | | | | | | | | |
100  .....ATCCCGAAGAAAGTTCCAGCATATTTTTCGAGTACTGACAGC 141
   || | | | | | | | | | | | | | | | | | | | | | | | | |
59  AsnLeuAsp 61
   || | | | | | | | | | | | | | | | | | | | | | | | | |
142  AACATTCGAT 150

seq_name: gb_estl:AV736082

seq_documentation_block:
LOCUS      AV736082      616 bp      mRNA      EST      17-OCT-2000
DEFINITION AV736082 CB Homo sapiens cDNA clone CBNABH09 5', mRNA sequence.
ACCESSION  AV736082
VERSION     AV736082.1 GI:10853663
KEYWORDS   EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 616)
REFERENCE   1 (bases 1 to 616)
AUTHORS    Zhang,Q., Ye,M., Wu,X., Gu,J., Huang,Q., Zhou,J., Shen,Y., Han,Z.,
            Chen,S., Mao,M. and Chen,Z.
            Homo sapiens CB library cDNA clones
            Unpublished (2000)
            Contact: Zhu Chen
            Shanghai Institute of Hematology, Rui-Jin Hospital
            197 Rui-Jin II Road, Shanghai 200025, P. R. China
            Tel: 86-21-64740490
            Fax: 86-21-64743206
            Email: mshlms.stn.sh.cn
            This clone is available at Shanghai Hematology Institute in
            Shanghai.
            Chinese National Human Genome Center at Shanghai
            351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong.
            Location/Qualifiers
                source
                    1. 616
                        /organism="Homo sapiens"
                        /db_xref="taxon:9606"
                        /clone="CBNABH09"
                        /clone_lib="CB"
                        /tissue_type="cord blood"
                        /cell_type="CD34+ hematopoietic stem/progenitor cell"
                        /lab_host="BM25.8"
                        /Note="Vector: pBluescript; Site_1: EcoRI; The insert is
cloned randomly with the EcoRI digestion"

```

```

'716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

BASE COUNT      60 a      98 c      90 g      70 t

ORIGIN

alignment_scores:
    quality:   73.50          length:       37
    ratio:     2.625         gaps:           1
Percent Similarity: 75.676        Percent Identity: 51.351

alignment_block:
US-09-289-346A-3 x AW753932 ..

Align seg 1/1 to: AW753932 from: 1 to: 318

5 GlytIupheGlnValAspGIyArGSerAlaArgly...GlyCysGlnTh 20
|||||:|||||::: ||::: |||||:|||| |||
96 GGACCTTTTCAGCTCATGCAGAAACTGGCGAGAAGCGGTGTAATCCAACT 145

20 rSerAnsppAlaaAlaAlaAlaAlaAlaAlaAlasrSeralAlaAlaAla 37
::: ||||||| ||||| |||||:|::: |||||
146 GCCAAGCACTGCTGCTGCTGCTGCCGCCGCCGCCAGCGCTGCTG 195

37 lalEuGlnlle 40
|||||:|:::
196 CCTTGCAACTG 206

seq_name: gb_estl:BEl155633

seq_documentation_block:
LOCUS      BEl155633             353 bp            mRNA                    EST              21-JUN-2000
DEFINITION PM2-HT0353-281299-003-h06 HT0353 Homo sapiens cDNA, mRNA sequence.
ACCESSION  BEl155633
VERSION    BEl155633.1 GI:8618354
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 353)
AUTHORS   Dias Neto,E., Garcia Correa,R., Vefjovski-Almeida,S., Briones,M.R.,
            Ngalai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,C.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
            Brunstein,A.H., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
TITLE      Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
JOURNAL    Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE    20202663
COMMENT    Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?lib=st2-PM2-HT0353-281)
            Seq primer: puc 18 forward
            High quality sequence stop: 353.
FEATURES
     source             location/Qualifiers
     1..353
     /organism="Homo sapiens"
     /db_xref="taxon:9606"
     /clone_lib="HT0353"
     /dev_stage="Adult"

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/note="Organ: head,neck; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESFES PCR (U.S. letters patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT      80 a      92 c      113 g      68 t
ORIGIN

```

[illegible]

```

alignment block:
US-09-289-346A-3 x BE155633/rev ..
Align seg 1/1 to reverse of: BE155633 From: 1 to: 353

```

20 rserasnaspialaliallialaleualalasereriallaialaa 37
 229 GCCAACCTACTGCGTGGTCGTGCTGCACGCCGCCGCCGCCAGGCTGTG 180

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37 laeuglnile 40
   |||||:::
179 CPTGCAACTG 169
seq_name: gfb_est2:BF837352

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seq_documentation_block:	
LOCUS	BF837352 360 bp mRNA EST 13-JAN-2001
DEFINITION	P42-H70353-211100-007-d09 H70353 Homo sapiens CDNA, mRNA sequence
ACCESSION	BF837352
VERSION	BF837352.1 GI:12189543
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens

REFERENCE	AUTHORS	TITLE
1 (bases 1 to 360)	Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Britones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordim, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bait, G.S., Simpson, D.R., Brumstein, A., deoliveira, P.S., Bucher, P., Jongsneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL MEDLINE	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)	
COMMENT	20202663	
	Contact: Simpson A.J.G.	

Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, São Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001

This sequence was derived from the FAPESP/ILICR Human Cancer Genome Project. This entry can be seen in the following URL (<http://www.ludwig.org.br/scripts/gechtml2.pl?rl=PM2&t2=PM2-HT0353211160-007-d09&t3=2000-11-21&t4=1>)

Seq primer: puc 18 forward

High quality sequence start: 27

High quality sequence stop: 360.

Location/Qualifiers

1..360

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_11b="HT0353"
/dev_stage="Adult"
/notes="Organ: head/neck; Vector: puc18; Site.1: SmaI;
Site.2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent Application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT. 72 a 112 c 93 g 83 t
ORIGIN

```

[illegible]

```
alignment_block:
US-09-289-346A-3 x BF837352  ..
Align seg 1/1  to: BF837352  from: 1  to: 360
```

```

5  GYGVVPEGVNVLAPSVLYAGSERIALAVGGLY...GLVYSGLINTH 20
   |||.....|.....|.....|.....|.....|.....|.....|
64  GGACGTTTCAGCTCATTGGCAAAAACGTGGCAAGGGCGCTGGATCCACT 111
   |||.....|.....|.....|.....|.....|.....|.....|
20  rserAsmAspAlaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 37
   |||.....|.....|.....|.....|.....|.....|.....|
114  GCCAAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 165
   |||.....|.....|.....|.....|.....|.....|.....|
37  IaleuGlnIle 40
   |||.....|.....|.....|.....|.....|.....|.....|
164  CCTTGCAACTG 174
   |||.....|.....|.....|.....|.....|.....|.....|

```


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OM of: US-09-289-346a-3 to: Issued_Patents_NA:* out_format : pfs

Date: Jan 3, 2002 3:37 PM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

-MODEL=trame-p2n.model -DEV=xlip
-O=/cgnl_1/USPRO.spool/US09289346/runatc_03012002_153304_16376/app_query.fasta-1.1163
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=p2n.rni
-GAPOP=12.000 -GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000
-LOOPEXT=0.000 -OGAPOP=4.500 -OGAPEXT=0.050 -XGAPOP=10.000
-XGAPEXT=0.500 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000
-YGAPEXT=0.500 -DELCP=6.000 -DELEXT=7.000 -START=1
-MATRIX=blotsum62 -TRANS=human40.coi -LIST=45 -DOCCALIG=200
-THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pfs -NORM=ext -MINLEN=0 -MAXLEN=200000000
-USER=US09289346_@cgnl_1_143 -NCPU=6 -ICPU=3 -LONGLOG -NO_XLPXY
-WAIT -THREADS=1

Search information block:

Query: US-09-289-346a-3
Query length: 70
Database: Issued_Patents_NA*
Database sequences: 351203
Database length: 113238999
Search time (sec): 264.020000

Score list:

Sequence	Strd Orig	ZScore	EScore	Len	Documentation
/cgnl_7/ptodata/1/ina/6B.COMB.seq:US-08-838-151A-59			237.00	566.83	6.4e-24
/cgnl_7/ptodata/1/ina/6B.COMB.seq:US-08-838-151A-1			218.00	527.98	9.3e-22
/cgnl_7/ptodata/1/ina/6B.COMB.seq:US-08-838-151A-3			218.00	527.91	9.4e-22
/cgnl_7/ptodata/1/ina/6B.COMB.seq:US-08-838-151A-5			218.00	527.91	9.4e-22
/cgnl_7/ptodata/1/ina/6B.COMB.seq:US-08-838-151A-7			218.00	527.91	9.4e-22
/cgnl_7/ptodata/1/ina/6B.COMB.seq:US-08-838-151A-17			218.00	518.94	3.0e-21
/cgnl_7/ptodata/1/ina/6B.COMB.seq:US-08-838-151A-48			217.00	526.44	1.1e-21
/cgnl_7/ptodata/1/ina/6B.COMB.seq:US-08-838-151A-51			217.00	526.44	1.1e-21
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/cgnl_7/ptodata/1/ina/6B.COMB.seq:US-08-793-634B-8 - 61.00 130.11 13.47 905
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seq_name: /cgnl_7/ptodata/1/ina/6B.COMB.seq:US-08-838-151A-59

seq_documentation_block:

Sequence 59, Application US/09838151A
Patent No. 6291743
GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Liu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Antikist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing GeminiVirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rocky, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 2744 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Tomato Leaf Curl GeminiVirus from Southern
INDIA
US-08-838-151A-59
alignment_scores:
Quality: 237.00 Length: 65
Ratio: 4.232 Gaps: 1
Percent Similarity: 86.154 Percent Identity: 72.308
alignment_block:
US-09-289-346a-3 x US-08-838-151A-59/rev ..
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54   H I S A S L E U A N S E R A N L E U A S P A R G I L P H E A S P L Y S T h P r o 68
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Patent No. 6291743
GENERAL INFORMATION:
APPLICANT: Scout, John T
APPLICANT: Lau, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing GeminiVirus
TITLE OF SEQUENCES: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rocky, Milanow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5460
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1162 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Tomato Mottle Gemini Virus
INDIVIDUAL ISOLATE: Florida
FEATURE:
NAME/KEY: CDS
LOCATION: 44..1127
PUBLICATION INFORMATION:
AUTHORS: Gilbertson, RL
AUTHORS: Hidayat, SH
AUTHORS: Paplomatas, EJ
AUTHORS: Rojas, MR
AUTHORS: Hou, YM
AUTHORS: Maxwell, DP
TITLE: Pseudorecombination between the infectious
TITLE: cloned DNA components of the tomato mottle and bean
TITLE: dwarf mosaic geminiviruses.
JOURNAL: Jour. General Virol.
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: VOLUME: 74
: PAGES: 23-31
: DATE: 1993
US-08-838-151A-1

Alignment_scores:
    Quality: 218.00      Length: 70
    Ratio: 3.695        Gaps: 0
    Percent Similarity: 84.286      Percent Identity: 57.143

alignment_block:
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   17 YcysGlnThrSerAsnAspAlaAlaAlaAlaAlaLeuAlaIleAsnSerA 34
   | |||:|||||:|||||:|||||: ||| ||||| |||||||:
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   34 lAlAlaAlaLeuGlnIlelleArgGluLysIleProGluLysTrpLeu 50
   :: |||||||: ||||:|||||: ||||: ||||: ||||: ||||:
471 TTCAATCTGCGCTTAGCAGTTCTTAAGGAGAAACAACCAAAATTTTGA 520
   51 PhgGlnPheIleAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
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: Patent No. 6291743
: GENERAL INFORMATION:
: APPLICANT: Scout, John T
: APPLICANT: Luu, Hang T
: APPLICANT: Maxwell, Douglas
: APPLICANT: Ahlquist, Paul
: APPLICANT: Hanson, Steve
: TITLE OF INVENTION: Transgenic Plants Expressing GeminiViruses
: NUMBER OF SEQUENCES: 63
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Dressler, Rocky, Milanow & Katz
: STREET: Two Prudential Plaza, Suite 4700
: CITY: Chicago
: STATE: Illinois
: COUNTRY: U.S.A.
: ZIP: 60601

COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/838,151A
: FILING DATE:
: CLASSIFICATION: 800
: ATTORNEY/AGENT INFORMATION:
: NAME: Mueller, Lisa V
: REGISTRATION NUMBER: 38,978
: REFERENCE/DOCKET NUMBER: SVS3801P0260
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312-616-5400
: TELEFAX: 312-616-5460

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; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1169 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Tomato Mottle Gemini Virus
; STRAIN: Florida
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 44..1127
; PUBLICATION INFORMATION:
; AUTHORS: Gilbertson, RL et al.
; TITLE: Pseudorecombination between the infectious
; TITLE: cloned DNA components of tomato mottle and bean
; TITLE: dwarf mosaic geminivirus.
; JOURNAL: Journal of General Virology
; VOLUME: 74
; PAGES: 23-31
; DATE: 1993
; US-08-838-151A-3

alignment_scores:
  Quality: 218.00      Length: 70
  Ratio: 3.695        Gaps: 0
  Percent Similarity: 84.286  Percent Identity: 57.143

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421 CCAGCAGTCTGATGATTCATATGCGAAGCGTTAAATGCAAGTTCCG 470
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51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
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521 TTACAAATCATATAACATCCGCTTAACCTTAACGTAAGATATTCCCAAAGGC 570
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; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Lau, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESS: Dressler, Rocky, Milnamow & Katz

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; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1169 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Tomato Mottle Gemini Virus
; STRAIN: Florida
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 44..1127
; US-08-838-151A-5

alignment_scores:
  Quality: 218.00      Length: 70
  Ratio: 3.695        Gaps: 0
  Percent Similarity: 84.286  Percent Identity: 57.143

alignment_block:
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17 yCysGlnThrSerAsnAspAlaAlaAlaAlaLeuAlaLeuAlaSerSer 34
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  :: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
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seq_documentation_block:
; Sequence 7, Application US/08838151A

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: Patent No. 6291743
: GENERAL INFORMATION:
: APPLICANT: Stout, John T
: APPLICANT: Luu, Hang T
: APPLICANT: Maxwell, Douglas
: APPLICANT: Ahlquist, Paul
: APPLICANT: Hanson, Steve
: TITLE OF INVENTION: Transgenic Plants Expressing Gemnivirus
: NUMBER OF SEQUENCES: 63
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Dressler, Rocky, Milnamow & Katz
: STREET: Two Prudential Plaza, Suite 4700
: CITY: Chicago
: STATE: Illinois
: COUNTRY: U.S.A.
: ZIP: 60601
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/838,151A
: FILING DATE:
: CLASSIFICATION: 800
: ATTORNEY/AGENT INFORMATION:
: NAME: Mueller, Lisa V
: REGISTRATION NUMBER: 38,978
: REFERENCE/DOCKET NUMBER: SVS3801P0260
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312-616-5400
: TELEFAX: 312-616-5460
: INFORMATION FOR SEQ ID NO: 7:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1169 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: circular
: MOLECULE TYPE: DNA (genomic)
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: ORIGINAL SOURCE:
: ORGANISM: Tomato Mottle Gemini Virus
: STRAIN: Florida
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 44..1127
: US-08-838-151A-7

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alignment_scores:
  Quality: 218.00      Length: 70
  Ratio: 3.695         Gaps: 0
  Percent Similarity: 84.286   Percent Identity: 57.143

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alignment_block:

US-09-289-346A-3 x US-08-838-151A-7

Align seg 1/1 to: US-08-838-151A-7 from: 1 to: 1169

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17  YCysGlnThrSerAsnAspAlaAlaAlaAlaAlaAlaAlaSerSerA 34
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421 CAGCGACTGCTGCTATGATTCATATCGCAAGCGTTAAATGCAAGTTCG 470
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34  laAlaAlaAlaLeuGlnIleIleArgGlyLysIleProGluLysTyrLeu 50
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51  PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
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seq_name: /cgnl_7/ptodata/1/lna/6B_COMB.seq:US-08-838-151A-17

seq_documentation_block:

: Sequence 17, Application US/08838151A

: Patent No. 6291743

: GENERAL INFORMATION:

: APPLICANT: Stout, John T

: APPLICANT: Luu, Hang T

: APPLICANT: Maxwell, Douglas

: APPLICANT: Ahlquist, Paul

: APPLICANT: Hanson, Steve

: TITLE OF INVENTION: Transgenic Plants Expressing Gemnivirus

: NUMBER OF SEQUENCES: 63

: CORRESPONDENCE ADDRESS:

: ADDRESSEE: Dressler, Rocky, Milnamow & Katz

: STREET: Two Prudential Plaza, Suite 4700

: CITY: Chicago

: STATE: Illinois

: COUNTRY: U.S.A.

: ZIP: 60601

: COMPUTER READABLE FORM:

: MEDIUM TYPE: Floppy disk

: COMPUTER: IBM PC compatible

: OPERATING SYSTEM: PC-DOS/MS-DOS

: SOFTWARE: Patent Release #1.0, Version #1.30

: CURRENT APPLICATION DATA:

: APPLICATION NUMBER: US/08/838,151A

: FILING DATE:

: CLASSIFICATION: 800

: ATTORNEY/AGENT INFORMATION:

: NAME: Mueller, Lisa V

: REGISTRATION NUMBER: 38,978

: REFERENCE/DOCKET NUMBER: SVS3801P0260

: TELECOMMUNICATION INFORMATION:

: TELEPHONE: 312-616-5400

: TELEFAX: 312-616-5460

: INFORMATION FOR SEQ ID NO: 17:

: SEQUENCE CHARACTERISTICS:

: LENGTH: 2602 base pairs

: TYPE: nucleic acid

: STRANDEDNESS: single

: TOPOLOGY: circular

: MOLECULE TYPE: DNA (genomic)

: HYPOTHETICAL: NO

: ORIGINAL SOURCE:

: ORGANISM: Tomato Mottle Gemnivirus

: STRAIN: Florida

: US-08-838-151A-17

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alignment_scores:
  Quality: 218.00      Length: 70
  Ratio: 3.695         Gaps: 0
  Percent Similarity: 84.286   Percent Identity: 57.143

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alignment_block:

US-09-289-346A-3 x US-08-838-151A-17/rev

Align seg 1/1 to reverse of: US-08-838-151A-17 from: 1 to: 2602

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1  ThrleuValTrpGlyGluPheGlnValAspGlyArgSerAlaArgGlyG1 17
   |||:| | | | | | | | | | | | | | | | | | | | | | |
2282 ACAATGAAATGGAGATTTCCAGATCGACGCGGATCTGCCAGAGAGG 2233

```

```

17 yCysGlnThrSerAsnAspAlaAlaAlaAlaLeuAlaAlaSerSerA 34
   |||:|||||:|||||: ||| ||||| |||||:
2232 CGAGCAGCTGCTGCTATGATCATATGCGAAAGCGTTAAATGCAAGTTCCG 2183
34 lAlaAlaAlaLeuGlnIleIleIleArgLysIleProGlnLysTyrLeu 50
   : : |||||: |||||: |||||: |||||:
2182 TTCAATCTGCTTACGATTCCTTAAGGAAAGAACACCAAAAGATTGTGTA 2133
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
   : |||: |||||: |||||: |||||: |||||: |||||: |||||:
2132 TTACAAATCTATACATCCGCTTAACTAAGAACGAAATATTGCAAAAGCG 2083
67 rProGlnPro 70
   : |||||:
2082 TCCGGAACCG 2073

seq_name: /cgnl_7/pdata/1/ina/6B_COMB.seq:US-08-838-151A-48

seq_documentation_block:
; Sequence 48, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Gemlinivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1062 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bean Golden Mosaic Gemlinivirus
; STRAIN: Type II
; INDIVIDUAL ISOLATE: Guatemala
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1059
; US-08-838-151A-48

alignment_scores:

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Quality: 217.00      Length: 70
Ratio: 3.741        Gaps: 0
Percent Similarity: 82.857      Percent Identity: 58.571

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alignment_block:

US-09-289-346a-3 x US-08-838-151A-48

Align seq 1/1 to: US-08-838-151A-48 from: 1 to: 1062

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1 ThrLeuValTrpGlyGluPheGlnValAspGlyArgSerAlaArgGlyL 17
   |||: |||||: |||||: |||||: |||||: |||||: |||||: |||||:
328 ACATCGAATGGGACATTCACAGTCGACGCGCATCTCTGCAAGAGAGG 377
17 yCysGlnThrSerAsnAspAlaAlaAlaAlaLeuAlaAlaSerSerA 34
   |||:|||||:|||||: ||| ||||| |||||:
378 TCAGCAGCTGCGCCACGACTCATATGCAAGGCAATTAAACGCAATTCA 427
34 lAlaAlaAlaLeuGlnIleIleIleArgLysIleProGlnLysTyrLeu 50
   : |||: |||||: |||||: |||||: |||||: |||||: |||||:
428 TTGAATCTGCTTACGATTCCTTAAGGAAAGCGTTAAATGCAAGTTACGTC 477
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
   : |||: |||||: |||||: |||||: |||||: |||||: |||||:
478 CTTCACATCATCAACAATCCGCTTAAATCTGCAAGCGATCTTCGTCAAAGT 527
67 rProGlnPro 70
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528 GCCGGAACCA 537

seq_name: /cgnl_7/pdata/1/ina/6B_COMB.seq:US-08-838-151A-51

seq_documentation_block:
; Sequence 51, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Gemlinivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1062 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)

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1 NAME: Mueller, Lisa V
2 REGISTRATION NUMBER: 38,978
3 REFERENCE/DOCKET NUMBER: SVS801P0260
4 TELECOMMUNICATION INFORMATION:
5 TELEPHONE: 312-616-5400
6 TELEFAX: 312-616-5460
7 INFORMATION FOR SEQ ID NO: 54:
8 SEQUENCE CHARACTERISTICS:
9 LENGTH: 1062 base pairs
10 TYPE: nucleic acid
11 STRANDEDNESS: single
12 TOPOLOGY: circular
13 MOLECULE TYPE: DNA (genomic)
14 HYPOTHEICAL: NO
15 ANTI-SENSE: NO
16 ORIGINAL SOURCE:
17 ORGANISM: Bean Golden Mosaic Geminiivirus
18 STRAIN: Type II
19 INDIVIDUAL ISOLATE: Guatemala
20 FEATURE:
21 NAME/KEY: CDS
22 LOCATION: 1..1059
23 US-08-838-151A-54
24
25 alignment_scores:
26     Quality: 217.00      Length: 70
27     Ratio: 3.741        Gaps: 0
28     Percent Similarity: 82.857      Percent Identity: 58.571
29
30 alignment_block:
31 US-05-289-346A-3 x US-08-838-151A-54 ..
32
33 Align seg 1/1 to: US-08-838-151A-54 from: 1 to: 1062
34
35 1 ThrleuValtrpGlyGluPheGlnValAspGlyArgSerAlaArgGlyG1 17
36   |||::: |||:::|||||:::|||||:::|||||:::|||||:::|||||
37 328 ACAGTACAGTATGGGACAAATTCACAGTCCAGCGCAGATCTGCAAGGAGG 377
38   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
39 17 ycySgIntHrSerAsnAspAlaAlaAlaAlaAlaAlaAlaAlaSerSera 34
40   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
41 378 TCAGCAGTCTGCGCAAGCAGCTCATATGCAAGGCAATTAAAGCAGATTCAA 427
42   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
43 34 laAlaAlaAlaLeuGlnIleIleArgGlyLysIleProGluLysIleu 50
44   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
45 428 TTGAACCTCGCTTGACAAATATTGTAAGGAGAACAACGAAAGATTACGTC 477
46   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
47 51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysH 67
48   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
49 478 CTTCACATCATCAACATCCGTTCTTAATCTCGAAGCGATCTTCGTCAAAAT 527
50   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
51 67 rProGluPro 70
52   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
53 528 GCCGGAACCA 537
54   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
55
56 seq_name: /cgnl_7/ptodata/1/lna/6B_COMB.seq:US-08-838-151A-43
57
58 seq_documentation_block:
59   Sequence 43, Application US/08638151A
60   Patent No. 6291743
61   GENERAL INFORMATION:
62     APPLICANT: Stout, John T
63     APPLICANT: Lou, Hang Y
64     APPLICANT: Maxwell, Douglas
65     APPLICANT: Ahlquist, Paul
66     APPLICANT: Hanson, Steve
67     TITLE OF INVENTION: Transgenic Plants Expressing Geminiivirus
68     TITLE OF INVENTION: Genes
69     NUMBER OF SEQUENCES: 3
70     CORRESPONDENCE ADDRESSES:
71     ADDRESSEE: Dressler, Rocky, Milnamow & Katz
72     STREET: Two Prudential Plaza, Suite 4700
73     CITY: Chicago

```

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STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838.151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 1183 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bean Golden Mosaic Geminivirus
STRAIN: Type II Isolates
INDIVIDUAL ISOLATE: Guatemala
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1059
PUBLICATION INFORMATION:
AUTHORS: Faria, JC
AUTHORS: Gilbertson, RL
AUTHORS: Hanson, SF
AUTHORS: Morales, FJ
AUTHORS: Ahlquist, P
AUTHORS: Ioniello, AO
AUTHORS: Maxwell, D
TITLE: Bean Golden Mosaic Geminivirus Type II
TITLE: Isolates from the Dominican Republic and
TITLE: Guatemala: Nucleotide Sequences, Infectious
JOURNAL: Pseudorecombinants, and Phylogenetic Relationships
VOLUME: 84
ISSUE: 3
PAGES: 321-329
DATE: 1994
US-08-838-151A-43

alignment_scores:
Quality: 217.00 Length: 70
Ratio: 3.741 Gaps: 0
Percent Similarity: 82.857 Percent Identity: 58.571

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328 ACAATCGAATGGGACAAATTCGACGCGCATCTGCAAGAGG 377
17 yCySglnThSerAsnAspAlaAlaAlaAlaAlaAlaSerSera 34
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
378 TCACGACTGCGCACGACATCATGCAAGGCAATTAACCGACATCTCAA 427

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34 laAlaAlaAlaLeuGlnIleIleArgGlnIuysIleProGlnIuysTyrIeu 50
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
428 TTGAATCTGCTTGACAAATATGAAAGACAGAACCGAAAGATTAGTC 477
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspIuysrh 67
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
478 CTTCAACATCATCAGACATCCGTTTCAATCTGCAAGCGATCTTCGTCAGAGT 527
67 rProGlnPro 70
||||| |||||
528 GCCGGAACCA 537

seq_name: /cgnl_7/ptodata/1/ina/6B_COMB.seq:US-08-838-151A-45
seq_documentation_block:
Sequence 45, Application US/08838151A
Patent No. 6291743
GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rocky, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838.151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 1183 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bean Golden Mosaic Geminivirus
STRAIN: Type II
INDIVIDUAL ISOLATE: Guatemala
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1059
US-08-838-151A-45

alignment_scores:
Quality: 217.00 Length: 70
Ratio: 3.741 Gaps: 0
Percent Similarity: 82.857 Percent Identity: 58.571

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alignment_block:

US-09-289-346A-3 x US-08-838-151A-45 ..

Align seg 1/1 to: US-08-838-151A-45 from: 1 to: 1183

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328 ACATCGAATGGGACAAATTCGAAGTCGACGCGAGATCTGCAAGAGGAGG 377
17 yCysGlnThrSerAsnAspAlaAlaAlaAlaLeuAlaAlaSerSera 34
   |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:|
378 TCACGAGCTGTCGCAACGCTCATATGCAAGGCAATTAAACGCAAGATTCAA 427
34 laAlaAlaAlaLeuGlnIleIleArgGluIysIleProGluIlySTyrlou 50
   |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:|
428 TTGAATCTGCTTGACATATTGAAGAGAGAACACCAAGATTACGTC 477
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
   |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:|
478 CTTCACATCTCACACATCCGTTTAATCTCGACGAGATCTTCGTCAAAGT 527
67 rProGluPro 70
   |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:|
528 GCCGGAACCA 537
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seq_name: /cgnl_7/pdata/1/lna/6A_COMB.seq:US-09-065-999-5

seq_documentation_block:

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; Sequence 5, Application US/09065999
; Patent No. 6118048
; GENERAL INFORMATION:
; APPLICANT: Hanson, Stephen F.
; TITLE OF INVENTION: TRANS-DOMINANT INHIBITION OF GEMINIVIRAL
; TITLE OF INVENTION: DNA REPLICATION BY GEMINIVIRUS REP GENE MUTANTS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: Quarles & Brady
; STREET: One South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/065,999
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27,386
; REFERENCE/DOCKET NUMBER: 960296,94754
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-251-5000
; TELEFAX: 608-251-9166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1651 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-065-999-5
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alignment_scores:

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Quality: 217.00 Length: 70
Ratio: 3.741 Gaps: 0
Percent Similarity: 82.857 Percent Identity: 58.571
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alignment_block:

US-09-289-346A-3 x US-09-065-999-5 ..

Align seg 1/1 to: US-09-065-999-5 from: 1 to: 1651

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796 ACATCGAATGGGACAAATTCGAAGTCGACGCGAGATCTGCAAGAGGAGG 845
17 yCysGlnThrSerAsnAspAlaAlaAlaAlaLeuAlaAlaSerSera 34
   |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:|
846 TCACGAGCTGTCGCAACGCTCATATGCAAGGCAATTAAACGCAAGATTCAA 895
34 laAlaAlaAlaLeuGlnIleIleArgGluIysIleProGluIlySTyrlou 50
   |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:|
896 TTGAATCTGCTTGACATATTGAAGAGAGAACACCAAGATTACGTC 945
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
   |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:|
946 CTTCACATCTCACACATCCGTTTAATCTCGACGAGATCTTCGTCAAAGT 995
67 rProGluPro 70
   |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:|
996 GCCGGAACCA 1005
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seq_name: /cgnl_7/pdata/1/lna/6A_COMB.seq:US-09-065-999-6

seq_documentation_block:

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; Sequence 6, Application US/09065999
; Patent No. 6118048
; GENERAL INFORMATION:
; APPLICANT: Hanson, Stephen F.
; TITLE OF INVENTION: TRANS-DOMINANT INHIBITION OF GEMINIVIRAL
; TITLE OF INVENTION: DNA REPLICATION BY GEMINIVIRUS REP GENE MUTANTS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: Quarles & Brady
; STREET: One South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/065,999
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27,386
; REFERENCE/DOCKET NUMBER: 960296,94754
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-251-5000
; TELEFAX: 608-251-9166
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1651 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-065-999-6
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alignment_scores:

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Quality: 217.00 Length: 70
Ratio: 3.741 Gaps: 0
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Percent Similarity: 82.857 Percent Identity: 58.571

alignment_block:
US-09-289-346a-3 x US-09-065-999-6 ..

Align seg 1/1 to: US-09-065-999-6 from: 1 to: 1651

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1 ThrleuValTrpGlyGluPheGlnValAspGlyArgSerAlaArgGly1 17
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17 yCysGlnThrSerAsnAspAlaAlaAlaAlaLeuAlaAlaSerSera 34
| ||||| ||||| ||||| ||||| ||||| |||||
846 TCAGCAGCTGCCACGACATCATGCAAGCGCATTTAAACGCAATTCGA 895
34 laAlaAlaAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeu 50
||||| ||||| ||||| ||||| ||||| |||||
896 TTGAATCTGCCCTTGACATATTGAGAGAACACACGCAAAAGATTACGTC 945
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
||||| ||||||| ||||||| ||||||| ||||||| |||||||
946 CTTCACATCACAACATCCGTTCTAATCTCGAACGCAATCTTCGCAAGT 995
67 rProGluPro 70
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996 GCCGGAACCA 1005
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seq_name: /cgnl_7/ptodata/1/lna/6A.COMB.seq:US-09-065-999-8

seq_documentation_block:

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; Sequence 8, Application US/09065999
; Patent No. 6118048
; GENERAL INFORMATION:
; APPLICANT: Hanson, Stephen F.
; APPLICANT: Maxwell, Douglas P.
; TITLE OF INVENTION: TRANS-DOMINANT INHIBITION OF GEMINIVIRAL
; TITLE OF INVENTION: DNA REPLICATION BY GEMINIVIRUS REP GENE MUTANTS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: One South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/065,999
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27,386
; REFERENCE/DOCKET NUMBER: 960296, 94754
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-251-5000
; TELEFAX: 608-251-9166
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1894 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-065-999-8
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alignment_scores:
Quality: 217.00 Length: 70

Ratio: 3.741 Gaps: 0
Percent Similarity: 82.857 Percent Identity: 58.571

alignment_block:
US-09-289-346a-3 x US-09-065-999-8 ..

Align seg 1/1 to: US-09-065-999-8 from: 1 to: 1894

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1 ThrleuValTrpGlyGluPheGlnValAspGlyArgSerAlaArgGly1 17
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796 ACATCGAATGGGGACATTCGCAAGTCGACGGCAGATCTCGAAGAGAGG 845
17 yCysGlnThrSerAsnAspAlaAlaAlaAlaLeuAlaAlaSerSera 34
| ||||| ||||| ||||| ||||| ||||| |||||
846 TCAGCAGCTGCCACGACATCATGCAAGCGCATTTAAACGCAATTCGA 895
34 laAlaAlaAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeu 50
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896 TTGAATCTGCCCTTGACATATTGAGAGAACACACGCAAAAGATTACGTC 945
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
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seq_name: /cgnl_7/ptodata/1/lna/6A.COMB.seq:US-09-065-999-7

seq_documentation_block:

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; Sequence 7, Application US/09065999
; Patent No. 6118048
; GENERAL INFORMATION:
; APPLICANT: Hanson, Stephen F.
; APPLICANT: Maxwell, Douglas P.
; TITLE OF INVENTION: TRANS-DOMINANT INHIBITION OF GEMINIVIRAL
; TITLE OF INVENTION: DNA REPLICATION BY GEMINIVIRUS REP GENE MUTANTS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: One South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/065,999
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27,386
; REFERENCE/DOCKET NUMBER: 960296, 94754
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-251-5000
; TELEFAX: 608-251-9166
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2072 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-065-999-7
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alignment_scores:


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seq_name: gb_vl:AY029750

seq_documentation block: 2588 bp DNA circular VRL 08-MAY-2001
LOCUS AY029750
DEFINITION Tomato severe rugose virus DNA-A, complete sequence.
ACCESSION AY029750
VERSION AY029750.1 GI:14009278
KEYWORDS
SOURCE
ORGANISM
Tomato severe rugose virus.
Tomato severe rugose virus.
VIRUSES: ssDNA viruses; Geminiviridae; Begomovirus.
REFERENCE
1 (bases 1 to 2588)
Rezende,W.L., Goulart,L.R., Parreira,K.S. and Figueiredo,J.E.F.
The full-length DNA-A nucleotide sequence of a novel
tomato-infecting begomovirus, Tomato severe rugose virus, in Brazil
JOURNAL
Unpublished
2 (bases 1 to 2588)
Rezende,W.L., Goulart,L.R., Parreira,K.S. and Figueiredo,J.E.F.
Direct Submision
TITLE
Submitted (03-APR-2001) Instituto de Genetica e Bioquimica,
Universidade Federal de Uberlandia, Av. Amazonas s/p, Bloco 2E,
Sala 24, Campus Umuarama, Uberlandia, Minas Gerais 38.400-000,
Brazil
FEATURES
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Location/Qualifiers
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/db_xref="taxon:158463"
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EQFHNLNSLDRIFARAPDPMAPTPELSSFTVPMEDQWADYFGCAARPERPISI
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/protein_id="AAK50359.1"
/db_xref="GI:14009281"
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BASE COUNT 660 a 525 c 598 g 805 t
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align_scores:
Ratio: 297.00 Length: 70
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Percent Identity: 78.571
alignment_block:
US-09-289-346a-4 x AY029750/rev ..
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2258 ACTATCGAATGAGGCGCAATTCGACGCGGCAAGTCTAGACGCGG 2209
|||||
17 YcysGlnThrSerAsnAspAlaAlaIleGluAlaLeuAsnAlaSerL 34
|||||
2208 TTGCGACAGACGCTAAGATGCTGCCGAGACCTTGACACCTTCCA 2159
|||||
34 ysglgluaAlaLeuGlnlleleAlaAlaIleProGluLysTyrLeu 50
|||||
2158 AAGAGAGCGCGCTGCACATATTCGGGAGAAAGTACCGGAAAAATTTTTA 2109
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51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTyr 67
|||||
2108 TTTCAGTTCCACATCTAAATAGCAATTTAGATAGCATATTGATTAAGAC 2059
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67 rProGluPro 70
|||||
2058 TCCTGAACCA 2049
seq_name: gb_vl:AF291705

seq_documentation block: 2622 bp DNA circular VRL 25-SEP-2000
LOCUS AF291705
DEFINITION Tomato rugose mosaic virus DNA-A, complete sequence.
ACCESSION AF291705
VERSION AF291705.1 GI:10281644

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KEYWORDS Tomato rugose mosaic virus.

SOURCE

ORGANISM Tomato rugose mosaic virus.

REFERENCE 1 (bases 1 to 2622)

AUTHORS Fernandes,J.J., Fontes,E.P.B., Brommonschenkel,S.H., Carvalho,M.G., Zambolim,E.M. and Zerbini,F.M.

TITLE Molecular Cloning and Characterization of Tomato rugose mosaic virus (TRMV), a Begomovirus isolated from Tomatoes at Triangulo Mineiro, Minas Gerais, Brazil

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 2622)

AUTHORS Fernandes,J.J. and Zerbini,F.M.

TITLE Direct Submission

JOURNAL Submitted (31-JUL-2000) Dept. de Fitopatologia, Universidade Federal de Vicosa, Av. P.H. Rolfs, s/n - Centro, Vicosa, MG 36571-000, Brazil

FEATURES

source Location/Qualifiers

1. 2622

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/db_xref="taxon:134599"

/country="Brazil: Uberlandia, Triangulo Mineiro, Mlans Gerais"

/note="previously referred to as Tomato geminivirus Uberlandia TRMV"

1. 227

/note="common region"

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/complement(240..992)

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342..1097

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/note="Rep"

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/db_xref="GI:10281648"

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/note="TtrAP"

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/note="Rep"

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/db_xref="GI:10281646"

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BASE COUNT 684 a 562 c 600 g 776 t

ORIGIN

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Quality: 295.00 Length: 70

Ratio: 4.683 Gaps: 0

Percent Similarity: 90.000 Percent Identity: 78.571

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US-09-289-346A-4 x AF291705/rev ..

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17 YCYGSLTThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerL 34

||||: |||||||

2248 TTGCGACACAGCTACGACGCTGCCGACGAAGCTTAAACGACACTTCCA 2199

34 YsglGluAlaLeuGlnIleleAlaAlaIleProGluLysTyrLeu 50

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2198 AAGACATCGCCTTCGACAGATATCCGGGAGAAAGCGGAAAGTCTCTA 2149

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2148 TTTCAGTTTTCACATCTTAATAGTAATTAGATATTTCGCAAGGC 2099

67 rProGluPro 70

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2098 TCCGGAGCCA 2089

seq_name: gb_vl:LM092532

seq_documentation_block: 1193 bp DNA VRL 01-APR-1997

LOCUS LM092532

DEFINITION Leonurus mosaic virus Rep protein (rep) and coat protein (cp)

genes, partial cds.

ACCESSION 092532

VERSION 092532.1 GI:1916344

KEYWORDS

SOURCE Leonurus mosaic virus.

ORGANISM Leonurus mosaic virus.

REFERENCE 1 (bases 1 to 1193)

AUTHORS Faria,J.C. and Maxwell,D.P.

TITLE Variability in geminivirus associated with Phaseolus vulgaris in Brazil


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37 lalenGlnlleleAlaAlaAlaIleProGluTylTyrLeuPheGlnPhe 53
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2205 CCATGCAAAATATCAAGAGAACTACCGGAAAGTTCTCTTCCATAT 2156
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2155 CACATATTATCCAGTAACCTGGATAGATATTCACAAAGCTCCGAGATCC 2106
70 o 70
2105 G 2105

seq_name: gb_v1:AF188708
seq_documentation_block: 1365 bp DNA VRL 07-NOV-1999
LOCUS AF188708
DEFINITION Cowpea golden mosaic geminivirus replication associated protein
(rep) and coat protein (cp) genes, partial cds.
ACCESSION AF188708
VERSION AF188708.1 GI:6273115
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
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/strain="CGMV-BR"
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BASE COUNT 339 a 259 c 332 g 435 t
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alignment_scores:
Quality: 277.00 Length: 67

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Ratio: 4.617 Gaps: 0
Percent Similarity: 89.552 Percent Identity: 77.612
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340 TGGGTCATTTTCAATCGACGAGATCTGCTAGACAGAGCTACAGAC 291
20 rSerAsnAspAlaAlaAlaGluAlaLeuAsnAlaSerLysGluGluA 37
|||||
290 AATTAATGATGACAGCATCGGAGCGCTTAATCCCTTCTTCAAGAGCAAG 241
37 lalenGlnlleleAlaAlaAlaIleProGluTylTyrLeuPheGlnPhe 53
|||||
240 CCATGCAAAATATCAAGAGAACTACCGGAGAGTTCTCTTCCAGTAT 191
54 HisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysThrProGluPr 70
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190 CACATATTATCCAGTAACCTGGATAGATATTCACAAAGCTCCGAGACC 141
70 o 70
140 A 140

seq_name: gb_v1:AF288227
seq_documentation_block: 1383 bp DNA VRL 20-AUG-2000
LOCUS AF288227
DEFINITION Sweet potato leaf curl virus replication association protein (Ac1)
and AC4 (Ac4) genes, complete cds.
ACCESSION AF288227
VERSION AF288227.1 GI:9658125
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
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US-09-289-346A-4 x AF288227/rev ..

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17 yCysGlnThrSerAsnAspAlaAlaAlaGluAlaLeuAsnAlaSerSerL 34
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852 CCAGCAGAGCTGCTACGACGACGCGCAGAGCTCTAAACGAGGTCTTA 803
34 yGluGluAlaLeuGlnIleIleAlaAlaAlaIleProGluIlySTyrlau 50
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802 AGAAACCTGCGTGCAGAAATATCAGGAGAAACTCCCTGAAATATTTA 753
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspIylStH 67
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752 TTTCATTTTCATATTAATTAGTTAGTAATTTAGATGAGATTTTTCCTC 703
67 rPro 68
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702 ACCT 699

seq_name: gb_vl:AF104036

seq_documentation_block:
LOCUS      AF104036      2828 bp      DNA      circular      VRL      05-AUG-1999
DEFINITION      Sweet potato leaf curl virus DNA A, complete sequence.
ACCESSION      AF104036
VERSION      AF104036.1      GI:5702158
KEYWORDS
SOURCE
ORGANISM
Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
1 (bases 1 to 2828)
Lotrakul,P., Valverde,R.A., Clark,C.A., Sim,J. and De La Torre,R.
Detection of a geminivirus infecting sweet potato in the United
States
Plant Dis. 82, 1253-1257 (1998)
2 (bases 1 to 2828)
Lotrakul,P. and Valverde,R.A.
Cloning of a DNA-A-like genomic component of sweet potato leaf curl
virus : nucleotide sequence and phylogenetic relationships
Molecular Plant Pathology On-line (1999)
http://www.bspp.org.uk/mpol/1999/0422lotrakul/
3 (bases 1 to 2828)
Lotrakul,P. and Valverde,R.A.
Direct Submission
Submitted (02-NOV-1998) Plant Pathology and Crop Physiology,
Louisiana State University, 302 Life Sciences Bldg., LSU, Baton
Rouge, LA 70803, USA
FEATURES
source      1..2828

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/db_xref="taxon:100755"
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/protein_id="AAD47172.1"
/db_xref="GI:5702162"
/translation="MSNPLSGYKRKCPIDQELHTLTAKKAKKRVBPQRTIRYKGGCGS
AFITTCYOHGFTHRGINKSCSDRESSIRHQPHVCGSDCTVPQSNVNCPRERHTEN
HPQIPAEGLGCKEATGIPDLPPIPDLDPSNMWCYSQLDWYFGTP"
complement(1587..2681)
/gene="AC1"
complement(1587..2681)
/gene="AC1"
/note="AL1; REP gene"
/codon_start=1
/product="replication initiation protein AC1"
/protein_id="AAD47173.1"
/db_xref="GI:5702163"
/translation="WAPKRRRIQAKNYFTYPRCSLSKEDCLAQLNIQTPSNKKYI
HYARLHEDGEPHLVAVQFEGKFCVTSRFDLSPNRSNHFHPIQGAKSSDYKS
VYDKDQDTTWGEFQVGRSARGGQCTANDAAEALINSGSKAALOITREKPEKYL
QPHNLVSNLDRIETSPSPVSSPSSSFNAPDILSDMAENWDSARAPRPSIV
IEGSRICKTYWARSLSGPHNTLCGHLSDSPKYSNSANTYNTDDVNPOTLKKRFEMG
AOKDQSNCKYKGVPRIRGGIPLTFLCNPGESSFKLMDKREGGALKMWAANAIFC
DVQSPFWQEEVSHGATAHREGDEOESS"
complement(2267..2524)
/gene="AC4"
complement(2267..2524)

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/gene="AC4"
/feature="AC1"
/codon_start=1
/product="AC4"
/protein_id="AAD47174.1"
/db_xref="GI:5702164"
/translation="MGNLTSMCMWSSKSSANSSAQIADSSIMSHRTDRIETPTPSRELNP
AFMSSPTSIKRTGIPSPGVNRSSTADILEASRLTLTQPLR"
BASE COUNT      741 a      606 c      675 g      806 t
ORIGIN

alignment_scores:
  Quality: 274.00      Length: 68
  Ratio: 4.567      Gaps: 0
Percent Similarity: 88.235      Percent Identity: 79.412

alignment_block:
US-09-289-346A-4 x AF104036/rev ..

Align seg 1/1 to reverse of: AF104036 from: 1 to: 2828

1   ThrleuValTrpGlyGluPheGlnValAspGlyArgSerAlaArgGlyG1 17
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
2354  ACCATCAGCTGGGGTGAATTCAGGCGAGGCTGTAAACGACGATCTTA 2305
    17  YCYSGlnThSerAsnSPAlaAlaGluAlaLeuAsnAlaSerSerL 34
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
2304  CCAGCACTGCTACGACGCGAGCGAGGCTGTAAACGACGATCTTA 2255
    34  YSGlGluAlaLeuGlnIleleAlaAlaAlaIleProGluLysTyrLeu 50
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
2254  AAGAGCGTGGCTTCAATATATATCAGGGAACATCCCTGAAATAATTTA 2205
    51  PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
2204  TTTCAATTTTCAATATTAGTTAGTAATTAGATTTTCTCTCTCC 2155
    67  rPro 68
    |||
2154  ACCT 2151

seq_name: gb_vi:SGU67926

seq_documentation_block: 554 bp      DNA      VRL      28-JAN-1998
LOCUS      SGU67926
DEFINITION Sida golden mosaic geminivirus Rep protein (AC1) gene, partial cds.
ACCESSION  U67926
VERSION     U67926.1 GI:1546801
KEYWORDS
SOURCE
ORGANISM   .
            sida golden mosaic virus.
            sida golden mosaic virus.
REFERENCE  1 (bases 1 to 554)
            Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
AUTHORS   Roye,M.E., McLaughlin,W.A., Nakhla,N.K. and Maxwell,D.P.
TITLE     Genetic diversity among geminiviruses associated with the weed
          species Sida spp. Macroptilium lathyroides, and Missadula
          amplissima from Jamaica
          Plant Dis. 81, 1251-1258 (1997)
JOURNAL   2 (bases 1 to 554)
          Direct Submission
          Submitted (23-AUG-1996) Plant Pathology, University of Wisconsin,
          1630 Linden Drive, Madison, WI 53706-1596, USA
FEATURES
          1..554
          Location/Qualifiers
            1..554
            /organism="sida golden mosaic virus"
            /strain="Jamaica"
            /isolate="Jamaica, May 1993"
            /db_xref="taxon:51034"
            /note="DNA A component"
            complement(1..554)
            /gene="AC1"
          gene

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complement(1..554)
/gene="AC1"
/feature="replication-associated protein"
/codon_start=1
/product="Rep protein"
/protein_id="AA097865.1"
/db_xref="GI:1546802"
/translation="STSKREALSLOTLKTPVKKFKIKTRELHNGEPHLLVLIQFE
GKYNCTNNRFPFLVSPTRSVHHPNIOGAKSSDVKSYERKGDITEMKVFQIDGRSA
RGQOOTANDAAALNSGTKEKDALKIRKLEPERLUFQYHNLSNIDRLFSKPEPWS
HPFPLPSFTVAVPGQWQEMWADGYFGR"
BASE COUNT      121 a      127 c      139 g      167 t
ORIGIN

alignment_scores:
  Quality: 271.00      Length: 70
  Ratio: 4.302      Gaps: 0
Percent Similarity: 90.000      Percent Identity: 70.000

alignment_block:
US-09-289-346A-4 x SGU67926/rev ..

Align seg 1/1 to reverse of: SGU67926 from: 1 to: 554

1   ThrleuValTrpGlyGluPheGlnValAspGlyArgSerAlaArgGlyG1 17
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
290  ACCATCAGATGGGGGTGTTTCCAGATGACGAGGAAGATGCTCTGGAGG 241
    17  YCYSGlnThSerAsnSPAlaAlaGluAlaLeuAsnAlaSerSerL 34
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
240  TCAGCAACAGCTTACGACGCGCGAGGATGATTCGTGGAACA 191
    34  YSGlGluAlaLeuGlnIleleAlaAlaAlaIleProGluLysTyrLeu 50
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
190  AGGAGGATGCACTGAATATCATCATCAGAGAGAGATTCACAGAAAGATATCTC 141
    51  PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
140  TTTCAATTTTCAACACTATCCAGTAATATGATAGATTTTCACTAAGCC 91
    67  rProGluPro 70
    |||
90  TCAGAAACCG 81

seq_name: gb_vi:YIE132548

seq_documentation_block: 2763 bp      DNA      circular VRL      01-FEB-1999
LOCUS      YIE132548
DEFINITION Ipomoea yellow vein virus V2, V1, C3 and C2 genes.
ACCESSION  AJ132548
VERSION     AJ132548.1 GI:4210720
KEYWORDS   C2 gene; C2 protein; C3 gene; C3 protein; coat protein; V1 gene; V2
            gene; V2 protein.
SOURCE
ORGANISM   Ipomoea yellow vein virus.
            Ipomoea yellow vein virus.
            Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
REFERENCE  1 (bases 1 to 2763)
            Banks,G.K.
AUTHORS   Banks,G.K.
TITLE     Direct Submission
            Submitted (26-JAN-1999) Banks G.K., Virus Research, John Innes
            Centre, Norwich Research Park, Colney Lane, Norwich, NR4 6JL, UK
JOURNAL   2 (bases 1 to 2763)
          Banks,G.K., Bedford,I.D., Beilts,F.J., Cerezo,E.R. and Markham,P.G.
          A novel geminivirus of Ipomoea indica (Convolvulaceae) from southern
          Spain
FEATURES
          Unpublished
          Location/Qualifiers
            1..2763
            /organism="Ipomoea yellow vein virus"
            /viralon
            /specific_host="Ipomoea indica"
            /db_xref="taxon:87832"

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gene      995..1390
CDS       /gene="V2"
          995..1390
          /gene="V2"
          /codon_start=1
          /product="V2 protein"
          /protein_id="CA10695.1"
          /db_xref="GI:4210721"
          /translation="MTLLYKDSDCRANCPSTAEKMDPLQNPLOTLYGFRCLSVKY
          LOGILKTEPGTGLFELCSGLRFRVROYDRANSFLETSLMGSETGTETSELRDSY
          RALHWCCPCNCCPKLCPGFKRPDEKEG"
gene      1215..1979
CDS       /gene="V1"
          1215..1979
          /gene="V1"
          /codon_start=1
          /product="coat protein"
          /protein_id="CA10696.1"
          /db_xref="GI:4210722"
          /translation="MTGRIRVSPRFHPYGGROVRSLNETAIVPYTGNAVPIARSY
          VPSRGVRRKRRGRDRIKGYCPCKIDYEFKMDVPHGTVCVSDPIRGCLTHRL
          GKRVCTKSHSIDGKWMDDNVAKRODHTNITLWLIRDRPNKDPINFGDFTMYDERP
          TPAKLRMDLRDMQVLAKFVSFVSGPSYSHKDALIRFKFKCLYNHVTYNHKEAKE
          NQLENALMLYSASHSNFVQTLRCRAFYDSHKV"
gene      complement(1976..2413)
CDS       /gene="C3"
          complement(1976..2413)
          /codon_start=1
          /product="C3 protein"
          /protein_id="CA10697.1"
          /db_xref="GI:4210723"
          /translation="MDSRGESLSHAQTRAAEFRRNPNSVQOTAFPHILRLMYVHTN
          LDKSTIMKQLOVNHRRNRKEIGFKIFLDFRIITPLRIGAITNMGTCSNRLKRWICNS
          IASIDYFSLFNLYVYIRHLPQQLWEEVDIDCKDILKVLVY"
gene      complement(2127..2576)
CDS       /gene="C2"
          complement(2127..2576)
          /codon_start=1
          /product="C2 protein"
          /protein_id="CA10698.1"
          /db_xref="GI:4210724"
          /translation="MSTAPSGYKRKCPAOPERPIHAAKRRORRTPPEPRTHIVKGGCS
          AFTINDCKRQHFTHRGVTKSCTDYESSRILOOSHVCSDCTIPSTTIDVCPKQPRLK
          DHESASASQPEQEGNWTPELPPIDHTNASDWCYSQLDWTFQSP"
BASE COUNT 734 a 570 c 671 g 788 t
ORIGIN

alignment_scores:
  Quality: 270.00 Length: 68
  Ratio: 4.576 Gaps: 0
  Percent Similarity: 86.765 Percent Identity: 76.471

alignment_block:
US-09-289-346A-4 x IYEL32548/rev ..
Align seg 1/1 to reverse of: IYEL32548 from: 1 to: 2763
1 ThrleuValTrpGlyGluPheGlnValAspGlyArgSerAlaArgGlyG1 17
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
469 ACCCTCATATGGGTGAATTCACATCGACGCGCATCTGCTAAGAGAGG 420
17 yCysGlnThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerL 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
419 TCACGACATCTCTAAGCAGCAGCGCAGAGCGCTAAACCATGTTCTA 370
34 ySgIuGluAlaLeuGlnIleIleAlaAlaAlaIleProGluLysTyleu 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
369 AAGAGACCTGCGCTTCAATATATCAGGAGAAATCTCCGAAATAATTTA 320
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAsnSprtGllPheAspLysTh 67

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|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
319 TTTCATATATCATATATTAGTAGTAATTAGATAGATATTTTCTCCTCC 270
67 rPro 68
269 TCCT 266

seq_name: gb_v1:MGU75278
seq_documentation_block:
LOCUS MGU75278 447 bp DNA VRL 27-NOV-1996
DEFINITION Macropitillium golden mosaic geminivirus replication-associated
ACCESSION protein (AC1) gene, partial cds.
VERSION 075278
KEYWORDS 075278.1 GI:168818
SOURCE Macropitillium golden mosaic geminivirus.
ORGANISM Macropitillium golden mosaic geminivirus
          Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
REFERENCE 1 (bases 1 to 447)
AUTHORS Roye,M.E.
TITLE Diversity and phylogeny of whitefly-transmitted geminiviruses from
JOURNAL Thesis (1996)
REFERENCE 2 (bases 1 to 447)
AUTHORS Roye,M.E., McLaughlin,W.A. and Maxwell,D.P.
TITLE Three distinct geminiviruses infecting M. lathyroides from Jamaica
          but not BGWV
JOURNAL Unpublished (1996)
REFERENCE 3 (bases 1 to 447)
AUTHORS Roye,M.E., McLaughlin,W.A. and Maxwell,D.P.
TITLE Direct Submission
JOURNAL Submitted (17-Oct-1996) Biochemistry, University of the West
          Indies, Mona, Kingston 7, Jamaica
FEATURES
  source
    1..447
    /organism="Macropitillium golden mosaic geminivirus"
    /strain="Jamaican"
    /isolate="2"
    /db_xref="taxon:51676"
    /clone="PMGJA2"
    complement(1..447)
    /gene="AC1"
    complement(<1..>447)
    /gene="AC1"
    /codon_start=1
    /product="replication-associated protein"
    /protein_id="AAB36919.1"
    /db_xref="GI:1688189"
    /translation="HYLIQFQKGFNCTNRLFDIVSPSPAHFHPNIOGAKSSDYKS
    YVEKDCDITEKGVFOIDGRSARGCQOTSNDAAAEALNSCTKAAARIVAEKLPEKFLF
    QYHNUSNINLDRIFMKDPEFWAPPPLPSSTFNVDEQEWATVFGK"
BASE COUNT 97 a 112 c 110 g 128 t
ORIGIN

alignment_scores:
  Quality: 266.00 Length: 70
  Ratio: 4.361 Gaps: 0
  Percent Similarity: 87.143 Percent Identity: 70.000

alignment_block:
US-09-289-346A-4 x MGU75278/rev ..
Align seg 1/1 to reverse of: MGU75278 from: 1 to: 447
1 ThrleuValTrpGlyGluPheGlnValAspGlyArgSerAlaArgGlyG1 17
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
294 ACCATTCGATGGGAGTGTTCCAGATCGACGAGAAAGACTGCTCAAGCGG 245
17 yCysGlnThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerL 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
244 TCACGAACATCTAAGCATGACGCGCGGAGCATTAATTCGTGACACAA 195

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34 yseluoluLauLeugInIlellelaAlAalAleProguLUvSYrUw 50
||||| |||||.....|||::: :::|||||.....|||
194 AGAGAGCGGCGCATGACATATGTCAAGAGAGAAGTGGCCGGAAAGATTCTC 145
51 pHeGlnPheHisAsnLeuAnsSerAsnLeuAspArgI]ePhAspLyStH 67
|||||.....|||.....|||.....|||.....|||
144 TTTCATATCACAACTATCTCACTAACCTCGAGATGATTTTCATGAAGA 95
67 rPGouPro 70
|||||.....|||
94 TCCGGAACA 85
seq_name= gb_v1:AF098940

seq_documentation_block:
LOCUS AF098940 1405 bp DNA VRL 04-MAR-1999
DEFINITION Macropittium golden mosaic geminivirus strain Jamaica 1
partial cds.
replication associated protein (rep) and coat protein (cp) genes,
partial cds.
AF098940
VERSION AF098940.1 GI:4336584
KEYWORDS
SOURCE
ORGANISM
Macropittium golden mosaic geminivirus.
Macropittium golden mosaic geminivirus
Virus; ssDNA viruses; Geminiviridae; Begomovirus.
REFERENCE
1 (bases 1 to 1405)
Royer,M.E., McLaughlin,W.A. and Maxwell,D.P.
Genetic diversity and phylogeny of whitefly-transmitted
geminiviruses from Jamaica
JOURNAL
TITLE Unpublished
2 (bases 1 to 1405)
Royer,M.E., McLaughlin,W.A. and Maxwell,D.P.
Molecular characterization of two distinct geminiviruses infecting
M. lathyroides from Jamaica
JOURNAL
TITLE Unpublished
3 (bases 1 to 1405)
Royer,M.E., McLaughlin,W.A. and Maxwell,D.P.
Direct Submission
Submitted (14-OCT-1998) Biotechnology Centre, University of the
West Indies, Mona, Kingston 7, Jamaica
FEATURES
source
1..1405
/oranism="Macropittium golden mosaic geminivirus"
/strain="Jamaica strain 1"
/specific_host="Macropittium lathyroides"
/db_xref="taxon:51676"
/country="Jamaica"
/clone="pmcJA3"
/complement(<1..701)
/gene="rep"
complement(<1..701)
/gene="rep"
/codon_start=1
/product="replication associated protein"
/protein_id="AADI7850.1"
/db_xref="GI:4336586"
/translation="MPKRSFSIKAKNYFLTYPOCSLTKEFALSOTNLNTPVKKFET
YVEKDQGTTEMGVQLDGRSARGCOQTNDAAALASGTEAMRAIVKELPKFTLE
OYNHLSSLDRIETMKDEPMWAPPLSLSTFWPDPEMDADYGRGSAAERPRMS
ITVEDSRTRGTMMAC"
702..1030
/note="intergenic region"
1031..>1405
/gene="cp"
1031..>1405
/gene="cp"
/codon_start=1
/product="coat protein"
/protein_id="AADI7849.1"
/db_xref="GI:4336585"
/translation="MPKRDSGSWRTPGVAKVSRLNTPRGVGPRSKAQAQEWNRPM

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YRKPRIRFTLSPGRCGECPCVQGEQEDRHDSHVKGVMCJSDVTRGVLTIRHVG
RFCVKFVYIIIGKIMMDNINOSC"
BASE COUNT      328 a      333 c      357 g      386 t      1 others
ORIGIN

alignment_scores:
    Quality: 266.00      Length: 70
    Ratio: 4.361      Gaps: 0
    Percent Similarity: 87.143      Percent Identity: 70.000

alignment_block:
US-09-289-346A-4 x AF098940/rev ..

Align seg 1/1 to reverse of: AF098940 from: 1 to: 1405

1  Thtleuvaltrpdyglnupheglnvalaspglyargseralarglyc1 17
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
374 ACCATTCGATTCGGGACTGTTCGAGATCGACGAGAGAGTCTCGAGCGG 325
17 ycygslnthrserasnaspalalalactlualaleuasnalaserse1 34
1 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
324 TAGAGCAAACTCATACGATGACGCCGCCGAGACATTAAATCTCGAACAA 275
34 ysglnclualaleucnllellelala1alaleproclustyrleu 50
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
274 AGAGAGCGGCCATGAGAAATAGTCAGAGAGAAAGTTTC 225
51 PhcglPhh1sasnleuasnsersasnleuasparg1laphasp1synh 67
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
224 TTTCATATTCACACACTATCCAGTACCTGATAGGATTTTCATGAGGA 175
67 rProGluPro 70
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
174 TCCGGAAACA 165

seq_name: gb_v1:AF026553

seq_documentation_block:
LOCUS AF026553 1165 bp DNA VRL 03-NOV-1997
DEFINITION Potato yellow mosaic virus Tomato strain AV1 and AC1 genes, partial cds.
ACCESSION AF026553
VERSION AF026553.1 GI:2583073
KEYWORDS
SOURCE
ORGANISM
Geminiviridae.
Geminiviridae
Viruses; ssDNA viruses.
1 (bases 1 to 1165)
Guzman,P., Arredondo,C.R., Emmatty,D., Portillo,R.J. and
Gilbertson,R.L.
Partial Characterization of Two Whitefly-Transmitted Geminiviruses
Infecting Tomatoes in Venezuela
Plant Dis. 81, 312-312 (1997)
2 (bases 1 to 1165)
Guzman,P., Arredondo,C.R., Emmatty,D., Portillo,R.J. and
Gilbertson,R.L.
Direct Submission
submitted (24-SEP-1997) Plant Pathology, University of
California-Davis, Department of Plant Pathology, Davis, CA 95616,
USA

FEATURES
source
1..1165
location/Qualifiers
/organism="Geminiviridae"
/strain="Tomato strain"
/db_xref="taxon:10811"
/note="bipartite genome; whitefly-transmitted; DNA-A
fragment obtained by PCR from tomato sample from State of
Monagagas (Venezuela)"
complement(<1..153)
/note="capsid protein"
/codon_start=1
/product="AV1"

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/feature_id="AAB82606.1"
/db_xref="GI:2583075"
/translation="MPKRDAPWRSMAGTSKYSRNANSPRSGIGPRINKAAEWNRPM
YRPGCSI
464..>1165
/note="replication-associated protein"
/codon_start=1
/product="AC1"
/protein_id="AAB82605.1"
/db_xref="GI:2583074"
/translation="MPKGSFSIKAKNYELTYPOCSLSEKDALSOIQMLTPVKKFI
KICRELNENGEPLHLVLIQEFKFNCTNNRLFDVSPRTYHFNIOGAKSSSVKS
YKEDGPTIEWGLFOIDGRSARGCOQTANDAAEAALNCGTKEAMKIRKLPKFLF
OYHNSLDRIEMKAPPMAPPPPLSFTVPHQMESHDFGRSAANGETISII
IESGRCKTMMACRC"
BASE COUNT      350 a      264 c      256 g      295 t
ORIGIN

alignment_scores:
  Quality: 260.00      Length: 70
  Ratio: 4.127      Gaps: 0
  Percent Similarity: 90.000      Percent Identity: 68.571

alignment_block:
US-09-289-346a-4 x AF026553 ..
Align seg 1/1 to: AF026553 from: 1 to: 1165

1 ThrleuValTrpGlyGluPheGlnValAspGlyArgSerAlaArgGlyG1 17
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
791 ACCATCGAATGGGGATTGTTCCAGATTGACGGAAGAAGTCTCGAGGTGG 840

17 yCysGlnThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSert 34
| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
841 CCACAGACCGCAACGACGACGCTGCGAGCATTTAACTCTGGAACAA 890

34 ysgGluAlaLeuGlnIleIleAlaAlaAlaIleProGluIuLysTyrLeu 50
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
891 AGGAAAGACCATGAAATCATATAAGAGACAGTTCGCCGAAAGTTTCTT 940

51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgTllePheAspLysTh 67
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
941 TTTCAGATCATCACTATCAGTACGACCTCGATGATTTTCATGAAGGC 990

67 rProGluPro 70
: ||||| |||||
991 TCCAAATCCG 1000

seq_name: gb_v1:AB001315

seq_documentation_block:
LOCUS      AB001315      570 bp      DNA      VRL      13-FEB-1999
DEFINITION Tobacco leaf curl virus C1 and C4 genes, clone YOKOHAMA3-1, partial
and complete cds.
ACCESSION      AB001315
VERSION      AB001315.1 GI:3798714
KEYWORDS
SOURCE
ORGANISM      tobacco leaf curl virus (isolate:YOKOHAMA3,
specific host:Eupatorium makinoi) DNA, clone:YOKOHAMA3-1.
Viruses: ssDNA viruses; Geminiviridae; Begomovirus.
1 (bases 1 to 570)
Ooi,K.
AUTHORS
TITLE      Direct Submission
JOURNAL
Submitted (19-FEB-1997) to the DDBJ/EMBL/GenBank databases.
Kazuyuki Ooi, Kyushu University, Department of Biology; 6-10-1
Hakozaki Higashi-ku, Fukuoka 812, Japan
(E-mail:kooi@chembox.nc.kyushu-u.ac.jp, Tel:+81-92-642-2624,
Fax:+81-92-642-2645)
2 (bases 1 to 570)
REFERENCE
Ooi,K., Onshita,S., Ishii,I. and Yahara,T.
Molecular phylogeny of geminivirus infecting wild plants in Japan

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JOURNAL      J. Plant Res. 110, 247-257 (1997)
FEATURES
SOURCE
1..570
/organism="tobacco leaf curl virus"
/isolate="YOKOHAMA3"
/specific_host="Eupatorium makinoi"
/db_xref="taxon:67762"
/clone="YOKOHAMA3-1"
complement(1..570)
/gene="C1"
complement(<1..>570)
/gene="C1"
CDS
/codon_start=1
/protein_id="BAA34033.1"
/db_xref="GI:4426541"
/translation="EALISQONITPTNKLTIKICRELNENGEPLHLVLIQEFK
YKONNEFDLVSPTRSARHFRPNTQAKSSSDVKSVIDKGDLTLEWTFQIDGRSARGC
ONANDACAEALNASKAEALAIIRKLPKDFIFOYHNLNLSIDRIAPPLLEVFVCPFT
ASSFDQVEBELLEMASENVMSAARPM"
complement(231..488)
/gene="C4"
complement(231..488)
CDS
/gene="C4"
complement(231..488)
/gene="C4"
/codon_start=1
/protein_id="BAA34034.1"
/db_xref="GI:3798715"
/translation="MEALISMGFCSKANTNKTIDSSSTWYPPQPHISIKTFRELNP
APTSSPTREIRNSGHSRSTEEVLEAAHMLTHVQR"
BASE COUNT      141 a      121 c      126 g      182 t
ORIGIN

alignment_scores:
  Quality: 254.00      Length: 85
  Ratio: 4.164      Gaps: 1
  Percent Similarity: 71.765      Percent Identity: 58.824

alignment_block:
US-09-289-346a-4 x AB001315/rev ..
Align seg 1/1 to reverse of: AB001315 from: 1 to: 570

1 ThrleuValTrpGlyGluPheGlnValAspGlyArgSerAlaArgGlyG1 17
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
318 ACGCTCCAGATGGGACACATTCCAGATCGACGGAAGAAGTGTAGAGAGG 269

17 yCysGlnThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSert 34
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
268 CTGCCAGATGCTTAACGACGACGCTGACAGAGCCTTAAATGCAAGTTCTA 219

34 ysgGluAlaLeuGlnIleIleAlaAlaAlaIleProGluIuLysTyrLeu 50
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
218 AGCGAGAGCATTTAGCAATATATTAGGAAAGCTCCCTAAAGATTATATA 169

51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgTllePheAspLysTh 63
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
168 TTTCATATATCATTAATTAAATAGTAATTTAGATAGAGATTTTGCTCTCC 119

64 .....PheAspLysThrP 68
118 GTTGAGAGTTTGTGTTGTCTTTCACAGCCTCATCCCTTATCATCAAGTTC 69

68 rGlu 69
|||||
68 CAGAA 64

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```

alignment_scores:
  Quality: 233.00      Length: 85
  Ratio: 3.820        Gaps: 1
  Percent Similarity: 71.765  Percent Identity: 54.118

alignment_block:
  US-09-289-346a-4 x AA084371

Align seg 1/1 to: AA084371 from: 1 to: 434

1  ThrleuValTrpGlyGluPheGlnValAspGlyArgSerAlaArgIyl 17
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
95  ACCCTCGAATGGGAGAGTTTCACATGCATGCATCTGCACAGCGCG 144
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
17  YCysGlnThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerL 34
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
145  ACAACAATCAGCCATGACGCTTACGCCACGCGCTTAACACTGGAAGTA 194
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
34  YsglGluAlaLeuGlnIleIleAlaAlaIleProGluLysTyrLeu 50
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
195  AGTCAGAGGCTTAACGCTTACGGAATTAAGCCCTTAAGCATTAATGTT 244
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
51  PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIle..... 63
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
245  TTACAAATTCATATTAATAATAGTAATTTAGATTTTACACCTCC 294
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
64  .....PheAspLysThrP 68
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
295  GTTGGAGGTTTATGTTCTCTTTTATCTTCTTCTTTCATCGAGCTTC 344
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
68  roglu 69
   |||||
345  CAGAA 394

seq_name: /cgnl_8/gcdata/geneseq/geneseqn/NA1995.DAT:AA084372
seq_documentation_block:
  ID AA084372 standard; DNA; 479 BP.
  XX
  AC AA084372;
  XX
  DF 19-AUG-1995 (first entry)
  XX
  DE Gemini virus-specific polyribozyme-F target sequence.
  XX
  KW ribozyme target sequence: polyribozyme-F;
  KM tomato leaf curl virus; RNA cleavage; tomato transgenic plant;
  KW virus disease-resistance; ss.
  XX
  OS Tomato leaf curl virus.
  XX
  PH Key Location/Qualifiers
  FT misc_feature 46..96
   /tag= a
   /note= "ribozyme R4-R5 target sequence"
  FT misc_feature 58..60
   /tag= b
   /note= "ribozyme R4 cleavage site"
  FT misc_feature 81..83
   /tag= c
   /note= "ribozyme R5 cleavage site"
  FT misc_feature 356..386
   /tag= d
   /note= "ribozyme R2 target sequence"
  FT misc_feature 370..372
   /tag= e
   /note= "ribozyme R2 cleavage site"
  FT misc_feature 429..459
   /tag= e
   /note= "ribozyme R3 target sequence"
  FT misc_feature 442..444

```

```

FT FT /*tag= d
FT FT /note= "ribozyme R3 cleavage site"
XX XX
XX PN W09503404-A.
XX PN
XX PD 02-FEB-1995.
XX PD
XX PF 22-JUL-1993; 93WO-EP01946.
XX PF
XX PR 22-JUL-1993; 93AU-0047014.
XX PR
XX PR 22-JUL-1993; 93WO-EP01946.
XX PR
XX PA (BIOC-) BIOCEM SA.
XX PA (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX PA
XX PI Baudino S, Comeau D, Dry IB, Gruber V, Lence P;
XX PI Mason J, Rezaiian MA, Rigen JE, Rezaiian MA;
XX PI
XX DR WPI; 1995-075232/10.
XX DR
XX PT Synthetic DNA virus ribozyme(s) - reduce replication, infection
XX PT and/or assembly of viruses by cleaving target virus sequence,
XX PT useful for preparing resistant plants, esp tomatoes.
XX PT
XX PS Example 10; Fig 11c; 90pp; English.
XX PS
XX CC The sequence is a tomato leaf curl virus target sequence for
XX CC polyribozyme-F, which hybridizes to and cleaves the sequence and
XX CC thereby reduces replication, infection and/or assembly of the virus
XX CC substantially. The ribozyme may be expressed in a transgenic plant,
XX CC e.g. tomato, to confer virus disease-resistance.
XX CC
XX SQ Sequence 479 BP; 145 A; 95 C; 97 G; 142 T; 0 other;

```

```

alignment_scores:
  Quality: 233.00      Length: 85
  Ratio: 3.820        Gaps: 1
  Percent Similarity: 71.765  Percent Identity: 54.118

alignment_block:
  US-09-289-346a-4 x AA084372

Align seg 1/1 to: AA084372 from: 1 to: 479

1  ThrleuValTrpGlyGluPheGlnValAspGlyArgSerAlaArgIyl 17
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
140  ACCCTCGAATGGGAGAGTTTCACATGCATGCATCTGCACAGCGCG 189
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
17  YCysGlnThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerL 34
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
190  ACAACAATCAGCCATGACGCTTACGCCACGCGCTTAACACTGGAAGTA 239
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
34  YsglGluAlaLeuGlnIleIleAlaAlaIleProGluLysTyrLeu 50
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
240  AGTCAGAGGCTTAACGCTTACGGAATTAAGCCCTTAAGCATTAATGTT 289
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
51  PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIle..... 63
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
290  TTACAAATTCATATTAATAATAGTAATTTAGATTTTACACCTCC 339
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
64  .....PheAspLysThrP 68
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
340  GTTGGAGGTTTATGTTCTCTTTTATCTTCTTCTTTCATCGAGCTTC 389
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
68  roglu 69
   |||||
390  CAGAA 394

seq_name: /cgnl_8/gcdata/geneseq/geneseqn/NA1995.DAT:AA084375
seq_documentation_block:
  ID AA084375 standard; DNA; 550 BP.

```



```

XX AA084375;
AC
XX 19-AUG-1995 (first entry)
DE Tomato leaf curl virus Australian strain DNA sequence.
XX
XX Tomato leaf curl virus; Australia strain; plant disease; ds.
XX
XX Tomato leaf curl virus (Australia).
XX
XX WO9503404-A.
XX
XX 02-FEB-1995.
XX
XX 22-JUL-1993; 93WO-EP01946.
XX
XX 22-JUL-1993; 93AU-0047014.
XX
XX 22-JUL-1993; 93WO-EP01946.
XX
XX (BIOC-) BIOCEM SA.
XX (CSTR) COMMONWEALTH SCI & IND RES ORG.
XX
XX Baudino S, Comeau D, Dry IB, Gruber V, Lencee P;
XX Mason J, Rezalian MA, Ridden JE, Rezanan MA;
XX
XX WPI: 1995-075232/10.
XX
XX Synthetic DNA virus ribozyme(s) - reduce replication, infection
XX and/or assembly of viruses by cleaving target virus sequence,
XX useful for preparing resistant plants, esp tomatoes.
XX
XX Disclosure: Fig 1; 90pp: English.
XX
XX The sequence represents the complementary sense DNA strand of an
XX Australian strain of tomato leaf curl virus. Ribozymes specific
XX for this sequence may be used in generation of transgenic plants
XX with disease-resistance.
XX
XX Sequence 550 BP; 148 A; 120 C; 134 G; 142 T; 6 other;
XX
alignment_scores:
Quality: 232.50 Length: 86
Ratio: 3.811 Gaps: 1
Percent Similarity: 70.930 Percent Identity: 53.488
alignment_block:
US-09-289-346A-4 x AA084375 ..
Align seg 1/1 to: AA084375 from: 1 to: 550
1 ThtleuValtrpGlyIupheGlnValAspGlyArgSerAlaArgGlyG1 17
||||| ||||||| ||||||| ||||||| ||||||| |||||||
201 ACCCTCGAATGGGAGAGTTTCAGATCGATGAGATCTGCACAGAGGGG 250
17 yCysGlnThrSerAsnAspAlaAlaGluAlaLeuAlaSerSerL 34
||||| ||||||| ||||||| ||||||| ||||||| |||||||
251 ACAACAATCGCAATGACGCTTACGCCAGCGCCTTAACACCTGGAAGTA 300
34 ySgIuGluAlaLeuGlnIleAlaAlaAlaIleProGluLysTYrLeu 50
||||| ||||||| ||||||| ||||||| ||||||| |||||||
301 AGTCAGAGGCTTAAACGCTCTTAGGGAATTAGCCCTTAAGATTATGTT 350
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIle..... 63
:::||||| ||||||| ||||||| ||||||| ||||||| |||||||
351 TTACAATTTCATTAATTAAATAGTAATTAGATTTNNNTACACC 400
64 ..... PheAspLysT 67
401 TCCGTTGACAGCTTATGTTCTCTCTTTTATCTCTCTTTGATGAG 450
67 hrpGlu 69

```

```

:::|||||
451 TTCACAGA 458
seq_name: /cgnl_8/gcdata/geneseq/geneseq/NM1997.DAT:AA093317
seq_documentation_block:
ID AA093317 standard; DNA: 2744 BP.
XX
XX AA093317;
AC
XX 27-APR-1998 (first entry)
DE Tomato leaf curl virus from Southern India (stem-loop begin).
XX
XX Geminiivirus; TLGV-IND; AC1 gene; transdominant mutation;
XX transgenic plant; disease resistance; ss; cyclic; circular.
XX
XX Tomato leaf curl virus from Southern India.
XX
XX WO9739110-A1.
XX
XX 23-OCT-1997.
XX
XX 15-APR-1997; 97WO-US06300.
XX
XX 16-APR-1996; 96US-0015517.
XX
XX (SEMI-) SEMINIS VEGETABLE SEEDS INC.
XX (WISC) WISCONSIN ALUMNI RES POUND.
XX
XX Ahlquist PG, Hanson SF, Luu HT, Maxwell DP, Stout JT;
XX
XX WPI: 1997-526447/48.
XX
XX Transgenic plants expressing geminivirus AC1 and CI wild-type and
XX mutant genes - have increased resistance to geminivirus infection
XX e.g. tomato mottle virus, tomato yellow leaf curl virus or bean
XX golden mosaic geminivirus
XX
XX Disclosure: Page 119-121; 132pp: English.
XX
XX This genomic DNA sequence comprises a full-length sequence
XX (stem-loop begin) from a tomato leaf curl virus from Southern
XX India. The invention involves production of transgenic plants
XX containing DNA comprising geminivirus AC1 or CI wild-type or mutant
XX sequences (see AA093282-93) that negatively interfere in trans with
XX geminiviral replication during infection. Such transgenic plants
XX are resistant to viral infection. The AC1/CI genes are especially
XX CC from tomato mottle virus, tomato yellow leaf curl virus or bean
XX golden mosaic virus.
XX
XX Sequence 2744 BP; 742 A; 539 C; 637 G; 826 T; 0 other;
XX
alignment_scores:
Quality: 229.00 Length: 65
Ratio: 4.241 Gaps: 1
Percent Similarity: 83.077 Percent Identity: 69.231
alignment_block:
US-09-289-346A-4 x AA093317/rev ..
Align seg 1/1 to reverse of: AA093317 from: 1 to: 2744
4 TTPGlyIupheGlnValAspGlyArgSerAlaArgGlyCysGlnTh 20
||||| ||||||| ||||||| ||||||| ||||||| |||||||
2266 TGGGTCAGTTTCAGATGATGAGAAATCTGCACAGAGGTCAACAGAC 2217
20 rSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerLysGluGua 37
||||| ||||||| ||||||| ||||||| ||||||| |||||||
2216 AGCTAATGATGCTGCGCACAGAGCCTTAATAATGACGTTACCTAAGC 2167
37 lAlaGlnIleAlaAlaAlaIleProGluLysTYrLeuPheGlnPhe 53

```

```

||||| ||||| ::|||::: |||||:::
2166 CTTTAGCAATATATAGGAAACTCCCTTAAGATTTATTTTCATAT 2117
54 HisAsnLeuAsnSerAsnLeuAspArg11IlePheAspLysThrPro 68
|||||::: |||||::: |||||:::
2116 CATTAATTTAAATGTAAATTTAGATAGATTTT.....ACACCT 2078
seq_name: /cgul_8/gcgdata/geneseq/geneseqn/NA1996.DAT:AAAT12904
seq_documentation_block:
ID AAAT12904 standard; DNA; 1080 BP.
XX
AC AAAT12904;
XX
DT 07-NOV-1996 (first entry)
XX
DE Sardinian tomato yellow leaf curl virus mutated CI gene (K227A).
XX
KW Nucleotide triphosphate binding site; DNA helicase; RNA helicase;
KW modification; mutation; viral replication; deficient; inhibition;
KW viral resistance; geminivirus; tomato yellow leaf curl virus;
KW Sardinian isolate; STYLCV; transgenic plant; P-loop; CI gene;
KW ALI gene; dominant negative phenotype; ss.
XX
OS Sardinian tomato yellow leaf curl virus.
XX
FH Key Location/Qualifiers
FT CDS 1..1080
FT /*tag= a
FT /product= Rep_(K227A)
FT /note= "encodes Rep protein in which wild-type Lys
FT at position 227, i.e. within the NTP-
FT binding site, is replaced by Ala"
XX
PN WO9608573-A1.
XX
PD 21-MAR-1996.
XX
PF 15-SEP-1995; 95WO-FR01192.
XX
PR 15-SEP-1994; 94FR-0011040.
XX
PA (CNRS ) CENT NAT RECH SCT.
XX
PI Gronenborn B;
XX
DR WPI: 1996-179947/18.
DR P-PSDB: AAR88870.
XX
PT Prod. of virus-resistant transgenic plants - using mutated genomic
PT sequence from phytopathogenic DNA virus
XX
PS Disclosure; Fig 13; 93pp; French.
XX
CC Mutation of consensus amino acids in the NTP-binding site of
CC geminivirus Rep protein is used to produce replication deficient
CC viruses. The mutated viral nucleic acid is used for producing
CC transgenic plants that are resistant to, or tolerant of, the native
CC virus. The present sequence encodes a mutant form of the Rep (or CI)
CC protein from the Sardinian isolate of tomato yellow leaf curl virus
CC (STYLCV) in which the wild-type Lys227 residue has been changed to an
CC Ala residue; transgenic Nicotiana benthamiana plants generated by
CC transformation with the mutated virus were found to be resistant to
CC STYLCV, i.e the mutation results in a dominant negative phenotype.
XX
SQ Sequence 1080 BP; 355 A; 248 C; 210 G; 267 T; 0 other:

```

```

alignment_scores:
Quality: 222.00 Length: 69
Ratio: 3.895 Gaps: 0
Percent Similarity: 82.609 Percent Identity: 57.971

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alignment_block:
US-09-289-346a-4 x AAAT12904 ..
Align seg 1/1 to: AAAT12904 from: 1 to: 1080
2 LeuValTrpGlyGluPheGlnValAspGlyArgSerAlaArgGlyGly 18
||| ||||| |||||::: |||||::: |||||::: |||||:::
331 CTTGAATGGGCTACTTCCAGATCGACGACGATCTGCTAGGGAGACA 380
18 sGlnThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerLys 35
|||||::: |||||::: |||||::: |||||::: |||||:::
381 ACAGACAGCCACGACGCTTACGCAAGGCATTAACGACGAAGTAAGT 430
35 LucAlaLeuGlnIleIleAlaAlaIleProGluLysTyrLeuPhe 51
::: |||||::: |||||::: |||||::: |||||::: |||||:::
431 CGCAGGCTCTTGATGTATTAAGATTTAGCGCTTACGATTTAGCTCTA 480
52 GluPheHisAsnLeuAsnSerAsnLeuAspArg11IlePheAspLysThrPr 68
::: |||||::: |||||::: |||||::: |||||::: |||||:::
481 CATTTTCATATATATAATTAATTTAGATTAAGSTTTTCCAGGTGCCCTCC 530
68 OGluPro 70
| |||
531 GGCACCT 537
seq_name: /cgul_8/gcgdata/geneseq/geneseqn/NA1996.DAT:AAAT12905
seq_documentation_block:
ID AAAT12905 standard; DNA; 1080 BP.
XX
AC AAAT12905;
XX
DT 07-NOV-1996 (first entry)
XX
DE Sardinian tomato yellow leaf curl virus mutated CI gene (K227H).
XX
KW Nucleotide triphosphate binding site; DNA helicase; RNA helicase;
KW modification; mutation; viral replication; deficient; inhibition;
KW viral resistance; geminivirus; tomato yellow leaf curl virus;
KW Sardinian isolate; STYLCV; transgenic plant; P-loop; CI gene;
KW ALI gene; ss.
XX
OS Sardinian tomato yellow leaf curl virus.
XX
FH Key Location/Qualifiers
FT CDS 1..1080
FT /*tag= a
FT /product= Rep_(K227H)
FT /note= "encodes Rep protein in which wild-type Lys
FT at position 227, i.e. within the NTP-
FT binding site, is replaced by His"
XX
PN WO9608573-A1.
XX
PD 21-MAR-1996.
XX
PF 15-SEP-1995; 95WO-FR01192.
XX
PR 15-SEP-1994; 94FR-0011040.
XX
PA (CNRS ) CENT NAT RECH SCT.
XX
PI Gronenborn B;
XX
DR WPI: 1996-179947/18.
DR P-PSDB: AAR88871.
XX
PT Prod. of virus-resistant transgenic plants - using mutated genomic
PT sequence from phytopathogenic DNA virus
XX
PS Disclosure; Fig 13; 93pp; French.
XX
CC Mutation of consensus amino acids in the NTP-binding site of

```

CC geminivirus Rep protein is used to produce replication deficient
 CC viruses. The mutated viral nucleic acid is used for producing
 CC transgenic plants that are resistant to, or tolerant of, the native
 CC virus. The present sequence encodes a mutant form of the Rep (or CI)
 CC protein from the Sardinian isolate of tomato yellow leaf curl virus
 CC (STYLCV) in which the wild-type Lys227 residue has been changed to a
 CC His residue; transgenic Nicotiana benthamiana plants generated by
 CC transformation with the mutated virus were not resistant to STYLCV.
 CC In contrast, plants transformed with a virus in which Lys227 had been
 CC replaced by Ala were found to be resistant.

XX Sequence 1080 BP; 356 A; 248 C; 208 G; 268 T; 0 other;

alignment_scores:
 Quality: 222.00 Length: 69
 Ratio: 3.895 Gaps: 0
 Percent Similarity: 82.609 Percent Identity: 57.971

alignment_block:

US-09-289-346A-4 x AAT12905 ..

Align seg 1/1 to: AAT12905 from: 1 to: 1080

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2 LeuValTrpGlyGluPheGlnValAlaSpGlyArgSerAlaArgGlyGlyC 18
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
331 CTTCGATGGGGTACTTCCAGATCGACGCGATCTCTTGGGAGACACA 380
18 sGlnTrpSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerLysG 35
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
381 ACAGACAGCCACGACGCTTACGCAAGGCAATTACGACGAGAACTAGT 430
35 LuGluAlaLeuGlnIleIleAlaAlaIleProGluLysTyrLeuPhe 51
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
431 CGCAGGCTCTTGATGTAATTAAAGCAATTACGCGCTTACGATCTCTA 480
52 GlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysThrPr 68
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
481 CATTTCATATATATAATAGTAATTAGATAGCTTTCCACAGTCCCTCC 530
68 oGluPro 70
|||
531 GGCACCT 537
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seq_name: /cgnl_8/gcgdata/geneseq/geneseqn/NA1996.DAT:AAT12906

seq_documentation_block:

ID AAT12906 standard; DNA; 1080 BP.

AC AAT12906;

DT 07-NOV-1996 (first entry)

DE Sardinian tomato leaf curl virus mutated CI gene (K227R).

XX Nucleotide triphosphate binding site; DNA helicase; RNA helicase;
 KM modification; mutation; viral replication; deficient; inhibition;
 KM viral resistance; geminivirus; tomato yellow leaf curl virus;
 KM Sardinian isolate; STYLCV; transgenic plant; P-loop; CI gene;
 KW All gene; ss.

XX Sardinian tomato yellow leaf curl virus.

OS Sardinian tomato yellow leaf curl virus.

PH Key Location/Qualifiers

FT CDS 1..1080

FT /tag= a

FT /product= Rep.(K227R)

FT /note= "encodes Rep protein in which wild-type Lys

FT at position 227, i.e. within the NTP-

FT binding site, is replaced by Arg"

XX WO9608573-A1.

PD 21-MAR-1996.

XX 15-SEP-1995: 95WO-FR01192.

XX 15-SEP-1994: 94FR-0011040.

XX (CNRS) CENT NAT RECH SCI.

XX Gronenborn B;

XX WPI: 1996-179947/18.

XX P-PSDB: AAR88872.

XX Prodn. of virus-resistant transgenic plants - using mutated genomic

XX sequence from phytopathogenic DNA virus

XX Disclosure: Fig 13; 93pp: French.

CC Mutation of consensus amino acids in the NTP-binding site of
 CC geminivirus Rep protein is used to produce replication deficient
 CC viruses. The mutated viral nucleic acid is used for producing
 CC transgenic plants that are resistant to, or tolerant of, the native
 CC virus. The present sequence encodes a mutant form of the Rep (or CI)
 CC protein from the Sardinian isolate of tomato yellow leaf curl virus
 CC (STYLCV) in which the wild-type Lys227 residue has been changed to an
 CC Arg residue; transgenic Nicotiana benthamiana plants generated by
 CC transformation with the mutated virus were not resistant to STYLCV.
 CC In contrast, plants transformed with a virus in which Lys227 had been
 CC replaced by Ala were found to be resistant.

XX Sequence 1080 BP; 356 A; 247 C; 210 G; 267 T; 0 other;

alignment_scores:
 Quality: 222.00 Length: 69
 Ratio: 3.895 Gaps: 0
 Percent Similarity: 82.609 Percent Identity: 57.971

alignment_block:

US-09-289-346A-4 x AAT12906 ..

Align seg 1/1 to: AAT12906 from: 1 to: 1080

```

2 LeuValTrpGlyGluPheGlnValAlaSpGlyArgSerAlaArgGlyGlyC 18
||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
331 CTTCGATGGGGTACTTCCAGATCGACGCGATCTCTTGGGAGACACA 380
18 sGlnTrpSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerLysG 35
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
381 ACAGACAGCCACGACGCTTACGCAAGGCAATTACGACGAGAACTAGT 430
35 LuGluAlaLeuGlnIleIleAlaAlaIleProGluLysTyrLeuPhe 51
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
431 CGCAGGCTCTTGATGTAATTAAAGCAATTACGCGCTTACGATCTCTA 480
52 GlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysThrPr 68
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
481 CATTTCATATATATAATAGTAATTAGATAGCTTTCCACAGTCCCTCC 530
68 oGluPro 70
|||
531 GGCACCT 537
```

seq_name: /cgnl_8/gcgdata/geneseq/geneseqn/NA1995.DAT:AAQ84378

seq_documentation_block:

ID AAQ84378 standard; DNA; 1695 BP.

AC AAQ84378;

DT 19-AUG-1995 (first entry)

DE Tomato yellow leaf curl virus DNA sequence.

```

XX XX Tomato yellow leaf curl virus; plant disease;
KM KM ribozyme target sequence; ds.
XX XX
OS OS Tomato yellow leaf curl virus (S).
XX XX
Key Location/Qualifiers
FH misc-feature 405
FT /tag= a
FT /note= "ribozyme cleavage site"
FT misc-feature 1065
FT /tag= b
FT /note= "ribozyme cleavage site"
FT misc-feature 1286
FT /tag= c
FT /note= "ribozyme cleavage site"
XX XX
PN W09503404-A.
XX XX
PD 02-FEB-1995.
XX XX
PF 22-JUL-1993; 93MO-EP01946.
XX XX
PR 22-JUL-1993; 93AU-0047014.
PR 22-JUL-1993; 93MO-EP01946.
XX XX
PA (BIOC-) BIOCEM SA.
PA (CSTR) COMMONWEALTH SCT & IND RES ORG.
XX XX
PI Baudino S, Comeau D, Dry IB, Gruber V, Lenee P;
PI Mason J, Rezaian MA, Rigden JE, Rezaian MA;
XX XX
DR WPI: 1995-075232/10.
XX XX
PT Synthetic DNA virus ribozyme(s) - reduce replication, infection
PT and/or assembly of viruses by cleaving target virus sequence,
PT useful for preparing resistant plants, esp tomatoes.
XX XX
PS Disclosure: Fig 8; 90pp; English.
XX XX
CC The sequence represents the complementary sense DNA strand of
CC tomato yellow leaf curl virus-S strain. Ribozyme cleavage sites
CC are indicated. Ribozymes against this sequence may be used in
CC generation of transgenic tomato plants with disease-resistance.
XX XX
SQ Sequence 1695 BP; 568 A; 366 C; 308 G; 453 T; 0 other;

alignment_scores:
Quality: 222.00 Length: 69
Ratio: 3.895 Gaps: 0
Percent Similarity: 82.609 Percent Identity: 57.971

alignment_block:
US-09-289-346A-4 x AA084378 ..
Align seg 1/1 to: AA084378 from: 1 to: 1695

2 LeuValTrpGlyIupheginValAspGlyArgSerAlaArgGlyIcy 18
||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
487 CTGGAATGGCGGTCTTCAGATCGACGACGATCTGCTAGGGAGGACCA 536
18 sginThrSerAspAlaAlaAlaGluAlaLeuAsnAlaSerSerIysG 35
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
537 ACAGACAGCCACGACGCTTACGCAAGGCAATTAAACGAGAAAGTAA 586
35 LuGluAlaLeuGlnIleIleAlaAlaAlaAlaIleProGlyIuTyLeuPhe 51
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
587 CGCAGCGCTCTGATGATTAATTAAGAATTACCGCTACAGATTACGTTCTA 636
52 GluPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspIysThrPr 68
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
637 CATTTCATATATATATAGTAATTAGATTAAGGTTTCCAGGTGCTCC 686

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68 oGluPro 70
| |||
687 GCGACCT 693

seq_name: /cgnl_8/gcgdata/geneseq/geneseqn/NA1997.DAT:AA93291
seq_documentation_block:
ID AA93291 standard; DNA; 1062 BP.
XX XX
AC AA93291;
XX XX
DT 27-APR-1998 (first entry)
XX XX
DE Bean golden mosaic geminivirus CI mutant ORF BGAC221.
XX XX
KW Geminivirus; BGWV; CI gene; transdominant mutation;
KM transgenic plant; disease resistance; ss; cyclic; circular.
XX XX
OS Bean golden mosaic virus type II isolate Guatemala.
XX XX
PN W09739110-A1.
XX XX
PD 23-OCT-1997.
XX XX
PF 15-APR-1997; 97MO-US06300.
XX XX
PR 16-APR-1996; 96US-0015517.
XX XX
PA (SEMI-) SEMINIS VEGETABLE SEEDS INC.
PA (MISC) WISCONSIN ALUMNI RES FOUND.
XX XX
PI Ahlquist PG, Hanson SF, Luu HF, Maxwell DP, Stout JT;
PI WPI: 1997-526447/48.
XX XX
DR P-PSDB; AAW34333.
XX XX
PT Transgenic plants expressing geminivirus AC1 and CI wild-type and
PT mutant genes - have increased resistance to geminivirus infection
PT e.g. tomato mottle virus, tomato yellow leaf curl virus or bean
PT golden mosaic geminivirus
XX XX
PS Claim 13; Page 107-109; 132pp; English.
XX XX
CC This DNA sequence comprises construct BGAC221 that codes for a
CC transdominant lethal mutant (see AAW34333) of the CI protein (see
CC AAW34338) of bean golden mosaic virus (BGWV). It was obtained by
CC Kunkel mutagenesis of the wild-type CI gene (see AAT93314). CI is
CC required for replication. The invention involves production of
CC transgenic plants containing DNA comprising geminivirus CI or AC1
CC wild-type or mutant sequences that negatively interfere in trans
CC with geminiviral replication during infection. Such transgenic
CC plants are resistant to viral infection. The AC1/CI genes are
CC especially from BGWV, tomato mottle virus or tomato yellow leaf
CC curl virus (see AAT93282-93) and encode polypeptides (see AAW34324-35)
CC that have mutations in the highly conserved DNA-nicking and/or the
CC MTP-binding domains.
XX XX
SQ Sequence 1062 BP; 339 A; 245 C; 219 G; 259 T; 0 other;

alignment_scores:
Quality: 219.00 Length: 70
Ratio: 3.776 Gaps: 0
Percent Similarity: 82.857 Percent Identity: 60.000

alignment_block:
US-09-289-346A-4 x AAT93291 ..
Align seg 1/1 to: AAT93291 from: 1 to: 1062

1 ThrLeuValTrpGlyIupheginValAspGlyArgSerAlaArgGlyI 17
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

```

328 ACAATCGAATGGGACAAATTCAGATCGACGGACGATCTGCAAGAGGAGG 377
17 YCysGlnThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerL 34
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
378 TCAGCACTGCGCAACGATCATATGCAAGGCAATTAAACGACGATTCAA 427
34 YsglGluAlaLeuGlnIleIleAlaAlaIleProGluLysTyrLeu 50
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
428 TTGAATCTGCTTGACAAATATTGAAGAGAACACACCGAAGATTACGTC 477
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
478 CTTCACATCATCAACATCCGTTCTTAATCTCGAACGATCTTCGTCANAAGT 527
67 rProGluPro 70
   :|||||
528 GCCGGAACCA 537

seq_name: /cgml_8/gcgdata/geneseq/geneseqn/NA1997.DAT:AA193292

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```

seq_documentation_block:
ID   AA193292 standard; DNA; 1062 BP.
XX
XX   AA193292;
AC   AA193292;
XX
XX   27-APR-1998 (first entry)
DT
XX
XX   Bean golden mosaic geminivirus C1 mutant ORF BGAC228.
DE
XX
XX   Geminivirus; BGMV; C1 gene; transdominant mutation;
KM   transgenic plant; disease resistance; ss: cyclic; circular.
XX
XX   Bean golden mosaic virus type II isolate Guatemala.
OS
XX
XX   WO9739110-A1.
PN
XX
XX   23-OCT-1997.
PD
XX
XX   15-APR-1997; 97WO-US06300.
PF
XX
XX   16-APR-1996; 96US-0015517.
PR
XX
XX   (SEMI-) SEMINIS VEGETABLE SEEDS INC.
PA   (WISC) WISCONSIN ALUMNI RES FOUND.
XX
XX   Ahlquist PG, Hanson SF, Luu HT, Maxwell DP, Stout JT;
PI
XX
XX   WPI: 1997-526447/48.
DR   P-PSDB: AAW34334.
XX
XX   Transgenic plants expressing geminivirus AC1 and C1 wild-type and
PT   mutant genes - have increased resistance to geminivirus infection
PT   e.g. tomato mottle virus, tomato yellow leaf curl virus or bean
PT   golden mosaic geminivirus
XX
XX   Claim 13; Page 111-112; 132pp; English.
XX
XX   This DNA sequence comprises construct BGAC228 that codes for a
CC   transdominant lethal mutant (see AAW34334) of the C1 protein (see
CC   AAW34338) of bean golden mosaic virus (BGMV). It was obtained by
CC   Kunze mutagenesis of the wild-type C1 gene (see AAT93314). C1 is
CC   required for replication. The invention involves production of
CC   transgenic plants containing DNA comprising geminivirus C1 or AC1
CC   wild-type or mutant sequences that negatively interfere in trans
CC   with geminiviral replication during infection. Such transgenic
CC   plants are resistant to viral infection. The AC1/C1 genes are
CC   especially from BGMV, tomato mottle virus or tomato yellow leaf
CC   curl virus (see AAT93282-93) and encode polypeptides (see AAW34324-35)
CC   that have mutations in the highly conserved DNA-nicking and/or the
CC   NTP-binding domains.
XX
XX   Sequence 1062 BP; 338 A; 247 C; 218 G; 259 T; 0 other;
CC

```

```

alignment_scores:
Quality: 219.00      Length: 70
Ratio: 3.776        Gaps: 0
Percent Similarity: 82.857  Percent Identity: 60.000

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alignment_block:
US-09-289-346A-4 x AA193292 ..

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Align seq 1/1 to: AA193292 from: 1 to: 1062

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1   ThrLeuValTrpGlyGluPheGlnValAspGlyValArgSerAlaArgLysL 17
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
328 ACAATCGAATGGGACAAATTCAGATCGACGGACGATCTGCAAGAGGAGG 377
17 YCysGlnThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerL 34
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
378 TCAGCACTGCGCAACGATCATATGCAAGGCAATTAAACGACGATTCAA 427
34 YsglGluAlaLeuGlnIleIleAlaAlaIleProGluLysTyrLeu 50
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
428 TTGAATCTGCTTGACAAATATTGAAGAGAACACACCGAAGATTACGTC 477
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
478 CTTCACATCATCAACATCCGTTCTTAATCTCGAACGATCTTCGTCANAAGT 527
67 rProGluPro 70
   :|||||
528 GCCGGAACCA 537

```

```

seq_name: /cgml_8/gcgdata/geneseq/geneseqn/NA1997.DAT:AA193293

```

```

seq_documentation_block:
ID   AA193293 standard; DNA; 1062 BP.
XX
XX   AA193293;
AC   AA193293;
XX
XX   27-APR-1998 (first entry)
DT
XX
XX   Bean golden mosaic geminivirus C1 mutant ORF BGAC262.
DE
XX
XX   Geminivirus; BGMV; C1 gene; transdominant mutation;
KM   transgenic plant; disease resistance; ss: cyclic; circular.
XX
XX   Bean golden mosaic virus type II isolate Guatemala.
OS
XX
XX   WO9739110-A1.
PN
XX
XX   23-OCT-1997.
PD
XX
XX   15-APR-1997; 97WO-US06300.
PF
XX
XX   16-APR-1996; 96US-0015517.
PR
XX
XX   (SEMI-) SEMINIS VEGETABLE SEEDS INC.
PA   (WISC) WISCONSIN ALUMNI RES FOUND.
XX
XX   Ahlquist PG, Hanson SF, Luu HT, Maxwell DP, Stout JT;
PI
XX
XX   WPI: 1997-526447/48.
DR   P-PSDB: AAW34335.
XX
XX   Transgenic plants expressing geminivirus AC1 and C1 wild-type and
PT   mutant genes - have increased resistance to geminivirus infection
PT   e.g. tomato mottle virus, tomato yellow leaf curl virus or bean
PT   golden mosaic geminivirus
XX
XX   Claim 13; Page 115-116; 132pp; English.
XX
XX   This DNA sequence comprises construct BGAC262 that codes for a
CC   transdominant lethal mutant (see AAW34335) of the C1 protein (see
CC   AAW34338) of bean golden mosaic virus (BGMV). It was obtained by

```



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KW transgenic plant; disease resistance; ss: cyclic; circular.
XX
OS Bean golden mosaic virus type II isolate Guatemala.
XX
FH Key Location/Qualifiers
FT CDS 1..1062
FT /tag= a
XX
PN MO9739110-A1.
XX
PD 23-OCT-1997.
XX
PF 15-APR-1997; 97WO-US06300.
XX
PR 16-APR-1996; 96US-0015517.
XX
PA (SEMT-) SEMINIS VEGETABLE SEEDS INC.
XX (WISC) WISCONSIN ALUMNI RES FOUND.
XX
PI Ahlquist PG, Hanson SF, Luu HT, Maxwell DP, Stout JT;
XX
DR WPI: 1997-526447/48.
DR P-PSDB: AAW34332.
XX
XX Transgenic plants expressing geminivirus AC1 and CI wild-type and
XX PT mutant genes - have increased resistance to geminivirus infection
XX PT e.g. tomato mottle virus, tomato yellow leaf curl virus or bean
XX PT golden mosaic geminivirus
XX
XX Claim 13; Page 103-105; 132pp; English.
XX
CC This DNA sequence comprises construct BGAC190 that codes for a
CC control mutant (see AAW34332) of the CI protein (see AAW34338) of bean
CC golden mosaic virus (BGWV). It was obtained by Kunkel mutagenesis
CC of the wild-type CI gene (see AAT93314). CI is required for
CC replication. The invention involves production of transgenic
CC plants containing DNA comprising geminivirus CI or AC1 wild-type or
CC mutant sequences that negatively interfere in trans with
CC geminivirus replication during infection. Such transgenic plants
CC are resistant to viral infection. The AC1/CI genes are especially
CC from BGWV, tomato mottle virus or tomato yellow leaf curl virus (see
CC AAT93282-93) and encode polypeptides (see AAW34324-35) that have
CC mutations in the highly conserved DNA-nicking and/or the NTP-binding
CC domains.
XX
SQ Sequence 1183 BP; 371 A; 277 C; 249 G; 286 T; 0 other:

```

```

alignment_scores:
    Quality: 219.00      Length: 70
    Ratio: 3.776        Gaps: 0
    Percent Similarity: 82.857    Percent Identity: 60.000

```

alignment_block:
US-09-289-346A-4 x AAT93290 ..

Align seg 1/1 to: AAT93290 from: 1 to: 1183

```

1  ThleuValTrpGlyGluPheGlnValAspGlyArgSerAlaArgGly 17
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
328 ACAATCGAATGGGACAAATTCGAAGTCGACGCGCATCTCGAAGACGAGG 377
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
17  YCYSGlThSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSer 34
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
378 TCAGCAGCTCTGCCAAGCATCTATTCGAAGGCACTTAACGCGACATTCAA 427
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
34  YSGlGluAlaLeuGlnIleIleAlaAlaAlaIleProGluLysTyrLeu 50
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
428 TTGAATCTGCTTGACAAATATTGAAGAGACACCGAAGGATTACGTC 477
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
51  PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgTlePheAspLysTh 67
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
478 CTTCACATCATCAACAATCGCTTCAATCTCGAAGCATCTTCGTCACAAAGT 527

```

```

67  rProGluPro 70
   :|||||||
528 GCCGGAGACCA 537
seq_name: /cgn1_8/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA94700
seq_documentation_block:
ID AAA94700 standard; DNA; 1651 BP.
XX
XX AAA94700;
XX
AC AAA94700;
XX
DF 15-JAN-2001 (first entry)
XX
DE PMRG 2288 35S-rep gene cassette.
XX
XX Geminivirus; DNA-A; geminivirus replication inhibitor; ac3 gene;
XX transgenic plant; antiviral; gene therapy; bean golden mosaic virus;
XX BGWV; alfalfa mosaic virus; AMV; cauliflower mosaic virus; CaMV; ds.
XX
XX Bean golden mosaic virus.
XX Cauliflower mosaic virus.
XX Alfalfa mosaic virus.
XX Synthetic.
XX
XX US6118048-A.
XX
XX 12-SEP-2000.
XX
XX 24-APR-1998; 98US-0065999.
XX
XX 25-APR-1997; 97US-0044925.
XX
XX (WISC) WISCONSIN ALUMNI RES FOUND.
XX
XX WPI: 2000-610861/58.
XX
XX Genetic construct comprising a mutant geminiviral rep gene, useful for
XX PT producing a plant resistant to geminiviral infection -
XX PT
XX Example; Column 15-16; 14pp; English.
XX
XX The present sequence is a 35S-rep gene cassette comprising the rep gene
XX of bean golden mosaic virus (BGWV)-GA cloned downstream of the CaMV
XX 35S promoter and an alfalfa mosaic virus (AMV) leader sequence. The
XX CC sequence was integrated into pSII-KS+ to produce a rep gene expression
XX CC vector. DNA-nicking domain mutations may be incorporated into rep gene
XX CC to produce a genetic construct that acts as a trans-dominant inhibitor
XX CC of geminiviral replication. When expressed in a plant cell, this
XX CC inhibitor is able to dramatically reduce replication of geminivirus.
XX CC Genetic constructs that include sequences containing a portion of the
XX CC ac3 gene in addition to the trans-dominant inhibitor exhibit increased
XX CC efficiency and broadened specificity of inhibition of geminiviral
XX CC replication. Geminiviruses are one of the greatest constraints on
XX CC production of important crops, including cassava, beans, cowpeas,
XX CC peppers, tomatoes and cotton. The effects of the virus can be overcome
XX CC by using the genetic construct.
XX
XX Sequence 1651 BP; 517 A; 393 C; 342 G; 399 T; 0 other:

```

```

alignment_scores:
    Quality: 219.00      Length: 70
    Ratio: 3.776        Gaps: 0
    Percent Similarity: 82.857    Percent Identity: 60.000

```

alignment_block:
US-09-289-346A-4 x AAA94700 ..

Align seg 1/1 to: AAA94700 from: 1 to: 1651

```

1  ThleuValTrpGlyGluPheGlnValAspGlyArgSerAlaArgGly 17
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

```

```

796 ACAATCGAATGGGACAAATTCAGTCAGCGACATCTCGAAGAGG 845
17 yCysGlnThrSerAsnAspAlaIaIaGluAlaLeuAsnAlaSerL 34
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
846 TCACGAGTCGCCAACAGCATCTATGCAAAAGCATTTAAACGACATTC 895
34 ySGlGluAlaLeuGlnIleIleAlaIaIaIaIleProGluLysTyrLeu 50
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
896 TTGAATCTGCCCTTGACAATATTGAAGACAGAACCCGAAGATTACGTC 945
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
946 CTTCAACATCATCAACAACATCCGTTTAATCTCGAACGATCTTCGCA 995
67 rProGluPro 70
   :|||||
996 GCCGGAACCA 1005

seq_name: /cgnl_8/gcgdata/geneseg/geneseqn/NA2000.DAT:AAA94701
seq_documentation_block:
ID   AAA94701 standard; DNA; 1651 BP.
XX
AC   AAA94701:
XX
DT   15-JAN-2001 (first entry)
XX
DE   pTrepN nucleotide sequence.
XX
KW   Geminivirus; DNA-A; geminivirus replication inhibition; ac3 gene;
KM   transgenic plant; antiviral; gene therapy; bean golden mosaic virus;
KM   BGWV; alfalfa mosaic virus; AMV; cauliflower mosaic virus; CaMV; ds.
XX
OS   Bean golden mosaic virus.
OS   Cauliflower mosaic virus.
OS   Alfalfa mosaic virus.
OS   Synthetic.
XX
PN   US6118048-A.
XX
PD   12-SEP-2000.
XX
PF   24-APR-1998: 9805-0065999.
XX
PR   25-APR-1997: 9705-0044925.
XX
PA   (WISC ) WISCONSIN ALUMNI RES FOUND.
XX
DR   MPI; 2000-610861/58.
XX
PT   Genetic construct comprising a mutant geminiviral rep gene, useful for
PT   producing a plant resistant to geminiviral infection -
XX
PS   Example: Column 17-18; 14pp: English.
XX
CC   The present sequence is pTrepN, a vector containing a CanV-35S
CC   promoter-driven rep gene derived from bean golden mosaic virus (BGWV)-GA.
CC   Site-directed mutagenesis was used to engineer an NcoI site in the start
CC   codon of the rep gene to facilitate cloning of DNA-nicking domain
CC   mutants. The resulting genetic constructs act as trans-dominant
CC   inhibitors of geminiviral replication. When expressed in a plant cell,
CC   these inhibitors are able to dramatically reduce replication of
CC   geminivirus. Genetic constructs that include sequences containing a
CC   portion of the ac3 gene in addition to the trans-dominant inhibitor
CC   exhibit increased efficiency and broadened specificity of inhibition of
CC   geminiviral replication. Geminiviruses are one of the greatest
CC   constraints on production of important crops, including cassava, beans,
CC   cowpeas, peppers, tomatoes and cotton. The effects of the virus can be
CC   overcome by using the genetic construct.
XX
SQ   Sequence 1651 BP; 517 A; 392 C; 343 G; 399 T; 0 other;

```

```

alignment_scores:
    Quality: 219.00      Length: 70
    Ratio: 3.776        Gaps: 0
    Percent Similarity: 82.857    Percent Identity: 60.000

alignment_block:
US-09-289-346A-4 x AAA94701  ..

Align seg 1/1 to: AAA94701 from: 1 to: 1651

1   ThrLeuValIrrpGlyGluPheGlnValAspGlyArgSeraIaArgIyl 17
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
796 ACAATCGAATGGGACAAATTCAGTCAGCGACATCTCGAAGAGG 845
17 yCysGlnThrSerAsnAspAlaIaIaGluAlaLeuAsnAlaSerL 34
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
846 TCACGAGTCGCCAACAGCATCTATGCAAAAGCATTTAAACGACATTC 895
34 ySGlGluAlaLeuGlnIleIleAlaIaIaIaIleProGluLysTyrLeu 50
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
896 TTGAATCTGCCCTTGACAATATTGAAGACAGAACCCGAAGATTACGTC 945
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
946 CTTCAACATCATCAACAACATCCGTTTAATCTCGAACGATCTTCGCA 995
67 rProGluPro 70
   :|||||
996 GCCGGAACCA 1005

```


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OM of: US-09-289-346a-4 to: EST:* out_format: pfs

Date: Jan 3, 2002 6:15 PM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

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-MODE=frame.p2n.model
-Q/cgml1/USFPro.spool/US09289346/runat_03012002_153303_16354/app-query.fasta_1.1163
-DB=EST -OFMT=fastap -SUFFIX=p2n.rst -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOPEXT=0.000 -LOOPEXT=0.500
-OCAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
-FCAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELDP=6.000
-DELEXT=7.000 -SPART=1 -MATRIX=bloms62 -TRANS=humand0.cdi
-LIST=45 -DOCLIN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0
-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
-MAJEN=2000000000 -USER=US09289346.qcgm1_1.6788 -NCPY=6
-ICPU=3 -LONGLOG -NO_XLPHY -WAIT -THREADS=1
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Search information block:

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Query: US-09-289-346a-4
Query length: 70
Database: EST:*
Database sequences: 11351937
Database length: 1077921985
Search time (sec): 8697.120000
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score list:

Sequence	strd Orig	ZScore	EScore	len	Documentation
gb_est2:H37423	-	73.50	163.56	6.03	513
gb_est1:AI959235	+	71.00	136.81	14.31	560
gb_est2:BG472333	+	71.00	136.81	21.38	789
gb_est2:BF030592	+	70.00	152.64	24.46	682
gb_est1:AA863354	+	69.50	152.72	12.74	343
gb_est1:AI731422	-	68.50	151.10	29.79	546
gb_gss:AO950848	-	68.00	149.49	36.64	572
gb_gss:AO947513	-	68.00	149.25	37.77	587
gb_gss:AO367423	+	68.00	144.58	46.81	705
gb_gss:AZ208697	+	67.50	144.06	73.51	910
gb_est1:AV744255	+	67.00	148.52	36.47	439
gb_est1:AV744255	+	67.00	148.08	43.86	514
gb_est1:AV737185	+	67.00	146.90	51.04	585
gb_est1:AV736532	+	67.00	146.89	51.14	586
gb_est1:AV741448	+	67.00	146.89	52.17	596
gb_est1:AV738839	+	67.00	146.45	54.12	615
gb_est2:BG024294	+	67.00	138.68	146.44	1439
gb_est1:BB574192	+	66.50	153.44	22.07	251
gb_est2:BF342302	+	66.50	144.81	66.77	646
gb_est2:BG595046	-	66.50	143.67	77.30	732
gb_est1:AV729475	+	66.00	149.81	35.17	328
gb_est1:AV741296	+	66.00	147.68	46.19	414
gb_gss:AO235923	-	66.00	145.56	60.60	522
gb_gss:AZ648984	-	66.00	143.67	77.21	642
gb_gss:CN50587	-	66.00	138.01	140.43	1070
gb_gss:AO233405	+	65.50	143.96	71.48	546
gb_est2:BI158930	+	65.50	140.33	118.58	813
gb_est1:AV701638	+	65.50	139.99	123.89	844
gb_est2:BF030456	+	65.50	137.56	169.13	1101
gb_est2:BG113570	+	65.50	137.23	176.53	1142
gb_est1:AI668333	+	64.50	143.25	81.53	455
gb_est1:AV739224	+	64.50	141.94	96.40	545
gb_gss:AO656777	-	64.50	140.15	106.16	570
gb_est2:BG595614	-	64.50	140.68	113.38	603
gb_gss:AZ972754	-	64.50	139.65	129.39	675
gb_est2:BG596652	-	64.50	139.05	139.77	721
gb_est2:BI406561	-	64.50	138.85	143.41	737
gb_est1:AV369952	+	64.00	148.86	33.69	216
gb_gss:AO908538	+	64.00	146.56	53.34	278
gb_est2:BF493366	+	64.00	146.24	55.59	288
gb_est1:AA133710	+	64.00	143.28	81.19	398

```
gb_gss:AZ967502 - 64.00 141.84 97.66 466 1 AZ967502 2M0238A03R Mouse 10
gb_est2:BG119947 - 64.00 137.55 169.43 716 1 BG119947 602352215F1 NIH.MGC
gb_est2:BG477162 - 64.00 137.30 174.77 766 1 BG477162 602524392F1 NIH.MGC
gb_gss:AZ296373 + 63.50 144.52 69.25 305 1 AZ296373 RFL1-23-108022.TJ R
```

seq_name: gb_est2:H37423

```
seq_documentation_block: 513 bp mRNA EST 30-DEC-1997
LOCUS H37423
DEFINITION 15552 Lambda-PRU2 Arabidopsis thaliana cDNA clone 181E577, mRNA
sequence.
ACCESSION H37423
VERSION H37423.1 GI:9069222
KEYWORDS EST.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1 (bases 1 to 513)

```

REFERENCE Newman,T., deBruin,J.F.J., Green,P., Keegstra,K., Kende,H., McIntosh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomashow,M., Retzel,E., and Somerville,C.

Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones Plant Physiol. 106, 1241-1255 (1994)

CONTACT: Thomas Newman

MSU-DOE Plant Research Laboratory

Michigan State University

MSU-DOE-PL, Michigan State University, Plant Biology Bldg., E. Lansing MI

Tel: 517-353-0854

Fax: 517-353-9168

Email: 22313cnc@lbm.cl.msu.edu

Seq primer: 77 dye primer.

Location/Qualifiers

1..513

/organism="Arabidopsis thaliana"

/strain="var Columbia"

/db_xref="taxon:3702"

/clone="181E577"

/note="Vector: lambda zip-lox; Site_1: Sal; Site_2: NotI;

lambda PRU2 is a cDNA library derived from equal

quantities of 4 pools of mRNA. The mRNA sources were 1) 7

day germinated etiolated seedlings; 2) tissue culture

grown roots; 3) staged plants half with 24 hour light

cycle, half on 16 hr light, 8 hour dark- rosettes; 4)

same plants as 3 but aerial tissue (stems, flowers and

siliques. The vector is BRU's lambda zip-lox. The cDNA

inserts were directionally cloned with Sal-NotI arms using

oligo dt primed cDNA. "

BASE COUNT 127 a 109 c 119 g 140 t 18 others

ORIGIN

alignment_scores:

Quality: 73.50 length: 57

Ratio: 1.885 Gaps: 1

Percent Similarity: 68.421 Percent Identity: 40.351

alignment_block:

US-09-289-346a-4 x H37423/rev ..

Align seg 1/1 to reverse of: H37423 from: 1 to: 513

12 ArgSerAlaArgGlyGlyCysGlnThrSerAsnAspAlaAlaGluAla 28

||||||| :||| ||||| ||||| :||| :||| :||| :|||

353 AGAAGTGCACCTAATAGCTCCAAAGTCCACGGGAGCTCAGCTCGGC 304

||||||| :||| ||||| ||||| :||| :||| :||| :|||

28 alauAsnAlaSerSerGlyGlnAlaLeuGlnIleIleAlaAlaAla 45

||||||| :||| ||||| ||||| :||| :||| :||| :|||

303 CTGAGACTGCTTACCTTGAAGACAGCAACATCTTCATTGCTCTTGTGA 254
 45 leprolulysrtyrleuphneglphehisasnlenuasnsersleuasp 61
 253 TCTTTGGACGTCTTACACATCTTCATGCGGTTACGACCATGAGTT 204

62 Arg1lePheAsp1yThrPro 68
 203 GAGATA...GATGCAACTCCA 186

seq_name: gb_est1:A1959235

seq_documentation_block:
 LOCUS A1959235 560 bp mRNA EST 20-AUG-1999
 DEFINITION f025909.y1 zebrafish Washu MPMG EST Danio rerio cDNA 5' similar to
 gb:X69150.405 RIBOSOMAL PROTEIN S18 (HUMAN); mRNA sequence.
 ACCESSION A1959235
 VERSION A1959235.1 GI:5751948
 KEYWORDS EST.
 SOURCE zebrafish.
 ORGANISM Danio rerio
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 Cypriniformes; Cyprinidae; Rasbortinae; Danio.
 1 (bases 1 to 560)
 Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy,
 S., Hillier,L., Knapa,T., Martin,D., Beck,C., Wylie,T., Underwood,
 K., Steppe,M., Theising,B., Allen,M., Bowers,Y., Person,B.,
 Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schur,R., Ritter,E.,
 Korn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R.
 and Wilson,R.
 Washu Zebrafish EST Project 1998
 Unpublished (1998)
 Contact: Stephen L. Johnson
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: zbrafish@wustl.edu
 CDNA Library Preparation: Matthew Clark, cDNA Library Arrayed by:
 Matthew Clark, DNA Sequencing by: Washington University Genome
 Sequencing Center Clone Distribution: Genome Systems, St. Louis,
 Missouri (web address: www.genomesystems.com) (email contact:
 info@genomesystems.com) and Research Genetics, Huntsville, Alabama
 (web address: www.resgen.com) (email contact: info@resgen.com) and
 Ressourcenzentrum Primatendatenbank, Berlin, Germany (web address:
 www.rzpd.de)
 Seq primer: T3 ET from Amersham
 High quality sequence stop: 491.
 Location/Qualifiers
 1..560
 /organism="Danio rerio"
 /db_xref="taxon:7955"
 /clone_lib="Zebrafish Washu MPMG EST"
 /sex="mixed"
 /tissue_type="26 somite embryos, adult livers, shield
 stage embryos"
 /lab_host="XLI-blue MRF"
 /note="Vector: pSPORT1; Site_1: NotI; Site_2: SalI; 1st
 strand cDNA was primed with a Not I - oligo(dT)15 primer
 (5' pGACTAGTTCAGATCGGACGCGCCGCTTTTCTTTTCTTTT3');
 double-stranded cDNA was ligated to Sal I adaptors (BRL),
 digested with Not I and cloned into the Not I and Sal I
 sites of the pSPORT1 vector (BRL). Library was constructed
 by Matthew Clark (Lehrach lab; ICRF, London and Max Planck
 Institut fuer Molekulare Genetik, Berlin). cDNAs for EST
 hybridization were selected following oligonucleotide
 hybridization fingerprinting of arrayed clones from
 zebrafish late somitogenesis (26 ss), adult liver or
 embryonic shield stage (5.6 h) libraries. Fingerprint
 data were used to computationally cluster cDNAs, and a
 single cDNA from each cluster was chosen for sequencing.
 In some cases multiple members of the same cluster were

sequenced to assess clustering parameters or single clones
 were sequenced additional times to assess quality
 control."

BASE COUNT 141 a 130 c 161 g 128 t
 ORIGIN

alignment_scores:
 Quality: 71.00 Length: 61
 Ratio: 1.919 Gaps: 2
 Percent Similarity: 60.656 Percent Identity: 29.508

alignment_block:
 US-09-289-346A-4 x A1959235 ..
 Align seg 1/1 to: A1959235 from: 1 to: 560

1 ThrLeuValTrpGlyGluPheGluValAspGlyArgSerAlaArgGlyG1 17
 ||||| |||||
 22 ACATGTGTCGTGGCGG.....GGGGGTGTCGGCGG 50
 17 ycygclntrhrSerAsnAspAlaAlaAlaGluAlaLeuAsnAlaSerG1 34
 ||||| |||||
 51 GTGTGACCCCTCCTCCACGCGCGCCGCCACGCGTCCGCGCGATC 100
 34 ysgclnluAlaLeuGlnIleIleAlaAlaAlaIleProGluTrpLeu 50
 ||||| |||||
 101 AACAT.....GTCTCTCTGTCATGTCGACAGAAAGTTTCAG 135
 51 PheGlnPheHisAsnLeuAsnSerAsnLeuAsp 61
 ||||| |||||
 136 CACATCTTCGTGTCCTCAACACGACGACATTGAT 168

seq_name: gb_est2:BG472323

seq_documentation_block:
 LOCUS BG472323 789 bp mRNA EST 21-MAR-2001
 DEFINITION 602513970F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:4645793 5',
 mRNA sequence.
 ACCESSION BG472323
 VERSION BG472323.1 GI:13404598
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 789)
 NIH-MGC http://mgc.ncl.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs@mail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Ling Hong/Rubin laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
 DNA sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LMNL at: image.lnl.gov
 Plate: L1CM1419 row: 1 column: 18
 High quality sequence stop: 745.
 Location/Qualifiers
 1..789
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="IMAGE:4645793"
 /clone_lib="NIH_MGC_16"
 /tissue_type="retinoblastoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2:
 EcoRI; cDNA made by oligo-dT priming. Directionality
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCAAGAG(G). Library constructed by Ling Hong
 in the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

BASE COUNT 162 a 265 c 211 g 151 t
ORIGIN

alignment_scores:
Quality: 71.00 Length: 78
Ratio: 1.578 Gaps: 2
Percent Similarity: 57.692 Percent Identity: 28.205

alignment_block:
US-09-289-346A-4 x BG472323 ..

Align seg 1/1 to: BG472323 from: 1 to: 789

```

1 ThleValTrpGlyGluPheGlnValAspGlyArgSerAlaArgGly1 17
||||| ||||||| ||||| ||||| ||||| ||||| ||||| |||||
480 ACCTTCACACGGGGGAGACCCGGAATTGACCCGACGGCTCTAGGCACG 529
17 yCysGlnThrSerAsnAspAlaAlaAlaGluAlaLeuAsn..... 30
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
530 ACCGTACAGCGACACACTTCGCCGCCGACGCTTCACATTGTCATT 579
31 .....AlaSerSerlySGluGlu 36
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
580 ATAACACAGACCTTATCTCGACGCCACGACCTCCAGACAGTCAGAA 629
37 AlaleGlnIleIleAlaAlaIleProGluIuIuIuIuIuIuIuIuIu 53
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
630 GGCCTCGCTCTCTGCTGCTTT.....CTCATGTAGAT 661
53 eHisAsnLeuAsnSerAsnLeuAspArgIlePhe 64
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
662 GGGCTCTTCATTCGTCCTATGACAGATCTTC 695

```

seq_name: gb_est2.BF030592

seq_documentation_block:

LOCUS BF030592 682 bp mRNA EST 10-OCT-2000
DEFINITION 60155952F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3829669 5',
mRNA sequence.

ACCESSION BF030592.1 GI:10738304

VERSION BF030592.1
KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

1 (bases 1 to 682)

REFERENCE NIH-MGC http://mgc.nci.nih.gov/.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE Unpublished (1999)

JOURNAL Contact: Robert Strausberg, Ph.D.

COMMENT Email: cgapbs@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: CLONTECH Laboratories, Inc.

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LICM502 row: 9 column: 14

High quality sequence stop: 630.

Location/Qualifiers

FEATURES

source

1..682
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3829669"
/clone_lib="NIH_MGC_58"
/tissue_type="hypernephroma"
/lab_host="DH10B (T1 phage-resistant)"

/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site.1:
SfiI (9ggccctcggcc); Site.2: SfiI (9ggccataggcc).
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCCATTATGACC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGGCCGCGGCGCCGACATG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.35 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."

BASE COUNT 183 a 154 c 166 g 179 t
ORIGIN

alignment_scores:
Quality: 70.00 Length: 51
Ratio: 2.059 Gaps: 2
Percent Similarity: 66.667 Percent Identity: 39.216

alignment_block:
US-09-289-346A-4 x BF030592 ..

Align seg 1/1 to: BF030592 from: 1 to: 682

```

23 ASPAlaAlaAlaGluAlaLeuAsnAlaSerSerlySGluGluAlaLeuG1 39
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
394 GATGCGGACTGATGACGAAGATGATTCGTGAATGTAAGCCCTCAG 443
39 nIleIleAlaAlaIleProGluIuIuIuIuIuIuIuIuIuIuIuIu 56
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
444 GCACATCTTCTGCGCTTTCAACAG.....TTCCGATTCAATCACC 484
56 euAsnSerAsnLeuAspArgIlePhe.....AspIuThrProGlu 69
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
485 TCGTGACTTCATCAGCGCTTATGATTTGACTGATGATTCACAGAT 534
70 Pro 70
|||
535 CCA 537

```

seq_name: gb_est1.AA863354

seq_documentation_block:

LOCUS AA863354 343 bp mRNA EST 13-MAY-1998
DEFINITION oh04e07.s1 NCI-CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1456836 3',
mRNA sequence.

ACCESSION AA863354.1 GI:2955833

VERSION AA863354.1
KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

1 (bases 1 to 343)

REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

TITLE Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

DNA Sequencing by: Greg Lennon, Ph.D.

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov/dbtrp/image/image.html

Insert length: 761 Std Error: 0.00

Seq primer: -40m13 fwd. ET from Amersham

High quality sequence stop: 328.

Location/Qualifiers

FEATURES

```

source
1. .343
/organism="Homo sapiens"
/db.xref="taxon:9606"
/clone="IMAGE:1456836"
/clone_lib="NCI_CGAP_K1d3"
/lab.host="DH10B"
/note="Organ: kidney; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer,
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pT73 vector. mRNA
source: 2 pooled kidneys. Library went through one round
of normalization. Library constructed by Bento Soares and
M. Fatima Bonaldo."

BASE COUNT      98 a      90 c      102 g      53 t
ORIGIN

alignment_scores:
Quality: 69.50      Length: 64
Ratio: 1.782      Gaps: 3
Percent Similarity: 60.938      Percent Identity: 37.500

alignment_block:
US-09-289-346a-4 x AA863354 ..

Align seg 1/1 to: AA863354 from: 1 to: 343

3 ValTRP..GlyGIuPheGlnVal.....AspGlyArgSerAlaIaR 15
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
43 GTGTGACGGCTCAATGCAATGCTCCCGAGAGACCCAGATCCGCTAC 92
15 GGIuGlyCysGlnThrSerAsnAspAlaIaIaGluAlaLeuAsnIaIa 32
||| ..... ||||| ||||| ||||| ||||| ||||| |||||
93 AGGACGGAGAGACGTGAAATGAAGCAAAAGTACCCGACTG..... 135
32 eSerLySGluGluAlaLeuGlnIleIleAlaIaIaIeProGluLys 48
||||| :: ||||| :: ||||| :: ||||| :: ||||| :: |||||
136 .....GAGGAGAGAGTGTTCATCACCACCAAGAGCGTCTCCAGG 177
49 TyrLeuPheGlnPheHisAsnLeuAsnSerAsnLeuAspArg 62
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
178 TACCGAGCTCGAGAGCACTGCTGCACCCCAAGCTGCAGAGA 219

seq_name: gb_est1:AT731422

seq_documentation_block:
LOCUS AT731422 546 bp mRNA EST 11-JUN-1999
DEFINITION BNLGH19563 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar
to mitochondrial processing peptidase (EC 3.4.99.41) alpha-II chain
precursor - potato g11587562 (X80236) mitochondrial processing
peptidase [Solanum tuberosum], mRNA sequence.
ACCESSION AT731422 GI:5050274
VERSION AT731422.1
KEYWORDS EST.
SOURCE upland cotton.
ORGANISM Gossypium hirsutum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eustosids II; Malvales; Malvaceae; Gossypium.
1 (bases 1 to 546)
Blewitt,M., Matz,E.C., Davy,D.F. and Burr,B.
ESTs from developing cotton fiber
unpublished (1999)
Contact: Ben Burr
Biology Department
Brookhaven National Laboratory
Upton, NY 11973, USA
Tel: 516-344-3396
Fax: 516-344-3407
Email: burrb@bnl.gov
Seq primer: T3 Primer.

```

```

FEATURES
source
1. .546
/organism="Gossypium hirsutum"
/cultivar="Acala Maxxa"
/db.xref="taxon:3635"
/clone_lib="Six-day Cotton fiber"
/tissue_type="Immature fiber"
/dev_stage="Six days post anthesis"
/lab.host="XLI-Blue"
/note="Vector: pBluescript II KS+"

BASE COUNT      151 a      99 c      134 g      160 t
ORIGIN

alignment_scores:
Quality: 68.50      Length: 60
Ratio: 1.671      Gaps: 1
Percent Similarity: 68.333      Percent Identity: 33.333

alignment_block:
US-09-289-346a-4 x AT731422/rev ..

Align seg 1/1 to reverse of: AT731422 from: 1 to: 546

11 GlyArgSerAlaArgGlyCysGlnThrSerAsnAspAlaIaIa.. 26
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
469 GGAAGATCTGACAGAACTGCTTCGACAGATACATATCTTCATGTTT 420
27 .GluAlaLeuAsnAlaSerSerLySGluGluAlaLeuGlnIleIleAla 43
:: ||||| :: ||||| :: ||||| :: ||||| :: ||||| :: |||||
419 TACACCGATGCTGCCGATCCGAGAGACAGATVMAAATTTTTCGAA 370
43 IaAlaIeProGluLysTyrLeuPheGlnPheHisAsnLeuAsnSerAsn 59
:: ||||| :: ||||| :: ||||| :: ||||| :: ||||| :: |||||
369 CAATATCTCCAAACTGACTGTTCAACATATTAATCTGCAGATTCTGGG 320
60 LeuAspArgIlePheAspLysThrProGlu 69
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
319 GCTAAAGAGCATTTGCCATGCACCGAGAA 290

seq_name: gb_gss:AQ950848

seq_documentation_block:
LOCUS AQ950848 572 bp DNA GSS 27-JAN-2000
DEFINITION Sheared DNA-51M3.TF Sheared DNA Trypanosoma brucei genomic clone
Sheared DNA-51M3, DNA sequence.
ACCESSION AQ950848 GI:6774113
VERSION AQ950848.1
KEYWORDS GSS.
SOURCE Trypanosoma brucei.
ORGANISM Trypanosoma brucei
Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 572)
El-Sayed,N., Zhao,H., Gill,S., Suh,E., Malek,J., Fujii,C.,
Gerrard,C., Leech,V., de Jong,P., Ullu,E., Melville,S., Donelson,J.,
Fraser,C. and Adams,M.
Determination of clone end sequences from Trypanosoma brucei GUTat
10.1 Sheared DNA Library
Unpublished (1999)
Other_GSSs: Sheared DNA-51M3.TF
Contact: Najib M. El-Sayed
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: nelsayed@igf.org
Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared
DNA library constructed at TIGR. Clones will be available for
distribution through ATCC. Sheared DNA end sequences search page:
http://www.tigr.org/tldb/mdb/tldb/.
Seq primer: M13-forward

```



```

DEFINITION AV742525 CB Homo sapiens cDNA clone CBMAUC12 5', mRNA sequence.
ACCESSION AV742525
VERSION AV742525.1 GI:10860106
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 439)
AUTHORS Zhang,Q., Ye,M., Wu,X., Gu,J., Huang,Q., Zhou,J., Shen,Y., Han,Z.,
Chen,S., Mao,M. and Chen,Z.
TITLE Homo sapiens CB library cDNA clones
JOURNAL Unpublished (2000)
COMMENT Contact: Zhu Chen
Shanghai Institute of Hematology, Rui-Jin Hospital
197 Rui-Jin II Road, Shanghai 200025, P. R. China
Tel: 86-21-64740490
Fax: 86-21-64743206
Email: mshhems.stn.sh.cn
This clone is available at Shanghai Hematology Institute in
Shanghai.
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong.
LOCATION/Qualifiers
1..439
FEATURES
source
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CBMAUC12"
/clone_lib="CB"
/tissue_type="cord blood"
/cell_type="CD34+ hematopoietic stem/progenitor cell"
/lab_host="BM25.8"
/note="Vector: pBluescript: Ste1: EcoRI: The insert is
cloned randomly with the EcoRI digestion"
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DEFINITION AV744255 CB Homo sapiens cDNA clone CBMAJD03 5', mRNA sequence.
ACCESSION AV744255
VERSION AV744255.1 GI:10861836
KEYWORDS EST.
SOURCE human.

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 514)
AUTHORS Zhang,Q., Ye,M., Wu,X., Gu,J., Huang,Q., Zhou,J., Shen,Y., Han,Z.,
Chen,S., Mao,M. and Chen,Z.
TITLE Homo sapiens CB library cDNA clones
JOURNAL Unpublished (2000)
COMMENT Contact: Zhu Chen
Shanghai Institute of Hematology, Rui-Jin Hospital
197 Rui-Jin II Road, Shanghai 200025, P. R. China
Tel: 86-21-64740490
Fax: 86-21-64743206
Email: mshhems.stn.sh.cn
This clone is available at Shanghai Hematology Institute in
Shanghai.
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong.
LOCATION/Qualifiers
1..514
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LOCUS AV737185 585 bp mRNA EST 17-OCT-2000
DEFINITION AV737185 CB Homo sapiens cDNA clone CBMARG03 5', mRNA sequence.
ACCESSION AV737185
VERSION AV737185.1 GI:10854766
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 585)
AUTHORS Zhang,Q., Ye,M., Wu,X., Gu,J., Huang,Q., Zhou,J., Shen,Y., Han,Z.,

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Shanghai.
 Chinese National Human Genome Center at Shanghai
 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong.
 Location/Qualifiers
 1. .596

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 Ratio: 1.811 Gaps: 2
 Percent Similarity: 69.811 Percent Identity: 32.075

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Date: Jan 3, 2002 3:37 PM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 CompuGen Ltd.

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Search information block:

Query: US-09-289-346a-4
Query length: 70
Database: Issued_Patents_NA.*
Database sequences: 351203
Search time (sec): 264.020000

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Patent No. 6291743
GENERAL INFORMATION:
APPLICANT: Scout, John T
APPLICANT: Liu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminalivirus
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rockey, Milanow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 2744 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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ORIGIN: India
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: APPLICANT: GROENBORN, Bruno
: TITLE OF INVENTION: PHOTOPHOTGENIC DNA VIRUS RESISTANT TO
: TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS
: NUMBER OF SEQUENCES: 17
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: YOUNG & THOMPSON
: STREET: 745 South 23rd Street
: CITY: Arlington
: STATE: Virginia
: COUNTRY: U.S.A.
: ZIP: 22202
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
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: APPLICATION NUMBER: US/08/809,103B
: FILING DATE: 17-MAR-1997
: CLASSIFICATION: 800
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: FR 94,11040
: FILING DATE: 15-SEP-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: WO PCT/FR95/01192
: FILING DATE: 15-SEP-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: PATCH, Andrew J.
: REGISTRATION NUMBER: 32,925
: REFERENCE/DOCKET NUMBER: US944L CNR TOM
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (703) 521-2297
: TELEFAX: (703) 685-0573
: TELEX: 248425 EMBON
: INFORMATION FOR SEQ ID NO: 7:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1145 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..1077
: US-08-809-103B-7

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: APPLICANT: GRONNBORN, Bruno
: TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
: TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
: NUMBER OF SEQUENCES: 17
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: YOUNG & THOMPSON
: STREET: 745 South 23rd Street
: CITY: Arlington
: STATE: Virginia
: COUNTRY: U.S.A.
: ZIP: 22202
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentln Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/809,103B
: FILING DATE: 17-MAR-1997
: CLASSIFICATION: 800
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: FR 94.11040
: FILING DATE: 15-SEP-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: WO PCT/FR95/01192
: FILING DATE: 15-SEP-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: PATCH, Andrew J.
: REGISTRATION NUMBER: 32,925
: REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (703) 521-2297
: TELEFAX: (703) 685-0573
: TELEX: 248425 EMBON
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1148 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..1077
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 Percent Similarity: 82.609 Percent Identity: 57.971

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35 LuGluAlaLeuGlnIleIleAlaAlaAlaIleProGluIysTyrLeuPhe 51
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431 CGCAGGCTCTTGATGTAATTAAGAATTACCGCTAGAGATTACGTTCTA 480
52 GlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspIysThrPr 68
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
481 CATTTTCATATATATAATAGTAATTAGATAGGTTTCCAGGTGCTCC 530
68 oGluPro 70
| |||
531 GGCACCT 537

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seq_name: /cgnl_7/plodata/1/lna/6A_COMB.seq:US-08-809-103B-3

seq_documentation_block:

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; Sequence 3, Application US/08809103B
; Patent No. 6133505
;
; GENERAL INFORMATION:
; APPLICANT: GRONENBORN, Bruno
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,103B
; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94.11040
; FILING DATE: 15-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR95/01192
; FILING DATE: 15-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 695-0573
; TELEX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1150 base pairs

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; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1077
; US-08-809-103B-3

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alignment_scores: Quality: 222.00 Length: 69
 Ratio: 3.895 Gaps: 0
 Percent Similarity: 82.609 Percent Identity: 57.971

alignment_block:

US-09-289-346A-4 x US-08-809-103B-3 ..

Align seg 1/1 to: US-08-809-103B-3 from: 1 to: 1150

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2 LeuValTTPGLyGluPhgInValAspGlyArgSerAlaArgGlyGlyC 18
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
331 CTGAAATGGGGTACTTCCAGATCGACGAGATCTGCTAGGGAGGACA 380
18 sGlnThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerIysG 35
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
381 ACAGACAGCCCAACGACGCTTACGCAAGCAATTAACGACGAGTAAGT 430
35 LuGluAlaLeuGlnIleIleAlaAlaAlaIleProGluIysTyrLeuPhe 51
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
431 CGCAGGCTCTTGATGTAATTAAGAATTACCGCTAGAGATTACGTTCTA 480
52 GlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspIysThrPr 68
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
481 CATTTTCATATATATAATAGTAATTAGATAGGTTTCCAGGTGCTCC 530
68 oGluPro 70
| |||
531 GGCACCT 537

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seq_name: /cgnl_7/plodata/1/lna/6A_COMB.seq:US-08-809-103B-5

seq_documentation_block:

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; Sequence 5, Application US/08809103B
; Patent No. 6133505
;
; GENERAL INFORMATION:
; APPLICANT: GRONENBORN, Bruno
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,103B
; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94.11040
; FILING DATE: 15-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR95/01192
; FILING DATE: 15-SEP-1995
; ATTORNEY/AGENT INFORMATION:

```

```

NAME: PATCH, Andrew J.
REGISTRATION NUMBER: 32,925
REFERENCE/DOCKET NUMBER: US894AL CNR TOM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 521-2297
TELEFAX: (703) 685-0573
TELEX: 248425 EMBON
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 1150 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1077
US-08-809-103B-5

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alignment_scores:
Quality: 222.00      Length: 69
Ratio: 3.895        Gaps: 0
Percent Similarity: 82.609      Percent Identity: 57.971

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alignment_block:

US-09-289-346A-4 x US-08-809-103B-5 ..

Align seg 1/1 to: US-08-809-103B-5 from: 1 to: 1150

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2 LeuValTrpGlyGluPheGlnValAspGlyArgSerAlaArgGlyGly 18
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
331 CTGAATGGGCTTCCACATCGACGACGACATCTGCTAGGAGGACCA 380
18 SGIrThSerAsnSpAlaAlaGluAlaLeuAsnAlaSerIysG 35
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
381 ACACAGCCACGACGCTTACGCAAGCAATTACGCAAGAGTAAGT 430
35 LuGluAlaLeuGlnIleIleAlaAlaIleProGluLysTyrLeuPhe 51
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
431 CGCAGGCTCTGATGATTAATTAAGCAATTACGCGCTAGAGATTGCTTA 480
52 GlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTrpPr 68
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
481 CATTTTCATATATATAATAGTAATTGATTAAGTTTCCAGTGCCCTCC 530
68 OGluPro 70
1 |||
531 GCGACCT 537

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seq_name: /cgnl_7/ptodata/1/lna/6B_COMB.seq:US-08-838-151A-48

seq_documentation_block:

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; Sequence 48, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahnquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Gemnivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rockey, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 1062 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bean Golden Mosaic Gemnivirus
STRAIN: Type II
INDIVIDUAL ISOLATE: Guatemala
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1059
US-08-838-151A-48

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alignment_scores:
Quality: 219.00      Length: 70
Ratio: 3.776        Gaps: 0
Percent Similarity: 82.857      Percent Identity: 60.000

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alignment_block:

US-09-289-346A-4 x US-08-838-151A-48 ..

Align seg 1/1 to: US-08-838-151A-48 from: 1 to: 1062

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1 ThrLeuValTrpGlyGluPheGlnValAspGlyArgSerAlaArgGly 17
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
328 ACATTCGACATGGGACCAATTCCAAAGTCGACGCGAGATCTGCAAGAGG 377
17 YcysGlnThrSerAsnSpAlaAlaGluAlaLeuAsnAlaSerIerL 34
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
378 TCACGAGCTGCGCAACGACATCATATGCAAGCAATTAAACGACGATTCAA 427
34 yscGluAlaLeuGlnIleIleAlaAlaIleProGluLysTyrLeu 50
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
428 TTGAATCTGCTTGACATATATTGAAGAGAACCAAGCAAGATTCATGTC 477
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTrp 67
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
478 CTTCACATCATCACACATCCGTTTAATCTCGAACGATCTTCGCAAGT 527
67 rProGluPro 70
1 |||||
528 GCGCGAACCA 537

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seq_name: /cgnl_7/ptodata/1/lna/6B_COMB.seq:US-08-838-151A-51

seq_documentation_block:

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; Sequence 51, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahnquist, Paul

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APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminiivirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESSES:
ADDRESS: Dressler, Rocky, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 1062 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bean Golden Mosaic Geminiivirus
STRAIN: Type II
INDIVIDUAL ISOLATE: Guatemala
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1059
US-08-838-151A-51

alignment_scores:
Quality: 219.00 Length: 70
Ratio: 3.776 Gaps: 0
Percent Similarity: 82.857 Percent Identity: 60.000

alignment_block:
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Align seg 1/1 to: US-08-838-151A-51 from: 1 to: 1062

1 ThleuValTrpGlyGluPheGlnValAspGlyArgSerAlaArgGlyG1 17
|||||
328 ACAATCGAATGGGAGCAATTCTCAAGTCGACGCGCATCTGCAAGAGGAGG 377
17 YCYGlnThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerL 34
|||||
378 TCAGCACTGCGCCAGACGATCATATGCAAGGCAATTAAAGCGCATTCOA 427
34 yselGuaAlaLeuGlnIleIleAlaAlaAlaIleProGluLysTyrLeu 50
|||||
428 TTGAATCTGCTTGACATATTTGAAGAGAGAACCAAGCAAGATTAGTC 477
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
|||||
478 CTTCAACATCATCAACATCGTTCTTAATCTCGAACGATCTTCGTCAAAGT 527
67 rProGluPro 70

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528 GCCGAGACCA 537
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seq_name: /cgnl7/ptodata/1/lna/6B.COMB.seq:US-08-838-151A-54
seq_documentation_block:
: Sequence 54, Application US/08838151A
: Patent No. 6291743
: GENERAL INFORMATION:
: APPLICANT: Stout, John T
: APPLICANT: Luu, Hang T
: APPLICANT: Maxwell, Douglas
: APPLICANT: Ahlquist, Paul
: APPLICANT: Hanson, Steve
: TITLE OF INVENTION: Transgenic Plants Expressing Geminiivirus
: TITLE OF INVENTION: Genes
: NUMBER OF SEQUENCES: 63
: CORRESPONDENCE ADDRESSES:
: ADDRESS: Dressler, Rocky, Milnamow & Katz
: STREET: Two Prudential Plaza, Suite 4700
: CITY: Chicago
: STATE: Illinois
: COUNTRY: U.S.A.
: ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 1062 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bean Golden Mosaic Geminiivirus
STRAIN: Type II
INDIVIDUAL ISOLATE: Guatemala
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1059
US-08-838-151A-54

alignment_scores:
Quality: 219.00 Length: 70
Ratio: 3.776 Gaps: 0
Percent Similarity: 82.857 Percent Identity: 60.000

alignment_block:
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Align seg 1/1 to: US-08-838-151A-54 from: 1 to: 1062

1 ThleuValTrpGlyGluPheGlnValAspGlyArgSerAlaArgGlyG1 17
|||||
328 ACAATCGAATGGGAGCAATTCTCAAGTCGACGCGCATCTGCAAGAGGAGG 377

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seq_name: /cgnl_7/ptodata/1/ina/6B_COMB.seq:US-08-838-151A-43
seq_documentation_block:
Sequence 43, Application US/08838151A
Patent No. 6291743
GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Gemnivirus
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSER: Dressler, Rockey, Milanow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS380JP0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 1183 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bean Golden Mosaic Gemnivirus
STRAIN: Type II Isolates
INDIVIDUAL ISOLATE: Guatemala
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1059
PUBLICATION INFORMATION:
AUTHORS: Faria, JC
AUTHORS: Gilbertson, RL
AUTHORS: Hanson, SF

17 ycgsglnthrSerAsnAspAlaIleValLeuAsnAlaSerLys 34
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
378 TCAGCACTGTGCCACGACTCATATGCACAAGCCATTAAACCAGTTTCAA 427
34 ysglgluaIaleugInlleIleIAlaIAlaIAleProGlulysTryLeu 50
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
428 TTGAATCTTCCTTGACATATTGACAGAAGAACCAACCGAAGATTACTCTC 477
51 pHeGLnPhelHisAnLeuAsnSerAsnLeuASPARgIIepheAsplystH 67
::: ||||| :::::::::::::::::::: ||||| :::::::::::::::::::: |||||
478 CTTCACATCATCACACATCCGTTCTTAATCTCGACGGATCTTCGTCANAAGT 527
67 rProGUlPro 70
: |||||||
528 GCCGGAACCA 537

seq_name: /cgnl_7/ptodata/1/ina/6B_COMB.seq:US-08-838-151A-43
seq_documentation_block:
Sequence 43, Application US/08838151A
Patent No. 6291743
GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Gemnivirus
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSER: Dressler, Rockey, Milanow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 1183 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bean Golden Mosaic Geminivirus
STRAIN: Type II
INDIVIDUAL ISOLATE: Guatemala
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1059
US-08-838-151A-45
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alignment_scores:
Quality: 219.00 Length: 70
Ratio: 3.776 Gaps: 0
Percent Similarity: 82.857 Percent Identity: 60.000
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alignment_block:
US-09-289-346A-4 x US-08-838-151A-45 ..
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Align seq 1/1 to: US-08-838-151A-45 from: 1 to: 1183
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1 ThrLeuValTrpGlyGluPheGlnValAspGlyArgSerAlaArgGly1 17
|||||
328 ACATTCGAATGGGGACAATTCGAAGTCACGCGCATCTGCAAGAGGAGG 377
17 yCysGlnThSerAsnSpAlaAlaGluAlaLeuAsnAlaSerL 34
|||||
378 TCACAGCTGCGCACAGCATCATATGCAAGAGGCAATTAACCGCAGATTCAA 427
34 ysgLgUAlaLeuGlnlleleAlaAlaAlaIleProGluLysTyrLeu 50
|||||
428 TTGAATCTGCTTGACAATATTTGAAGAGAGAACGAAAGATTAGTCTC 477
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLys7th 67
|||||
478 CTTCACATCATCAACACATCCGTTCTAATCTCGAACGATCTTCGTAAGT 527
67 rProGluPro 70
|||||
528 GCCGGAAACCA 537
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seq_name: /cgnl_7/ptodata/1/lna/6A_COMB.seq:US-09-065-999-5
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seq_documentation_block:
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; Sequence 5, Application US/09065999
; Patent No. 6118048
; GENERAL INFORMATION:
; APPLICANT: Hanson, Stephen F.
; APPLICANT: Maxwell, Douglas P.
; TITLE OF INVENTION: TRANS-DOMINANT INHIBITION OF GEMINIVIRAL
; TITLE OF INVENTION: DNA REPLICATION BY GEMINIVIRUS REP GENE MUTANTS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Quarles & Brady
; STREET: One South Pinckney Street
```

```
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/065,999
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 960296,94754
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-9166
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1651 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-065-999-5
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alignment_scores:
Quality: 219.00 Length: 70
Ratio: 3.776 Gaps: 0
Percent Similarity: 82.857 Percent Identity: 60.000
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alignment_block:
US-09-289-346A-4 x US-09-065-999-5 ..
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Align seq 1/1 to: US-09-065-999-5 from: 1 to: 1651
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1 ThrLeuValTrpGlyGluPheGlnValAspGlyArgSerAlaArgGly1 17
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796 ACATTCGAATGGGGACAATTCGAAGTCACGCGCATCTGCAAGAGGAGG 845
17 yCysGlnThSerAsnSpAlaAlaGluAlaLeuAsnAlaSerL 34
|||||
846 TCACAGCTGCGCACAGCATCATATGCAAGAGGCAATTAACCGCAGATTCAA 895
34 ysgLgUAlaLeuGlnlleleAlaAlaAlaIleProGluLysTyrLeu 50
|||||
896 TTGAATCTGCTTGACAATATTTGAAGAGAGAACGAAAGATTAGTCTC 945
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLys7th 67
|||||
946 CTTCACATCATCAACACATCCGTTCTAATCTCGAACGATCTTCGTAAGT 995
67 rProGluPro 70
|||||
996 GCCGGAAACCA 1005
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seq_name: /cgnl_7/ptodata/1/lna/6A_COMB.seq:US-09-065-999-6
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seq_documentation_block:
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; Sequence 6, Application US/09065999
; Patent No. 6118048
; GENERAL INFORMATION:
; APPLICANT: Hanson, Stephen F.
; APPLICANT: Maxwell, Douglas P.
; TITLE OF INVENTION: TRANS-DOMINANT INHIBITION OF GEMINIVIRAL
; TITLE OF INVENTION: DNA REPLICATION BY GEMINIVIRUS REP GENE MUTANTS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Quarles & Brady
```

```
STREET: One South Pinckney Street
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/065,999
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 960296, 94754
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ. ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1651 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-065-999-6
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alignment_scores:
  Quality: 219.00      Length: 70
  Ratio: 3.776        Gaps: 0
Percent Similarity: 82.857  Percent Identity: 60.000
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alignment_block:
US-09-289-346A-4 x US-09-065-999-6 ..
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Align seg 1/1 to: US-09-065-999-6 from: 1 to: 1651
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1 ThrleuValTrrpGlyGluPheGlnValAspGlyArgSerAlaArgGlyL 17
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796 ACAATCGAATGGGACAAATTCGAAGTCGACGCGAGATCTGCAAGAGGAG 845
17 YCysGlnThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerL 34
  |||:| | | | | | | | | | | | | | | | | | | | | | | | |
846 TCACGACGCTCCCAACGACTCATATGCAAAAGCATTAACCGACGATTC 895
34 YsGluGluAlaLeuGlnIleIleAlaAlaAlaIleProGluLysTyrLeu 50
  |||:| | | | | | | | | | | | | | | | | | | | | | | | |
896 TTGAATCTGCTTGACAAATATGGAAGAGAACACCAAGATTACGTC 945
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
  |||:| | | | | | | | | | | | | | | | | | | | | | | | |
946 CTTCAACATCAACACATCCGTTTAATCTCGAACGAGATCTTCGTCAG 995
67 rProGluPro 70
  |||:| | | | | | | | | | | | | | | | | | | | | | | | |
996 GCCGGAACCA 1005
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seq_name: /cgnl_7/ptodata/1/lna/6A_COMB.seq:US-09-065-999-8
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seq_documentation_block:
; Sequence 8, Application US/09065999
; Patent No. 6118048
; GENERAL INFORMATION:
; APPLICANT: Hanson, Stephen F.
; APPLICANT: Maxwell, Douglas P.
; TITLE OF INVENTION: TRANS-DOMINANT INHIBITION OF GEMINIVIRAL
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
```

```
ADDRESSEE: Quarles & Brady
STREET: One South Pinckney Street
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/065,999
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 960296, 94754
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ. ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1894 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-065-999-8
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alignment_scores:
  Quality: 219.00      Length: 70
  Ratio: 3.776        Gaps: 0
Percent Similarity: 82.857  Percent Identity: 60.000
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alignment_block:
US-09-289-346A-4 x US-09-065-999-8 ..
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Align seg 1/1 to: US-09-065-999-8 from: 1 to: 1894
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```
1 ThrleuValTrrpGlyGluPheGlnValAspGlyArgSerAlaArgGlyL 17
  |||:| | | | | | | | | | | | | | | | | | | | | | | | |
796 ACAATCGAATGGGACAAATTCGAAGTCGACGCGAGATCTGCAAGAGGAG 845
17 YCysGlnThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerL 34
  |||:| | | | | | | | | | | | | | | | | | | | | | | | |
846 TCACGACGCTCCCAACGACTCATATGCAAAAGCATTAACCGACGATTC 895
34 YsGluGluAlaLeuGlnIleIleAlaAlaAlaIleProGluLysTyrLeu 50
  |||:| | | | | | | | | | | | | | | | | | | | | | | | |
896 TTGAATCTGCTTGACAAATATGGAAGAGAACACCAAGATTACGTC 945
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
  |||:| | | | | | | | | | | | | | | | | | | | | | | | |
946 CTTCAACATCAACACATCCGTTTAATCTCGAACGAGATCTTCGTCAG 995
67 rProGluPro 70
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996 GCCGGAACCA 1005
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seq_name: /cgnl_7/ptodata/1/lna/6A_COMB.seq:US-09-065-999-7
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seq_documentation_block:
; Sequence 7, Application US/09065999
; Patent No. 6118048
; GENERAL INFORMATION:
; APPLICANT: Hanson, Stephen F.
; APPLICANT: Maxwell, Douglas P.
; TITLE OF INVENTION: TRANS-DOMINANT INHIBITION OF GEMINIVIRAL
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
```

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: One South Pinckney Street
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/065,999
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 960296.94754
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2072 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-065-999-7
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alignment_scores:
Quality: 219.00      Length: 70
Ratio: 3.776         Gaps: 0
Percent Similarity: 82.857      Percent Identity: 60.000
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alignment_block:
US-09-289-346A-4 x US-09-065-999-7  ..
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Align seg 1/1 to: US-09-065-999-7 from: 1 to: 2072

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1 ThrleuValITrpglyGluPheGlnValAspGlyArgSerAlaArgGlyGI 17
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796 ACAATCGAATGGGAGCAATTCCAAATCGACGGCAGATCTGCAGAGGAGG 845
17 YcysGlnThrsrAsnspAlaAlaAlaGluAlaLeuAsnAlaSerSerL 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
846 TCACGAGTCTGCCAAGCAGCATCATATGCAAGCAATTAAAGCAGATTCOA 895
34 ysgluGluAlaLeuGlnIleIleAlaAlaAlaIleProGluIlystIleu 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
896 TTGAATCTGCTTGACATATTGAGAGGAACAACCGAAAGATTACCTC 945
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAsnParGlyIlePheAspIysth 67
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:
946 CTTCAACGTCACCAACATCCGTTTAAATCTCGAACGGATCTTCGCAAGT 995
67 rProGluPro 70
:|||||:
996 GCCCGAACCA 1005
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seq_name: /cgnl_7/ptodata/1/ina/6B_COMB.seq:US-08-838-151A-1
seq_documentation_block:
; Sequence 1, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Lou, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
```

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APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rockey, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1162 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Tomato Mottle Geminivirus
INDIVIDUAL ISOLATE: Florida
FEATURE:
NAME/KEY: CDS
LOCATION: 44..1127
PUBLICATION INFORMATION:
AUTHORS: Gilbertson, RL
AUTHORS: Hidayat, SH
AUTHORS: Paplomatas, EJ
AUTHORS: Rojas, MR
AUTHORS: Hou, YM
AUTHORS: Maxwell, DP
TITLE: Pseudorecombination between the infectious
TITLE: cloned DNA components of tomato mottle and bean
TITLE: dwarf mosaic geminiviruses.
JOURNAL: Jour. General Virol.
VOLUME: 74
PAGES: 23-31
DATE: 1993
US-08-838-151A-1
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alignment_scores:
Quality: 214.00      Length: 70
Ratio: 3.690         Gaps: 0
Percent Similarity: 82.857      Percent Identity: 55.714
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alignment_block:

US-09-289-346A-4 x US-08-838-151A-1 ..

Align seg 1/1 to: US-08-838-151A-1 from: 1 to: 1162

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1 ThrleuValITrpglyGluPheGlnValAspGlyArgSerAlaArgGlyGI 17
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
371 ACAATCGAATGGGAGCAATTCCAGATCGACGGCAGATCTGCCAGAGGAGG 420
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34 ysglunluatlaeuuglnlellearglulustleproalaiaaleu 50
|||||
2171 AACAGAGAGCCCTGCAGATTAATTAGAGAGAAATCCACAGAAAATATTTA 2122
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArg1IlePheAspLysThr 67
|||||
2121 TTTCAGTTCACAACTCAATCTAAATAGCAATTGATGATATTGATTAGAC 2072
67 rProGluPro 70
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2071 TCCTGAGCCA 2062
seq_name: gb_v1:AY029750
seq_documentation_block: 2588 bp DNA circular VRL 08-May-2001
LOCUS AY029750
DEFINITION Tomato severe rugose virus DNA-A, complete sequence.
ACCESSION AY029750
VERSION AY029750.1 GI:14009278
KEYWORDS
SOURCE Tomato severe rugose virus.
ORGANISM Tomato severe rugose virus.
REFERENCES
1 (bases 1 to 2588)
Rezende,W.L., Goulart,L.R., Parreira,K.S. and Figueiredo,J.E.F.
The full-length DNA-A nucleotide sequence of a novel
tomato-infecting begomovirus, Tomato severe rugose virus, in Brazil
Unpublished
2 (bases 1 to 2588)
Rezende,W.L., Goulart,L.R., Parreira,K.S. and Figueiredo,J.E.F.
Direct Submission
Submitted (03-Apr-2001) Instituto de Genetica e Bioquimica,
Universidade Federal de Uberlandia, Av. Amazonas s/n, Bloco 2E,
Sala 24, Campus Umuarama, Uberlandia, Minas Gerais 38.400-000,
Brazil

FEATURES
source Location/Qualifiers
1..2588
/organism="Tomato severe rugose virus"
/strain="Minas Gerais"
/db_xref="taxon:158463"
/country="Brazil"
/note="segment: DNA-A"
305..1060
/gene="AV1"
305..1060
/gene="AV1"
305..1060
/codon_start=1
/product="coat protein"
/protein_id="AAK50360.1"
/db_xref="GI:14009282"
/translation="MPKRDAPRLMAGTSKVSRSANSPRAGYGPKYIKAAEWNRP
YRKPRVTLRGPDPVRCGEPCVKVSYESRHDVSHVKVLCVSDVTGKGLTHRVGK
RFVYSILYTLKVMDESIKLNHTNSYFMVLVRRRRYGTPTMDGQVFNMDNEPST
ATVKNLDRDFQVMHMFYAKVTGQGYASNEQALYRFKVVNNNVYNNHQEAGKYNHT
ENALLVMACTHASNPYATLKRIRYFYDSITN"
complement(1057..1455)
/gene="AC3"
complement(1057..1455)
/gene="AC3"
/codon_start=1
/product="enhancer protein"
/protein_id="AAK50358.1"
/db_xref="GI:14009280"
/translation="WDSRTGLITARQAENGVIWEISNPLYFKINRVEDPMYTTSRV
YHVOIRFHNHLRALHLKSEINFQIMTSTLJASGTYLNRKYLVLLYLDRLGVISI
NNVIRAVFATDKSYNAVLENHLIKFKFY"
complement(1202..1591)
/gene="AC2"
complement(1202..1591)
/codon_start=1
/product="trap"

gene
CDS
gene
CDS

/protein_id="AAK50361.1"
/db_xref="GI:14009283"
/translation="WRNSSSLTPPSIKYQVRAAKKRGRIRRRIRIDEGCCSYVHNGCR
GHGTHRGTHTNCTSGREMLYGLDKSLFPODKSGGSVNHEDSLPRPNTVOPOPEE
STASPOLHLQLPDMDDPFDSPWDIFK"
complement(1533..2588)
/gene="AC1"
complement(1533..2588)
/gene="AC1"
complement(1533..2588)
/codon_start=1
/product="rep protein"
/protein_id="AAK50357.1"
/db_xref="GI:14009279"
/translation="WPSATRRRFOIRAKNYFLTPKCSLSKEBALSQLKLNTPTKKF
IKVRELHENGEPHLHYLDFEGNYCRONORFPDLYSPRSTHHPNTORAKSSSDVK
SYVDKDGTTIMGEFOIDGRSARGCOTANDAAEALAPSKDALOTIRKLPKPEFL
FOPHLNSNLDRIFAFAPEWAPTEPLSSFTNVPREMDMADDFGKAAPERTISI
LIEGDSRTGKTMMARAFCAGAHNYLSCHLDNFPRVYSNHVEYVIDIAPHYLYLKHKE
LLGAOKDMOSNCKYKGPVOIKGGLPCIEBLCNPDGASYSKVPFRHKENASLNNWTKHNA
KFVFLNPLPYOGTTQSC"
complement(2171..2434)
/gene="AC4"
complement(2171..2434)
/gene="AC4"
/codon_start=1
/product="AC4 protein"
/protein_id="AAK50359.1"
/db_xref="GI:14009281"
/translation="WRKMSLISTCFEFSKAITAAKINDSTWSPOQGOHISIRFREL
NHRPTSPMSTRTEILNSGANSKSTAEVLEAVAROLTMLPKP"
join(2583..2588,1..304)
/note="common region"
rep_origin
BASE COUNT 660 a 525 c 598 g 805 t
ORIGIN

alignment_scores:
Quality: 298.00 Length: 70
Ratio: 4.730 Gaps: 0
Percent Similarity: 90.000 Percent Identity: 80.000

alignment_block:
US-09-289-346a-5 x AY029750/rev ..
Align seg 1/1 to reverse of: AY029750 from: 1 to: 2588

1 ThrLeuValTrpGlyLupheGlnValAspGlyArgSerAlaArgGly1 17
|||||
2258 ACTATCGAATGGGGCAATTCGAAATCGACGCGAGAAAGTCCTAGAGCGG 2209
17 yCysGlnThrSerAsnAspAlaAlaGlnAlaLeuAsnAlaSerSerL 34
|||||
2208 TTCCCGACAGCAGCTAACGATGCTGCCGAGAGCCTTGACACCTTCCA 2159
34 ysglunluatlaeuuglnlellearglulustleproalaiaaleu 50
|||||
2158 AACAGAGAGCCCTGCAGATTAATCCGGAGAGACTACCGGAAAAGTTTTA 2109
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArg1IlePheAspLysThr 67
|||||
2108 TTTCAGTTCACAACTCAATCTAAATAGTAATTGATGATATTGTCAGAGCG 2059
67 rProGluPro 70
|||||
2058 TCCTGAGGCCA 2049
seq_name: gb_v1:AF291705
seq_documentation_block: 2622 bp DNA circular VRL 25-SEP-2000
LOCUS AF291705
DEFINITION Tomato rugose mosaic virus DNA-A, complete sequence.
ACCESSION AF291705
VERSION AF291705.1 GI:10281644

vegetable-infecting geminiviruses in Central America

JOURNAL
Unpublished
2 (bases 1 to 1345)REFERENCE
Nakhla, M.K., Weiland, G., Kamal, S. and Maxwell, D.P.
Direct SubmissionJOURNAL
Submitted (25-FEB-1999) Plant Pathology, University of
Wisconsin-Madison, 1630 Linden Dr., Madison, WI 53706-1598, USAFEATURES
Location/Qualifiers
1.1345

/organism="tomato mild mottle geminivirus"

/isolate="HN96-H5Kv"

/specimen_voucher="H5"

/db_xref="taxon:92943"

/chromosome="segment A"

/clone="pHNH5akv"

/country="Honduras: Comayagua Valley"

/note="Obtained from a tomato plant collected in Dec. 1996
by M.K. Nakhla and D.P. Maxwell"

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/gene="rep"

/note="ac1"

complement(<1..678)

/gene="rep"

/note="rep protein"

/codon_start=1

/product="replication-associated protein"

/protein_id="AAD33471.1"

/db_xref="GI:4928224"

/translation="MPLPKPLINSKNYELTYPHCSLKEETLEQLLNTPTNKY
IKIARELHEDGEYHLHLVLIQFEGKEFTQCFEDYVSSSTRFHFNVGAKSSTDK
SYVDKGDITLWNGEFOIDGRSARGOQTNDAAAEELNASSKEEMRIIKELKEPEL
FOYHNSNLDRIFAKAPEPWIPLPLSFTWVDEMOMWTDYGRGVAARPERIS
IIEEDSR"rep_origin
676..832

/note="ori"

1001..>1345

/gene="cp"

/note="av1"

1001..>1345

/gene="cp"

/note="capsid protein"

/codon_start=1

/product="coat protein"

/protein_id="AAD33472.1"

/db_xref="GI:4928225"

/translation="MPKRDAPRMHSATPKVSRSSNYVPPDGLGRFTDKSSAMNPM
YKRPRTYRVSADVPKRGCEPKIOSFEORHDSHTGKWCISDVTNRNGILTHRVGK
RRCVSVYILGKV"BASE COUNT
329 a 289 c 313 g 414 t

ORIGIN

alignment_scores:

quality: 287.00 length: 70

Ratio: 4.484 gaps: 0

Percent similarity: 91.429 Percent identity: 77.143

alignment_block:

US-09-289-346a-5 x AF131071/rev ..

Align seg 1/1 to reverse of: AF131071 from: 1 to: 1345

1 ThrleuValTrpglyglupheglnValaspolyargserAlaarglycl 17

348 ACAATCGAATGGGAGAAATTCAGATCGACGCAATCTCTAGAGAGG 299

17 ycyglnThrsrnsapalaalaalagualaaleuasnalaserserl 34

298 TCACGAAACAGCTAACGAGCTGCCGAGAGCCCTAAATCCCTCGA 249

34 ysgluglualaleuglnlelleargclutylsileproalalaaleu 50

248 AAGAAAGAGCATCGAATATTAAGAGAGAGCTCCCAAGAGTTCCTT 199

51 PhedlnpHeHIsanleuAsnSerAsnleuAsparTllepHeAsplysth 67
198 TTTCAATATTCACACCTGTCTAGTACCTAGACAGATTTCCGTAAGGC 149

67 rProgluPro 70

148 TCCGCAACCG 139

seq_name: gb_v1:MBGARAL

seq_documentation_block:

LOCUS MBGARAL 2617 bp ss-DNA circular VR 02-AUG-1993

DEFINITION Bean golden mosaic geminivirus viral coat protein (ARI) gene,
complete cds; putative replicative protein (AL1) gene, putative
cds; AL2 gene, complete cds; and AL3 gene, complete cds.

ACCESSION M88686

VERSION M88686.1 GI:331462

KEYWORDS coat protein; replicative protein.

SOURCE Bean golden mosaic virus (individual isolate Brazil, strain Type I)

ORGANISM Replicative form DNA.

REFERENCE 1 (sites)

AUTHORS Gilbertson, R.L., Faria, J.C., Hanson, S.F., Morales, F.J.,
Abulquist, P.G., Maxwell, D.P. and Russell, D.R.TITLE Cloning of the Complete DNA Genomes of Four Bean-Infecting
Geminiviruses and Determining Their Infectivity by Electric
Discharge Particle Acceleration

JOURNAL Phytopathology 81, 980-985 (1991)

AUTHORS Gilbertson, R.L., Hidayat, S.H., Martinez, R.T., Leong, S.A., Faria, J.C.,
Morales, F.J. and Maxwell, D.P.TITLE Differentiation of bean-infecting geminiviruses by nucleic acid
hybridization probes and aspects of bean golden mosaic in Brazil

JOURNAL Plant Dis. 75, 336-342 (1991)

AUTHORS Gilbertson, R.L., Faria, J.C., Abulquist, P.G. and Maxwell, D.P.

TITLE Genetic diversity in geminiviruses causing bean golden mosaic
disease: The nucleotide sequence of the infectious cloned DNA
components of a Brazilian isolate of bean golden mosaic geminivirus
Unpublished (1992)

JOURNAL Location/Qualifiers

FEATURES 1..2617

source /organism="bean golden mosaic virus"

/proviral

/isolate="Brazil"

/strain="Type I"

/db_xref="taxon:10839"

/dev_stage="Replicative form"

/gemline

misc_feature 1..181

/standard_name="Common Region"

/note="putative"

/function="putative origin of replication"

gene 358..1113

/gene="ARI"

358..1113

/gene="ARI"

CDS /codon_start=1

/function="coat protein"

/protein_id="AA44613.1"

/db_xref="GI:331464"

/translation="MPKRDAPRMHSGTSSIRSNFSPRCNGPKRYNKAADVNPM
YKRPRTYRVSADVPKRGCEPKIOSFEORHDSHTGKWCISDVTNRNGILTHRVGK
RRCVSVYILGKV"

gene EXALLIYACTASNPVATLKIRITFDISTN"

complement(1110..1508)

/gene="AL3"

CDS complement(1110..1508)


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34 yscgluaialaueglnllelearglulysileproalaalaaleu 50
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248 AACGACGGCTCTCAATAATATTAGAGAAATGCCGAGAAATATCTT 199
51 PhcglInPhetHisasleuAsnSerAsnLeuAspArgllepheasplysth 67
||||| ||||||||| |||
198 TTTCAATTTCATTAATTTAAATTTGATGATGAAATTTTCGCAAGGC 149

seq_name: gb_v1:AF188708
seq_documentation_block: 1365 bp DNA VRL 07-NOV-1999
LOCUS AF188708
DEFINITION Cowpea golden mosaic geminivirus replication associated protein
(rep) and coat protein (cp) genes, partial cds.
ACCESSION AF188708
VERSION AF188708.1 GI:6273115
KEYWORDS
SOURCE cowpea golden mosaic geminivirus.
ORGANISM cowpea golden mosaic geminivirus.
REFERENCE 1 (bases 1 to 1365)
AUTHORS Faria,J.C.
TITLE Partial nucleotide sequence of cowpea golden mosaic geminivirus
from Brazil
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1365)
AUTHORS Faria,J.C.
TITLE Direct Submission
JOURNAL Submitted (21-SEP-1999) Biotechnology Laboratory, EMBRAPA, Caixa
Postal 179, Golandia, GO 75375, Brazil
FEATURES
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1..1365
/organism="cowpea golden mosaic geminivirus"
/strain="CGMV-BR"
/specific_host="cowpea"
/db_xref="taxon:69263"
complement(<1..676)
/gene="rep"
complement(<1..676)
/gene="cp"
note="AC1"
/codon_start=1
/product="replication associated protein"
/protein_id="AAF06318.1"
/db_xref="GI:6273117"
/translation="MPPPRKFKINAKNYFLTYPOCSIGKESAI EQLQTLQTPVNNKI
RYCRLEHNGEPHLLALQIEGKFOCTNRLFDLHNPHTSSVSHNIOGAKSSDVKS
YLEKGDYVEMGHFOIDGSAAGOOTINDASALNASSKEAMQIIKEKLPKELF
OYHNLSSNIDRFKKKPEPWPSPPLSSFTNVPKQMDWADYFGRDAAARERVSIT
IIEGDSR"
rep_origin
674..820
gene
1021..>1365
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YRKPIYHNRKRDVPRCGEGCKVQSEQKHDSHGICLVLTSDVTGGGITHRVGK
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BASE COUNT 339 a 259 c 332 g 435 t
alignment_scores: 275.00 Length: 67
Quality:
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Ratio: 4.583 Gaps: 0
Percent Similarity: 89.552 Percent Identity: 77.612
alignment_block:
US-09-289-346a-5 x AF188708/rev.
Align seg 1/1 to reverse of: AF188708 from: 1 to: 1365

4 TTPGLYGLUPHGINVALAEPGLYARGSERIALARGLYGLYCYSGINPH 20
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340 TGGGTCATTTTCATAATCGACGAGATCTGTACAGAGCTCAGCAGAC 291
20 rSerAsnAspAlaAlaAlaGlnAlaLeuAsnAlaSerSerLysGlnGln 37
||||| ||||||||| |||
290 AATTAATGATCGACGATCGAGCGGTTAATGCTTCTTCAAGACAGAAC 241
37 laueglnllelearglulysileproalaalaaleupheglnphe 53
||||| ||||||||| |||
240 CCATGCAAAATATCAAGAAAGAACTACCCGCAAGATTCTCTCCAGTAT 191
54 HisAsnLeuAsnSerAsnLeuAspArgllepheasplysthproglupr 70
||||| ||||||||| |||
190 CACACTTATTCAGTACCTGATGATATTCMAAAGCCTCCGAAAC 141
70 o 70
140 A 140

seq_name: gb_v1:SGU67926
seq_documentation_block: 554 bp DNA VRL 28-JAN-1998
LOCUS SGU67926
DEFINITION Sida golden mosaic geminivirus Rep protein (AC1) gene, partial cds.
ACCESSION U67926
VERSION U67926.1 GI:1546801
KEYWORDS
SOURCE sida golden mosaic virus.
ORGANISM sida golden mosaic virus.
REFERENCE 1 (bases 1 to 554)
AUTHORS Roys,M.E., McLaughlin,W.A., Nakhla,N.K. and Maxwell,D.P.
TITLE Genetic Diversity among geminiviruses associated with the weed
species Sida spp, Macroptilium lathyroides, and Wissadula
amplissima from Jamaica
Plant Dis. 81, 1251-1258 (1997)
JOURNAL 2 (bases 1 to 554)
REFERENCE Roys,M.E., McLaughlin,W.A. and Maxwell,D.P.
AUTHORS Direct Submission
TITLE Submitted (23-AUG-1996) Plant Pathology, University of Wisconsin,
1630 Linden Drive, Madison, WI 53706-1598, USA
JOURNAL Location/Qualifiers
1..554
/organism="sida golden mosaic virus"
/strain="Jamaica"
/isolate="Jamaica, May 1993"
/db_xref="taxon:51034"
note="DNA A component"
complement(1..554)
/gene="AC1"
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/product="Rep protein"
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/db_xref="GI:1546802"
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KYNCTNNRPFDLVSPTRSVHHPNIOGAKSSDVKSVEKGDYVEMGHFOIDGSA
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BASE COUNT 121 a 127 c 139 g 167 t
Quality:
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alignment_scores:
Quality: 271.00 Length: 70
Ratio: 4.302 Gaps: 0
Percent Similarity: 90.000 Percent Identity: 71.429

alignment_block:
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Align seq 1/1 to reverse of: SCU67926 from: 1 to: 554

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1 ThrleuValTrpGlyGluPheGlnValAlaSpGlyArgSerAlaArgGlyG1 17
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17 yCysGlnThrSerAsnAspAlaAlaIaGluAlaLeuAsnAlaSerI 34
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240 TCAGCAAAACGCTAACGACGACGCCGAGCATTTGAATCTTGGAACAA 191

34 ySgIuGluAlaLeuGlnIleIleArgGluLysIleProAlaAlaAlaLeu 50
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190 AGCAGAGTGCACCTGAATATCATCAGACAGAACTTACCAGAAAGTATCTC 141

51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
140 TTTCAGTATCAACAACCTATCCAGTAAATATGATATTTTCACTAGAGCC 91

67 rProGluPro 70
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90 TCCAGAACCG 81
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seq_name: gb_vl:AF288227

seq_documentation_block:
LOCUS AF288227 1383 bp DNA VRL 20-AUG-2000
DEFINITION Sweet potato leaf curl virus replication association protein (AC1)
and AC4 (AC4) genes, complete cds.
ACCESSION AF288227
VERSION AF288227.1 GI:9858125
KEYWORDS sweet potato leaf curl virus.
SOURCE sweet potato leaf curl virus
ORGANISM Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
REFERENCE 1 (bases 1 to 1383)
AUTHORS Lottakul,P., Valverde,R.A., Clark,C.A., Sim,J. and De la Torre,R.
TITLE Detection of a geminivirus infecting sweet potato in the United States
JOURNAL Plant Dis. 82, 1253-1257 (1998)
REFERENCE 2 (bases 1 to 1383)
AUTHORS Lottakul,P. and Valverde,R.A.
TITLE Direct Submission
JOURNAL Submitted (18-JUL-2000) Plant Pathology and Crop Physiology,
Louisiana State University, 302 Life Sciences Bldg., Baton Rouge,
LA 70803, USA

FEATURES
source location/Qualifiers
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HVARLHEDGEPHLVLOVEGKFWCTNSRFDLVSPNSNHFHPIIDGAKSSDVKS
IYVDKGDITWGEFQVDRSARGGQOTANDAAEALNMGSKRAALQIIREKLPEYLF
GFHNLVSNIDRIFFPPPSVYSSPSSSFNNAVDDILSDPAENVMSAARPRPISIV
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BASE COUNT 359 a 296 c 327 g 401 t
ORIGIN

alignment_scores:
Quality: 271.00 Length: 68
Ratio: 4.517 Gaps: 0
Percent Similarity: 88.235 Percent Identity: 79.412

alignment_block:
US-09-289-346a-5 x AF288227/rev ..

Align seq 1/1 to reverse of: AF288227 from: 1 to: 1383

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902 ACCATCACTGGGGTGAATTCAGGTGACGCGAGTCTGTAGAGGAGG 853

17 yCysGlnThrSerAsnAspAlaAlaIaGluAlaLeuAsnAlaSerI 34
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852 CCAGCACTGCTTACGACGACGCCGAGCTCTTAACGACAGTCTA 803

34 ySgIuGluAlaLeuGlnIleIleArgGluLysIleProAlaAlaAlaLeu 50
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802 AAGAGCTGCGTTCGAATATTCAGGAGGAACCTCGTGAATAATTATTA 753

51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
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752 TTTCATATTCATATTTAGTACTAATTTAGATTTTCTCTCTCC 703

67 rPro 68
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702 ACCT 699
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seq_name: gb_vl:AF104036

seq_documentation_block:
LOCUS AF104036 2828 bp DNA circular VRL 05-AUG-1999
DEFINITION Sweet potato leaf curl virus DNA A, complete sequence.
ACCESSION AF104036
VERSION AF104036.1 GI:5702158
KEYWORDS sweet potato leaf curl virus.
SOURCE sweet potato leaf curl virus.
ORGANISM Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
REFERENCE 1 (bases 1 to 2828)
AUTHORS Lottakul,P., Valverde,R.A., Clark,C.A., Sim,J. and De la Torre,R.
TITLE Detection of a geminivirus infecting sweet potato in the United States
JOURNAL Plant Dis. 82, 1253-1257 (1998)
REFERENCE 2 (bases 1 to 2828)
AUTHORS Lottakul,P. and Valverde,R.A.
TITLE Cloning of a DNA-A-like genomic component of sweet potato leaf curl
virus : nucleotide sequence and phylogenetic relationships
JOURNAL Molecular Plant Pathology On-line (1999)
REMARK http://www.bspp.org.uk/mpol/1999/0422lottakul/
AUTHORS Lottakul,P. and Valverde,R.A.
TITLE Direct Submission
JOURNAL Submitted (02-NOV-1998) Plant Pathology and Crop Physiology,
Louisiana State University, 302 Life Sciences Bldg., LSU, Baton

FEATURES
 source Rouge, LA 70803, USA
 Location/Qualifiers
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 132..476
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 GKRVCKSMGIDGKWMNDNNAKRDHTNLIITWALJDRPNKDPINFQIFPMYNEDP
 TTAKTIMDLRDMQVLCKFSYVSGGPGYSHKQDALIRKFFKGLYNHVTNHNKEAKE
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 VYDKGDPITTWGEFOYDGRSARGGQOTANDAAEALNAGSKFAALQITIREKPEYLF
 QPHNLVSNLDRLTFSPPSYVSSPFSSSSNAVPDITSDMAENVMDSARPRPISIV
 IEGPRIGKTWARSLGPHNYLCGLDLSPKYVSNAMYNIDVNPQYLKPKFEFG
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gene complement(2267..2524)
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 /translation="MGNLISMCMGSSKANSSAOIADSSIMSHRTDRITFTPTSRRLNP
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 BASE COUNT 741 a 606 c 675 g 806 t
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 Alignment scores:
 Quality: 271.00 Length: 68
 Ratio: 4.517 Gaps: 0
 Percent Similarity: 88.235 Percent Identity: 79.412
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 17 yCySgLinThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerL 34
 |||:::|||||
 2304 CCACGACAGCTCTTAACGACGCGGCGGAGCGCTTAACGACGAGTTCTTA 2255
 34 ySgLinGluAlaLeuGlnIleLeuArgGlyLysIleProAlaAlaAlaLeu 50
 |||:::|||||
 2254 AAGAACGCTGCTTCAATATATCATGAGGAGAAACCTCGAAAAATATTTA 2205
 51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgGlyIlePheAspLysTh 67
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 2204 TTTCATTTTCATATTTAGTTAGTATTTAGATTTGATTTTCTCTCTCC 2155
 67 rPro 68
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 2154 ACCT 2151
 seq_name: gb_v1:Y1E132548
 seq_documentation_block:
 LOCUS Y1E132548 2763 bp DNA circular VR1 01-FEB-1999
 DEFINITION Ipomoea yellow vein virus V2, V1, C3 and C2 genes.
 ACCESSION AJ132548
 VERSION AJ132548.1 GI:4210720
 KEYWORDS C2 gene; C2 protein; C3 gene; C3 protein; coat protein; V1 gene; V2
 gene; V2 protein.
 SOURCE
 Ipomoea yellow vein virus.
 ORGANISM
 Ipomoea yellow vein virus.
 Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 1 (bases 1 to 2763)
 REFERENCES
 Banks,G.K.
 Direct Submission
 Submitted (26-JAN-1999) Banks G.K., Virus Research, John Innes
 Centre, Norwich Research Park, Colney Lane, Norwich, NR4 6UL, UK
 2 (bases 1 to 2763)
 Banks,G.K., Bedford,I.D., Beitia,F.J., Cerezo,E.R. and Markham,P.G.
 A novel geminivirus of Ipomoea indica (Convolvulaceae) from southern
 Spain
 JOURNAL
 Unpublished
 FEATURES
 source Location/Qualifiers
 1..2763
 /organism="Ipomoea yellow vein virus"
 /villon
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 /db_xref="taxon:87832"

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           /db_xref="GI:4210721"
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           RALHWECCPNCCPKLCPGFKRRDEKEG"
gene      1215..1979
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CDS        1215..1979
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           TTAKIRMDLRDMQVLAKRESVYSGSPYSHKQALIRKFEKCLYNHVTYNNHEEPAKE
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gene      complement(2127..2576)
CDS        complement(2127..2576)
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           /protein_id="CA10698.1"
           /db_xref="GI:4210724"
           /translation="MSTAPSGYKKRKCPRQEPRIHAAKKROKRTPEPRTRIVAKGGCCS
           AFITNDCKFQHGFTIRGVKSCSTDESSFILOQSHVCSDDCTPSFTDVCPRKQPRLK
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BASE COUNT 734 a 570 c 671 g 788 t
ORIGIN
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  Ratio: 4.525        Gaps: 0
  Percent Similarity: 86.765      Percent Identity: 76.471
alignment_block:
US-09-289-346a-5 x IYE132548/rev ..
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469 ACCCTCATATGGGGTGAATTCACAGATCGACGGCGATCTGCTACAGGAGG 420
17 yCySGInThrSerAsnAspAlaAlaIaGluAlaLeuAsnAlaSerI 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
419 TCACCACTGCTACGACGACGACGACGACGACGCTAACCGCATGTTCTA 370
34 ySGIuAlaLeuGInIleIeArgIuIySIIeProAlaAlaLeu 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
369 AAGAAAGCTGGCTTGCAATATATACGAGGAAGAACCTGAAATAATATT 320
51 PheGInPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspIyStH 67

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67 rPro 68
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269 TCCT 266
seq_name: gb_v1:MGU75278
seq_documentation_block:
LOCUS      MGU75278          447 bp      DNA
DEFINITION Macropitillium golden mosaic geminivirus replication-associated
protein (AC1) gene, partial cds.
ACCESSION  U75278
VERSION    075278.1  GI:1688188
KEYWORDS
SOURCE
ORGANISM   Macropitillium golden mosaic geminivirus.
            Viruses: ssDNA viruses; Geminiviridae: Begomovirus.
REFERENCE  1 (bases 1 to 447)
            Roye,M.E.
            Diversity and phylogeny of whitefly-transmitted geminiviruses from
            Jamaica
            Thesis (1996)
            2 (bases 1 to 447)
            Roye,M.E., McLaughlin,W.A. and Maxwell,D.P.
            Three distinct geminiviruses infecting M. jathroides from Jamaica
            but not BGMV
            Unpublished (1996)
            3 (bases 1 to 447)
            Roye,M.E., McLaughlin,W.A. and Maxwell,D.P.
            Direct Submission
            Submitted (17-Oct-1996) Biochemistry, University of the West
            Indies, Mona, Kingston 7, Jamaica
            Location/Qualifiers
            1..447
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            /strain="Jamaican"
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            /protein_id="AAB36919.1"
            /db_xref="GI:1688189"
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BASE COUNT 97 a 112 c 110 g 128 t
ORIGIN
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  Ratio: 4.328        Gaps: 0
  Percent Similarity: 87.143      Percent Identity: 70.000
alignment_block:
US-09-289-346a-5 x MGU75278/rev ..
Align seq 1/1 to reverse of: MGU75278 from: 1 to: 447
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294 ACCATCGAATGGGAGTGTTCACAGATCGACGAGAAAGTCTCGAGCGG 245
17 yCySGInThrSerAsnAspAlaAlaIaGluAlaLeuAsnAlaSerI 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
244 TCACCAACATCTACAGATGACGCGCGCAAGCATTAATTTCTGACACA 195

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34 ysglgluaialaenglillelearglulysileproalialaaleu 50
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194 AGGAGGGCGCATGACATAGTCAAGGAGAGTCCGGAATTTCTC 145
51 pheglpnheliasnleuasenserasnleuaspargillephaslysth 67
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144 TTTCATATATCATCAACCTATCCAGTACCTGATGATTTTCATGAAGA 95
67 rproglupro 70
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94 TCCGGAACCA 85

seq_name: gb_v1:AB001315

seq documentation block:
LOCUS AB001315 570 bp DNA VRL 13-FEB-1999
DEFINITION Tobacco leaf curl virus CI and C4 genes, clone YOKOHAMA3-1, partial
and complete cds.
ACCESSION AB001315
VERSION AB001315.1 GI:3798714
KEYWORDS
SOURCE tobacco leaf curl virus (isolate:YOKOHAMA3,
specific_host:Eupatorium makinoi) DNA, clone:YOKOHAMA3-1.
Tobacco leaf curl virus
Virus; ssDNA viruses; Geminiviridae; Begomovirus.
ORGANISM
1 (bases 1 to 570)
Ooi.K.
REFERENCE
AUTHORS Direct Submission
SUBMITTED (19-FEB-1997) to the DDBJ/EMBL/GenBank databases.
Kazuyuki Ooi, Kyushu University, Department of Biology; 6-10-1
Hakozaki Higashi-ku, Fukuoka 812, Japan
(E-mail:kooiscdbmbox.nc.kyushu-u.ac.jp, Tel:+81-92-642-2624,
Fax:+81-92-642-2645)
2 (bases 1 to 570)
Ooi.K., Onshita,S., Ishii,I. and Yahara,T.
REFERENCE
AUTHORS Molecular phylogeny of geminivirus infecting wild plants in Japan
JOURNAL J. Plant Res. 110, 247-257 (1997)
FEATURES
location/Qualifiers
source 1..570
/organism="tobacco leaf curl virus"
/isolate="YOKOHAMA3"
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/complement(<1..>570)
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/codon_start=1
/db_xref="GI:4426541"
/translation="EBALSQLONITPTNKLYIKICRELHEDGSPHLVLLQPECKY
CONNRFEDVSPTRSAHFHPNIOGAKSSSDVKSITDKDGTLEWGTFQIDGSAAGC
QANADACAEALNASSKAELAIIREKLPRDFIYOYHNLSNIDRIEAPPLVEVFCPT
ASSPQVPEELEEMASENWSAARWBRM"
complement(231..488)
/gene="C4"
/complement(231..488)
/gene="C4"
/codon_start=1
/protein_id="BAA34034.1"
/db_xref="GI:3798715"
/translation="MEALISMGCSSKANTNKTIDSSWYPOPOHISIRFREINP
APTSPSTRIRKSRNGEHSRSTEEVLEFAHMLTHVQR"
BASE COUNT 141 a 121 c 126 g 182 t
ORIGIN
alignment_scores:
Quality: 264.00 Length: 85
Ratio: 4.258 Gaps: 1
Percent Similarity: 72.941 Percent Identity: 62.353

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alignment_block:
us-09-289-346a-5 x AB001315/rev ..
Align seq 1/1 to reverse of: AB001315 from: 1 to: 570

1 ThrdValuAlrrpGlyGluPheGlnValAspGlyArgSerAlaArgGlyC1 17
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
318 ACCTCGAATGCGGACATTCACATGACGACGAGAGAGTCTAGAGAGG 269
17 yCysGlnThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerC1 34
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
268 CTCGCAAGATGCTAACGACGATGCGAGCCCTTAATGCAAGTCTA 219
34 ysglgluaialaenglillelearglulysileproalialaaleu 50
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
218 AGCGAGAGACATTTGCAATATTTAGGAGAAAGCTCCCTAAAGATTTTATA 169
51 pheglpnheliasnleuasenserasnleuaspargille..... 63
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
168 TTTCATATATCATATTTAAATAGTATTTAGATTTTGTGCTCTCC 119
64 .....Phasplysthrp 68
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
118 GTTGAGAGTTTGTGTTGTCCTTTCACAGCCTCATCTTGATCAAGTTC 69
68 roglu 69
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
68 CAGAA 64

seq_name: gb_v1:AB001318

seq documentation block:
LOCUS AB001318 570 bp DNA VRL 13-FEB-1999
DEFINITION Tobacco leaf curl virus CI and C4 genes, clone YOKOHAMA5-2, partial
and complete cds.
ACCESSION AB001318
VERSION AB001318.1 GI:3798720
KEYWORDS
SOURCE tobacco leaf curl virus (isolate:YOKOHAMA5,
specific_host:Eupatorium makinoi) DNA, clone:YOKOHAMA5-2.
Tobacco leaf curl virus
Virus; ssDNA viruses; Geminiviridae; Begomovirus.
ORGANISM
1 (bases 1 to 570)
Ooi.K.
REFERENCE
AUTHORS Direct Submission
SUBMITTED (19-FEB-1997) to the DDBJ/EMBL/GenBank databases.
Kazuyuki Ooi, Kyushu University, Department of Biology; 6-10-1
Hakozaki Higashi-ku, Fukuoka 812, Japan
(E-mail:kooiscdbmbox.nc.kyushu-u.ac.jp, Tel:+81-92-642-2624,
Fax:+81-92-642-2645)
2 (bases 1 to 570)
Ooi.K., Onshita,S., Ishii,I. and Yahara,T.
REFERENCE
AUTHORS Molecular phylogeny of geminivirus infecting wild plants in Japan
JOURNAL J. Plant Res. 110, 247-257 (1997)
FEATURES
location/Qualifiers
source 1..570
/organism="tobacco leaf curl virus"
/isolate="YOKOHAMA5"
/specific_host="Eupatorium makinoi"
/db_xref="taxon:67762"
/clone="YOKOHAMA5-2"
/complement(1..570)
/gene="C1"
/complement(<1..>570)
/gene="C1"
/codon_start=1
/protein_id="BAA34039.1"
/db_xref="GI:4426544"
/translation="EBALSQLONITPTNKLYIKICRELHEDGSPHLVLLQPECKY
CONNRFEDVSPTRSAHFHPNIOGAKSSSDVKSITDKDGTLEWGTFQIDGSAAGC
QANADACAEALNASSKAELAIIREKLPRDFIYOYHNLSNIDRIEAPPLVEVFCPT
ASSPQVPEELEEMASENWSAARWBRM"
BASE COUNT 141 a 121 c 126 g 182 t
ORIGIN
alignment_scores:
Quality: 264.00 Length: 85
Ratio: 4.258 Gaps: 1
Percent Similarity: 72.941 Percent Identity: 62.353

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gene      complement(231..488)
          /gene="C4"
CDS       complement(231..488)
          /gene="C4"
          /codon_start=1
          /protein_id="BAA34040.1"
          /db_xref="GI:3798721"
          /translation="MEALISNGCCSSKANTNAKITDSSSTWYPPQPHISIRTFRELNP
          AFTSSPTSTRFIRNSNGEHSRSTEEVLEAARMILTHVORR"
BASE COUNT      140 a      121 c      129 g      180 t
ORIGIN

alignment_scores:
  Quality: 264.00      Length: 85
  Ratio: 4.258      Gaps: 1
  Percent Similarity: 72.941      Percent Identity: 62.353

alignment_block:
  us-09-289-346a-5 x AB001318/rev ..

Align seg 1/1 to reverse of: AB001318 from: 1 to: 570

1   ThrleuValTrpGlyGluPheGlnValAspGlyArgSerAlaArgGlyG1 17
    ||||| ||||| |||||:||||| ||||| ||||| |||||
318  ACGCTCGAATGGGACATTCACATTCACGACGAGAGAGTGTACAGCAGG 269
    |||||:||||| |||||:||||| ||||| ||||| |||||
17  YCysGlnThrSerAsnAspAlaAlaGluAlaLeuAsnAspSerL 34
    |||||:||||| |||||:||||| ||||| ||||| |||||
268  CTGGCAGAAATGCTAACGACGATGTCGACGAGCGCTTAATGCAAGTTCTA 219
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
34  YSGluGluAlaLeuGlnIleLeaArgLysIleProAlaAlaLeu 50
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
218  AGCGAGAGACATTAGCAATATTAGGAAAAGCTCCCTAAAGATTGTATA 169
    |||||:||||| |||||:||||| ||||| ||||| |||||
51  PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIle..... 63
    |||||:||||| |||||:||||| ||||| ||||| |||||
168  TTTCATATATCATATTAAATAGTAATTGATTTGCTGCTCC 119
    |||||:||||| |||||:||||| ||||| ||||| |||||
64  .....PheAspLysThrP 68
    |||||:||||| |||||:||||| ||||| ||||| |||||
118  GTTGGAGGTTTTGTTGCTCTTCACAGCGCTCATCTTCATCAAGTTC 69
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
68  rogiu 69
    |||||
68  CAGAA 64

seq_name: gb_v1:AF098940

seq_documentation_block:
LOCUS      AF098940      1405 bp      DNA      VRL      04-MAR-1999
DEFINITION Macropitillium golden mosaic geminivirus strain Jamaica strain 1
            replication associated protein (rep) and coat protein (cp) genes,
            partial cds.
ACCESSION  AF098940
VERSION    AF098940.1      GI:4336584
KEYWORDS   Macropitillium golden mosaic geminivirus.
SOURCE     Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
ORGANISM   1 (bases 1 to 1405)
REFERENCE  1 (bases 1 to 1405)
AUTHORS    Roye,M.E.
TITLE      Genetic diversity and phylogeny of whitefly-transmitted
            geminiviruses from Jamaica
JOURNAL    2 (bases 1 to 1405)
AUTHORS     Roye,M.E., McLaughlin,W.A. and Maxwell,D.P.
TITLE      Molecular characterization of two distinct geminiviruses infecting
            M. lathyroides from Jamaica
JOURNAL    3 (bases 1 to 1405)
AUTHORS     Roye,M.E., McLaughlin,W.A. and Maxwell,D.P.
TITLE      Direct Submission

```

```

JOURNAL    Submitted (14-Oct-1998) Biotechnology Centre, University of the
            West Indies, Mona, Kingston 7, Jamaica
FEATURES
source     1..1405
            /organism="Macropitillium golden mosaic geminivirus"
            /strain="Jamaica strain 1"
            /specific_host="Macropitillium lathyroides"
            /db_xref="taxon:51676"
            /country="Jamaica"
            /clone="PMGJAZ; PMGJAZ3"
            /complement(<1..701)
            /gene="rep"
            /complement(<1..701)
            /gene="rep"
            /complement(<1..701)
            /product="replication associated protein"
            /protein_id="AAD17850.1"
            /db_xref="GI:4336586"
            /translation="MPKRGSPFSIRKANYFLTYPOCSLIRKEFALSQLTNLNPVKKFI
            KICRPHEDGQVHLHLVLIPOKGFNCTNNRLFDLYSPRSARFHNIGAKSSDYSK
            YVEKGDITENGVFQIDGRSARGGQSTSDAAALNSGTGFAAMRIYKELPERFLF
            OYHNLSSNLDRIFMKDPPEWAPPPLSLSTNVPMQWADYFGRGSAAREPMSI
            IVEGDSRTGKTMWAC"
            /note="intergenic region"
            /complement(>1405)
            /gene="cp"
            /complement(>1405)
            /gene="cp"
            /complement(>1405)
            /codon_start=1
            /product="coat protein"
            /protein_id="AAD17849.1"
            /db_xref="GI:4336585"
            /translation="MPKRGCSWRTTPGVAKYSRLNYSFPGYGPBSNKAQEWVRPM
            YKRPRIYRTSPDVPKCGECPKQVSYEQRHDSHVGVKMCISDTYGVYTHRVGK
            RCFVFEVYLKIMDENINCSC"
BASE COUNT      328 a      333 c      357 g      386 t      1 others
ORIGIN

alignment_scores:
  Quality: 264.00      Length: 70
  Ratio: 4.328      Gaps: 0
  Percent Similarity: 87.143      Percent Identity: 70.000

alignment_block:
  us-09-289-346a-5 x AF098940/rev ..

Align seg 1/1 to reverse of: AF098940 from: 1 to: 1405

1   ThrleuValTrpGlyGluPheGlnValAspGlyArgSerAlaArgGlyG1 17
    ||||| ||||| |||||:||||| ||||| ||||| |||||
374  ACCATCGAATGGGACGATGCTTCACATTCACGACGAGAGTGTCCGAGCGG 325
    |||||:||||| |||||:||||| ||||| ||||| |||||
17  YCysGlnThrSerAsnAspAlaAlaGluAlaLeuAsnAspSerL 34
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
324  TCAGCAACATCTAACGATGCGCGGAGCAATTAATCTCGAACA 275
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
34  YSGluGluAlaLeuGlnIleLeaArgLysIleProAlaAlaLeu 50
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
274  AGCAGCGCGCCATGACAAATGTCAGGAGAAAGTCCGGAATAATTCTC 225
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
224  TTTCATATATCACAACCTATCCAGTAACCTGATGATTTCATGAAGA 175
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
67  rProGluPro 70
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
174  TCCGGAACA 165

```


OM of: US-09-289-346a-5 to: N_Geneseq_1101.* out_format : pfs

Date: Jan 3, 2002 3:50 PM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

```
-MODEL=frame+P2n_model -DEV=xlp
-Q=/cgnl_1/USPTO.spool/US09289346/runat_03012002_153304_15393/app_query.fasta.1.1163
-DB=N_Geneseq_1101 -OFMT=fastap -SUFFIX=P2n.rng -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-OGAPOP=4.500 -OGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATH=BLX-blossum2
-TRANS-human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
-NOR=ext -MINLEN=0 -MAXLEN=200000000
-USER=US09289346.ecgnl_1.396 -NCPU=6 -ICPU=3 -LONGLOG -NO_XLPEX
-WAIT -THREADS=1
```

Search information block:

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Query: US-09-289-346a-5
Query length: 70
Database: N_Geneseq_1101.*
Database sequences: 930621
Database length: 428662619
Search time (sec): 715.120000
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Score list:

Sequence	Std Orig	ZScore	EScore	len	Documentation
/cgnl_8/gcgdata/geneseq/geneseq/NA1997.DAT:AAAT93317 +	239.00	564.82	2.2e-23	2744	
/cgnl_8/gcgdata/geneseq/geneseq/NA1995.DAT:AAQ84371 +	232.00	566.48	1.8e-23	434	
/cgnl_8/gcgdata/geneseq/geneseq/NA1995.DAT:AAQ84372 +	232.00	565.45	2.0e-23	479	
/cgnl_8/gcgdata/geneseq/geneseq/NA1995.DAT:AAQ84375 +	231.50	562.76	2.9e-23	550	
/cgnl_8/gcgdata/geneseq/geneseq/NA1998.DAT:AAV92761 +	226.00	532.17	1.4e-21	2766	
/cgnl_8/gcgdata/geneseq/geneseq/NA1997.DAT:AAAT93294 +	220.00	526.19	3.1e-21	1160	
/cgnl_8/gcgdata/geneseq/geneseq/NA1997.DAT:AAAT93282 +	220.00	526.11	3.1e-21	1169	
/cgnl_8/gcgdata/geneseq/geneseq/NA1997.DAT:AAAT93283 +	220.00	526.11	3.1e-21	1169	
/cgnl_8/gcgdata/geneseq/geneseq/NA1997.DAT:AAAT93284 +	220.00	526.11	3.1e-21	1169	
/cgnl_8/gcgdata/geneseq/geneseq/NA1997.DAT:AAAT93309 +	219.00	517.78	9.2e-21	2602	
/cgnl_8/gcgdata/geneseq/geneseq/NA1996.DAT:AAAT12904 +	219.00	524.43	3.9e-21	1080	
/cgnl_8/gcgdata/geneseq/geneseq/NA1996.DAT:AAAT12905 +	219.00	524.43	3.9e-21	1080	
/cgnl_8/gcgdata/geneseq/geneseq/NA1996.DAT:AAAT12906 +	219.00	524.43	3.9e-21	1080	
/cgnl_8/gcgdata/geneseq/geneseq/NA1995.DAT:AAQ84378 +	219.00	519.74	7.1e-21	1695	
/cgnl_8/gcgdata/geneseq/geneseq/NA1997.DAT:AAAT93291 +	218.00	532.10	5.3e-21	1062	
/cgnl_8/gcgdata/geneseq/geneseq/NA1997.DAT:AAAT93292 +	218.00	532.10	5.3e-21	1062	
/cgnl_8/gcgdata/geneseq/geneseq/NA1997.DAT:AAAT93293 +	218.00	532.10	5.3e-21	1062	
/cgnl_8/gcgdata/geneseq/geneseq/NA1997.DAT:AAAT93314 +	218.00	520.98	6.1e-21	1183	
/cgnl_8/gcgdata/geneseq/geneseq/NA1997.DAT:AAAT93290 +	218.00	520.98	6.1e-21	1183	
/cgnl_8/gcgdata/geneseq/geneseq/NA1997.DAT:AAQ84370 +	218.00	517.51	9.5e-21	1651	
/cgnl_8/gcgdata/geneseq/geneseq/NA2000.DAT:AAA94700 +	218.00	517.51	9.5e-21	1651	
/cgnl_8/gcgdata/geneseq/geneseq/NA2000.DAT:AAA94701 +	218.00	516.08	1.1e-20	1894	
/cgnl_8/gcgdata/geneseq/geneseq/NA2000.DAT:AAA94703 +	218.00	516.08	1.1e-20	1894	
/cgnl_8/gcgdata/geneseq/geneseq/NA2000.DAT:AAA94702 +	218.00	515.14	1.3e-20	2072	
/cgnl_8/gcgdata/geneseq/geneseq/NA1986.DAT:AAAN60611 +	216.00	507.59	3.4e-20	2647	
/cgnl_8/gcgdata/geneseq/geneseq/NA1986.DAT:AAAT93287 +	216.00	507.59	3.4e-20	2647	
/cgnl_8/gcgdata/geneseq/geneseq/NA1995.DAT:AAQ84377 +	213.00	516.43	1.1e-20	550	
/cgnl_8/gcgdata/geneseq/geneseq/NA1995.DAT:AAQ84378 +	213.00	516.43	1.1e-20	550	
/cgnl_8/gcgdata/geneseq/geneseq/NA1999.DAT:AAZ11646 +	213.00	499.72	9.3e-21	2739	
/cgnl_8/gcgdata/geneseq/geneseq/NA1987.DAT:AAAT70897 +	208.50	498.10	1.1e-19	1083	
/cgnl_8/gcgdata/geneseq/geneseq/NA1987.DAT:AAAT70899 +	207.50	486.00	5.4e-19	2723	
/cgnl_8/gcgdata/geneseq/geneseq/NA1987.DAT:AAAT70893 +	203.00	483.75	7.2e-19	1145	
/cgnl_8/gcgdata/geneseq/geneseq/NA1997.DAT:AAAT93287 +	203.00	483.75	7.2e-19	1145	
/cgnl_8/gcgdata/geneseq/geneseq/NA1997.DAT:AAAT93288 +	203.00	483.75	7.2e-19	1145	
/cgnl_8/gcgdata/geneseq/geneseq/NA1995.DAT:AAQ84376 +	203.00	486.37	5.1e-19	550	
/cgnl_8/gcgdata/geneseq/geneseq/NA1997.DAT:AAAT93311 +	195.00	463.71	9.4e-18	1145	
/cgnl_8/gcgdata/geneseq/geneseq/NA1997.DAT:AAAT93285 +	193.50	459.77	1.6e-17	1166	
/cgnl_8/gcgdata/geneseq/geneseq/NA1997.DAT:AAAT93286 +	170.00	400.22	3.2e-14	1246	
/cgnl_8/gcgdata/geneseq/geneseq/NA1987.DAT:AAAT70900 +	125.00	302.44	9.0e-09	1403	
/cgnl_8/gcgdata/geneseq/geneseq/NA1997.DAT:AAAT93318 +	96.00	213.65	0.0008	1403	
/cgnl_8/gcgdata/geneseq/geneseq/NA1998.DAT:AAV60753 +	66.50	138.81	11.78	1539	
/cgnl_8/gcgdata/geneseq/geneseq/NA1998.DAT:AAV60751 +	66.50	120.21	127.89	9183	

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/cgnl_8/gcgdata/geneseq/geneseq/NA2000.DAT:AAQ94675 + 65.00 146.75 4.25 500
/cgnl_8/gcgdata/geneseq/geneseq/NA1997.DAT:AAAT85163 + 63.50 135.18 18.75 105
/cgnl_8/gcgdata/geneseq/geneseq/NA2000.DAT:AAAC83718 + 63.50 118.68 155.70 517
/cgnl_8/gcgdata/geneseq/geneseq/NA2000.DAT:AAAC83717 + 63.50 118.46 160.14 528
/cgnl_8/gcgdata/geneseq/geneseq/NA2000.DAT:AAAC83720 + 63.50 118.28 163.91 537
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seq_name: /cgnl_8/gcgdata/geneseq/geneseq/NA1997.DAT:AAAT93317

seq_documentation_block:

```
ID AAAT93317 standard; DNA; 2744 BP.
XX
AC AAAT93317;
XX
DT 27-APR-1998 (first entry)
XX
DE Tomato leaf curl virus from Southern India (stem-loop begin).
XX
KW Geminivirus; TLICV-IND; AC1 gene; transdominant mutation;
XX transgenic plant; disease resistance; ss; cyclic; circular.
XX
OS Tomato leaf curl virus from Southern India.
XX
PN WO9739110-A1.
XX
PD 23-OCT-1997.
XX
PF 15-APR-1997; 97WO-US06300.
XX
PR 16-APR-1996; 96US-0015517.
XX
PA (SEMI-) SEMINIS VEGETABLE SEEDS INC.
XX (WISC) WISCONSIN ALUMNI RES FOUND.
XX
PI Ahlquist PG, Hanson SF, Luu HT, Maxwell DP, Stout JT;
XX WPI; 1997-526447/48.
XX
PT Transgenic plants expressing geminivirus AC1 and CI wild-type and
XX mutant genes - have increased resistance to geminivirus infection
XX e.g. tomato mottle virus, tomato yellow leaf curl virus or bean
XX golden mosaic geminivirus
XX
PS Disclosure; Page 119-121; 132pp; English.
XX
CC This genomic DNA sequence comprises a full-length sequence
XX (stem-loop begin) from a tomato leaf curl virus from Southern
XX India. The invention involves production of transgenic plants
XX containing DNA comprising geminivirus AC1 or CI wild-type or mutant
XX sequences (see AAAT93282-93) that negatively interfere in trans with
XX geminiviral replication during infection. Such transgenic plants
XX are resistant to viral infection. The AC1/CI genes are especially
XX from tomato mottle virus, tomato yellow leaf curl virus or bean
XX golden mosaic virus.
XX
SQ Sequence 2744 BP; 742 A; 539 C; 637 G; 826 T; 0 other;
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alignment_scores:

```
Quality: 239.00 Length: 65
Ratio: 4.345 Gaps: 1
Percent Similarity: 84.615 Percent Identity: 73.846
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alignment_block:

```
US-09-289-346a-5 x AAAT93317/rev ..
Align seg 1/1 to reverse of: AAAT93317 from: 1 to: 2744
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4 TTPGGLYGLuPhcGLInVaLaSpGLyATgSerAlaATgGLyGLySGLInH 20
|||||
2266 TGGGCTGACGTTTCAGATCGATGAGACATCTGCACGAGGAGCTCACACGAC 2217
|||||
20 rTSPASrASpAlaAlaLaGLuLaLeuASrASrASrSGLyGLuGLuA 37
|||||
```



```

FT misc-feature 429..459
FT /tag= e
FT /note= "ribozyme R3 target sequence"
FT misc-feature 442..444
FT /tag= d
FT /note= "ribozyme R3 cleavage site"
XX
XX WO9503404-A.
XX
XX 02-FEB-1995.
XX
XX 22-JUL-1993; 93WO-EP01946.
XX
XX 22-JUL-1993; 93AU-0047014.
XX
XX 22-JUL-1993; 93WO-EP01946.
XX
XX (BIOC-) BIOCEM SA.
XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX
XX Baudino S, Comeau D, Dry IB, Gruber V, Lenee P;
XX Mason J, Rezaian MA, Rigden JE, Rezaian MA;
XX
XX WPI: 1995-075232/10.
XX
XX Synthetic DNA virus ribozyme(s) - reduce replication, infection
XX and/or assembly of viruses by cleaving target virus sequence,
XX useful for preparing resistant plants, esp tomatoes.
XX
XX Example 10; Fig 11c; 90pp; English.
XX
XX The sequence is a tomato leaf curl virus target sequence for
XX poliribozyme-P, which hybridizes to and cleaves the sequence and
XX thereby reduces replication, infection and/or assembly of the virus
XX substantially. The ribozyme may be expressed in a transgenic plant,
XX e.g. tomato, to confer virus disease-resistance.
XX
XX Sequence 479 BP; 145 A; 95 C; 97 G; 142 T; 0 other;

alignment_scores:
Quality: 232.00 Length: 85
Ratio: 3.803 Gaps: 1
Percent Similarity: 71.765 Percent Identity: 55.294

alignment_block:
US-09-289-346A-5 x AA084372 ..

Align seg 1/1 to: AA084372 from: 1 to: 479

1 ThleuValTrpGlyGluPheGlnValAspClyArgSerAlaArgGly 17
||||| ||||||||| ||||||||| ||||||||| |||||||||
140 ACCCTCGAATGGGAGAGTTTCAGATCGAGGAGATCTCGAAGGGGG 189
17 YCYSGlThrSerAsnSpAlaAlaGluAlaLeuAsnAlaSerSerL 34
| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
190 ACAACATATGACCATGACGCTTACGCCAGCCCTTAACACTGAGTA 239
34 YSGlGluAlaLeuGlnIleIleArgGluLysIleProAlaAlaLeu 50
| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
240 AGTCAGAGGCTCTTAACGCTTAGGGAATTAGCCCTTAAGATTATGTT 289
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAsnArgIle..... 63
290 TTTCATTTCATATTAATTAATAGTAATTAAGATTATTTTACACCTTC 339
64 ..... PheAspLysThrP 68
340 GTTGAGAGTTTATGTTCTGCTTTTATGCTTCTTTGATGAGACTTC 389
68 roGlu 69
|||||
390 CAGAA 394

```

```

seq_name: /cgn1_8/gcycdata/geneseq/geneseqn/NA1995.DAT:AA084375
seq_documentation_block:
ID AA084375 standard; DNA; 550 BP.
XX
XX AA084375;
XX
XX 19-AUG-1995 (first entry)
XX
XX Tomato leaf curl virus Australian strain DNA sequence.
XX
XX Tomato leaf curl virus; Australia strain; plant disease; ds.
XX
XX
XX
XX OS Tomato leaf curl virus (Australia).
XX
XX WO9503404-A.
XX
XX 02-FEB-1995.
XX
XX 22-JUL-1993; 93WO-EP01946.
XX
XX 22-JUL-1993; 93AU-0047014.
XX
XX 22-JUL-1993; 93WO-EP01946.
XX
XX (BIOC-) BIOCEM SA.
XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX
XX Baudino S, Comeau D, Dry IB, Gruber V, Lenee P;
XX Mason J, Rezaian MA, Rigden JE, Rezaian MA;
XX
XX WPI: 1995-075232/10.
XX
XX Synthetic DNA virus ribozyme(s) - reduce replication, infection
XX and/or assembly of viruses by cleaving target virus sequence,
XX useful for preparing resistant plants, esp tomatoes.
XX
XX Disclosure; Fig 1; 90pp; English.
XX
XX The sequence represents the complementary sense DNA strand of an
XX Australian strain of tomato leaf curl virus. Ribozymes specific
XX for this sequence may be used in generation of transgenic plants
XX with disease-resistance.
XX
XX Sequence 550 BP; 148 A; 120 C; 134 G; 142 T; 6 other;

alignment_scores:
Quality: 231.50 Length: 86
Ratio: 3.795 Gaps: 1
Percent Similarity: 70.930 Percent Identity: 54.651

alignment_block:
US-09-289-346A-5 x AA084375 ..

Align seg 1/1 to: AA084375 from: 1 to: 550

1 ThleuValTrpGlyGluPheGlnValAspClyArgSerAlaArgGly 17
||||| ||||||||| ||||||||| ||||||||| |||||||||
201 ACCCTCGAATGGGAGAGTTTCAGATCGAGGAGATCTCGAAGGGGG 250
17 YCYSGlThrSerAsnSpAlaAlaGluAlaLeuAsnAlaSerSerL 34
| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
251 ACAACATATGACCATGACGCTTACGCCAGCCCTTAACACTGAGTA 300
34 YSGlGluAlaLeuGlnIleIleArgGluLysIleProAlaAlaLeu 50
| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
301 AGTCAGAGGCTCTTAACGCTTAGGGAATTAGCCCTTAAGATTATGTT 350
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAsnArgIle..... 63
351 TTTCATTTCATATTAATTAATAGTAATTAAGATTATTTTNNNTACACC 400
64 ..... PheAspLysT 67

```

```
401 TCCGTTGAGGTTATGTTCTCCTTTTATCTTCTTTGATGAG 450
67 hrpGlu 69
:::|||||
451 TTCAGAA 458

seq_name: /cgml_8/gcdata/geneseq/geneseqn/NA1998.DAT:AAV29761
seq_documentation_block:
ID AAV29761 standard; DNA: 2766 BP.
XX
AC AAV29761;
XX
DT 11-AUG-1998 (first entry)
XX
DE Tobacco leaf curling virus gene.
XX
KM Tobacco leaf curling virus gene; TlCV; promoter; ds.
XX
OS Tobacco leaf curling virus.
XX
PN JP10070982-A.
XX
PD 17-MAR-1998.
XX
PF 30-AUG-1996; 96JP-0230394.
XX
PR 30-AUG-1996; 96JP-0230394.
XX
PA (NORQ ) NORINSUISANSHO KYUSHU NOGYO SHIKENJO.
XX
DR MPI; 1998-233630/21.
XX
PT Tobacco leaf curling virus gene - useful for inserting into vectors
XX for expression in, e.g. tomato plants
XX
PS Claim 1: Figs 1-3; 9pp; Japanese.
XX
CC This sequence represents the tobacco leaf curling virus (TlCV) gene of
CC the invention. TlCV gene or its promoter can be inserted into a vector
CC for expression in plants, e.g. tobacco and tomato. This sequence is
CC believed to encode the TlCV proteins shown in AAW56493-W56498.
XX
SQ Sequence 2766 BP; 722 A; 576 C; 609 G; 859 T; 0 other;

alignment_scores:
Quality: 226.00 Length: 84
Ratio: 3.705 Gaps: 1
Percent Similarity: 72.619 Percent Identity: 55.952

alignment_block:
US:09-289-346a-5 x AAV29761/rev ..

Align seg 1/1 to reverse of: AAV29761 from: 1 to: 2766

2 LeuValTrrpGlyGluPheGlnValAlaSpGlyArgSerAlaAargGlyGlyCy 18
||| ::||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2436 CTGATTTTGGAGTTTCCAGTCGATGAGATGAGATGAGTACGAGGAGTTG 2387

18 sGltThSerAsnSppAlaAlaAlaGluAlaLeuAsnAlaSerIysG 35
||||| ::||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2386 CCAATTCGCCACGACGATATGCGCGAGCAATCACTCAGATCAAGT 2337

35 IugIuAlaLeuGlnIleIleargGluIysIleProAlaAlaIleAlaPhe 51
:::||||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
2336 CATCGGCACTCAATATATTAAGGAGAAAGCTCCCAAGATTTGTTTA 2287

52 GlnPheHisAsnLeuAsnSerAsnLeuAspArgIle..... 63
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2286 CAATTCAATATTAAATTCAAATTTAGATGATTTTTCCTCCTCATT 2237
```

```
64 ..... PheAspIysThrProG 69
2236 GCAGCTTTTGTGCTTCTTCTAGTTCATTGATCAAGTCTCTG 2187
69 Lu 69
||
2186 AA 2185

seq_name: /cgml_8/gcdata/geneseq/geneseqn/NA1997.DAT:AAAT93294
seq_documentation_block:
ID AAT93294 standard; DNA: 1160 BP.
XX
AC AAT93294;
XX
DT 27-APR-1998 (first entry)
XX
DE Tomato mottle virus AC1 open reading frame.
XX
KM Geminivirus; TOMOV; AC1 gene; transdominant mutation;
XX transgenic plant; disease resistance; ss; cyclic; circular.
XX
OS Tomato mottle virus isolate Florida.
XX
FH Key Location/Qualifiers
FT CDS 44..1129
FT /tag= a
XX
PN WO9739110-A1.
XX
PD 23-OCT-1997.
XX
PF 15-APR-1997; 97WO-US06300.
XX
PR 16-APR-1996; 96US-0015517.
XX
PA (SEMI-) SEMINIS VEGETABLE SEEDS INC.
XX (WISC ) WISCONSIN ALUMNI RES FOUND.
XX
PI Ahlquist PG, Hanson SF, Lou HT, Maxwell DP, Stout JT;
XX
DR MPI; 1997-526447/48.
XX
PT Transgenic plants expressing geminivirus AC1 and CI wild-type and
XX mutant genes - have increased resistance to geminivirus infection
XX e.g. tomato mottle virus, tomato yellow leaf curl virus or bean
XX golden mosaic geminivirus
XX
PS Example 3.3: Page 57-58; 132pp; English.
XX
CC This genomic DNA sequence includes the open reading frame of the
XX wild-type AC1 gene of tomato mottle virus (TOMOV), a geminivirus
XX that has a bipartite genome. The AC1 gene must be expressed for
XX efficient replication of the two genomic components, DNA-A and
XX DNA-B. It encodes a protein (see AAW34336) having a DNA binding
XX site specific to the DNA-A common region, a DNA nicking activity,
XX and an NTP binding activity. The invention involves production of
XX transgenic plants containing DNA comprising AC1 or CI wild-type or
XX mutant sequences that negatively interfere in trans with
XX geminiviral replication during infection. Such transgenic plants
XX are resistant to viral infection. The AC1/CI genes are especially
XX from TOMOV, tomato yellow leaf curl virus or bean golden mosaic
XX geminivirus (see AAT93282-93) and encode polypeptides (see AAW34324-35)
XX CC that have mutations in the highly conserved DNA-nicking domain
XX and/or the NTP-binding domain.
XX
SQ Sequence 1160 BP; 360 A; 276 C; 257 G; 267 T; 0 other;

alignment_scores:
Quality: 220.00 Length: 70
Ratio: 3.729 Gaps: 0
```

Percent Similarity: 84.286 Percent Identity: 58.571

alignment_block:

US-09-289-346a-5 x AAT93294 ..

Align seg 1/1 to: AAT93294 from: 1 to: 1160

```

1 ThrLeuValTrpGlyGluPheGlnValAspGlyArgSerAlaArgGly1 17
||||| ||||||| ||||||| ||||||| ||||||| |||||||
371 ACAATCGAATGGGAGATTTCACGATGACGCGAGATCTCCAGAGG 420
17 yCysGlnThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerL 34
||||| ||||||| ||||||| ||||||| ||||||| |||||||
421 CCAGCACTCGCTAATGATTCATATGCGAAGCGCTTAATGCAAGTTCG 470
34 ysgLgUaAlaLeuGlnIleIleArgGlyLysIleProAlaAlaLeu 50
||||| ||||||| ||||||| ||||||| ||||||| |||||||
471 TTCAACTCGCTTAGCAGTTCTAAGCGAACAACCAAGATTGTTGTA 520
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLys 67
||||| ||||||| ||||||| ||||||| ||||||| |||||||
521 TTACAAATATCATACATCCGCTTAACCTAGAACGAATATTGCAAGGC 570
67 rProGluPro 70
||||| |||||||
571 TCCGGAACCG 580

```

seq_name: /cgnl_8/gcdata/geneseq/geneseqn/NA1997.DAT:AAT93282

seq_documentation_block:

ID AAT93282 standard; DNA; 1169 BP.

AC AAT93282;

DT 27-APR-1998 (first entry)

DE Tomato mottle virus AC1 mutant TOMOV-AC1dlm gene.

DE GeminiVirus: TOMOV-AC1dlm; AC1 gene; transdominant mutation;

KW Transgenic plant; disease resistance; ss; cyclic; circular.

OS Tomato mottle virus isolate Florida.

OS Synthetic.

XX Key Location/Qualifiers

FT CDS 44..1129

FT CDS /*tag= a

PN WO9739110-A1.

PD 23-OCT-1997.

PF 15-APR-1997; 97WO-US06300.

PR 16-APR-1996; 96US-0015517.

PA (SEMI-) SEMINIS VEGETABLE SEEDS INC.

PA (WISC) WISCONSIN ALOMNI RES FOUNDD.

XX Ahlquist PG, Hanson SF, Luu HT, Maxwell DP, Stout JT;

DR MPI: 1997-526447/48.

DR P-PSDB: AAM34324.

XX Transgenic plants expressing geminivirus AC1 and CI wild-type and

PT mutant genes - have increased resistance to geminivirus infection

PT e.g. tomato mottle virus, tomato yellow leaf curl virus or bean

PT golden mosaic geminivirus

XX Claim 11: Page 60-62; 132pp: English.

XX This DNA sequence comprises a transdominant lethal mutant,

CC designated TOMOV-AC1dlm, of the AC1 gene of tomato mottle virus

CC virus (TOMOV). It encodes an AC1 protein (see AAM34324) that carries
 CC mutations in its NTP-binding domains. The AC1 gene (see also
 CC AAT93294) must be expressed for efficient replication of the two
 CC genomic components, DNA-A and DNA-B, of the bipartite TOMOV genome.
 CC The invention involves production of transgenic plants containing
 CC DNA comprising geminivirus AC1 or CI wild-type or mutant sequences
 CC that negatively interfere in trans with geminiviral replication
 CC during infection. Such transgenic plants are resistant to viral
 CC infection. The AC1/CI genes are especially from TOMOV, tomato
 CC yellow leaf curl virus or bean golden mosaic geminivirus (see
 CC AAT93282-93) and encode polypeptides (see AAM34324-35) that have
 CC mutations in the highly conserved DNA-nicking and/or the NTP-binding
 CC domains.

SQ Sequence 1169 BP; 363 A; 281 C; 255 G; 270 T; 0 other;

alignment_scores:

Quality: 220.00

Ratio: 3.729

Percent Similarity: 84.286

Percent Identity: 58.571

alignment_block:

US-09-289-346a-5 x AAT93282 ..

Align seg 1/1 to: AAT93282 from: 1 to: 1169

```

1 ThrLeuValTrpGlyGluPheGlnValAspGlyArgSerAlaArgGly1 17
||||| ||||||| ||||||| ||||||| ||||||| |||||||
371 ACAATCGAATGGGAGATTTCACGATGACGCGAGATCTCCAGAGG 420
17 yCysGlnThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerL 34
||||| ||||||| ||||||| ||||||| ||||||| |||||||
421 CCAGCACTCGCTAATGATTCATATGCGAAGCGCTTAATGCAAGTTCG 470
34 ysgLgUaAlaLeuGlnIleIleArgGlyLysIleProAlaAlaLeu 50
||||| ||||||| ||||||| ||||||| ||||||| |||||||
471 TTCAACTCGCTTAGCAGTTCTAAGCGAACAACCAAGATTGTTGTA 520
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLys 67
||||| ||||||| ||||||| ||||||| ||||||| |||||||
521 TTACAAATATCATACATCCGCTTAACCTAGAACGAATATTGCAAGGC 570
67 rProGluPro 70
||||| |||||||
571 TCCGGAACCG 580

```

seq_name: /cgnl_8/gcdata/geneseq/geneseqn/NA1997.DAT:AAT93283

seq_documentation_block:

ID AAT93283 standard; DNA; 1169 BP.

AC AAT93283;

DT 27-APR-1998 (first entry)

DE Tomato mottle virus AC1 mutant TOMOV-AC1dlm1 gene.

DE GeminiVirus: TOMOV-AC1dlm1; AC1 gene; transdominant mutation;

KW Transgenic plant; disease resistance; ss; cyclic; circular.

OS Tomato mottle virus isolate Florida.

OS Synthetic.

XX Key Location/Qualifiers

FT CDS 44..1129

FT CDS /*tag= a

PN WO9739110-A1.

PD 23-OCT-1997.

PF 15-APR-1997; 97WO-US06300.

```

XX PR 16-APR-1996; 96US-0015517.
XX (SEMI-) SEMINIS VEGETABLE SEEDS INC.
PA (WISC ) WISCONSIN ALUMNI RES FOUND.
XX PI Ahlquist PG, Hanson SF, Lou HT, Maxwell DP, Stout JT;
XX WPI: 1997-526447/48.
XX DR P-PSDB; AAW34325.
XX PT Transgenic plants expressing geminivirus AC1 and CI wild-type and
XX mutant genes - have increased resistance to geminivirus infection
XX e.g. tomato mottle virus, tomato yellow leaf curl virus or bean
XX PT golden mosaic geminivirus
XX PS Claim 11; Page 64-65; 132pp; English.
XX CC This DNA sequence comprises a transdominant lethal mutant,
XX designated TOMOV-AC1dim1, of the AC1 gene of tomato mottle virus
XX CC virus (TOMOV). It encodes an AC1 protein (see AAW34325) that carries
XX CC a mutation in its NTP-binding domains. The AC1 gene (see also
XX CC AAT93294) must be expressed for efficient replication of the two
XX CC genomic components, DNA-A and DNA-B, of the bipartite TOMOV genome.
XX CC The invention involves production of transgenic plants containing
XX CC DNA comprising geminivirus AC1 or CI wild-type or mutant sequences
XX CC that negatively interfere in trans with geminiviral replication
XX CC during infection. Such transgenic plants are resistant to viral
XX CC infection. The AC1/CI genes are especially from TOMOV, tomato
XX CC yellow leaf curl virus or bean golden mosaic geminivirus (see
XX CC AAT93282-93) and encode polypeptides (see AAW34324-35) that have
XX CC mutations in the highly conserved DNA-nicking and/or the NTP-binding
XX CC domains.
XX SQ Sequence 1169 BP; 361 A; 280 C; 258 G; 270 T; 0 other:

alignment_scores:
Quality: 220.00 Length: 70
Ratio: 3.728 Gaps: 0
Percent Similarity: 84.286 Percent Identity: 58.571

alignment_block:
US-09-289-346a-5 x AAT93283 ..

Align seg 1/1 to: AAT93283 from: 1 to: 1169

1 ThrleuValTTPGlyGluPheGlnValAspGlyArgSerAlaArgGlyG1 17
||||| ||||||| ||||||| ||||||| ||||||| |||||||
371 ACATTCGAATGGGAGATTCACATCGACGCGAGATCTGCCAGAGGAGG 420
17 yCySGlnThSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerL 34
| ||||| ||||| ||||| ||||| ||||| |||||
421 CCACAGCTGCTATCATGATCGCAAGCGTTAAATCGCAAGTTCCG 470
34 ySGlUGlAlaLeuGlnlelleArgGluyslleProAlaAlaAlaLeu 50
||||| ||||| ||||| ||||| ||||| |||||
471 TTCATCTGCTTAGCACTTCTAAGGGAGACAAACCAAAAGATTGTA 520
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
||||| ||||||| ||||||| ||||||| ||||||| |||||||
521 TTACAAATCATACATCGCTCTAACCTAGCAAGAAATATTCGCAAGGC 570
67 rProGluPro 70
||||| ||||| ||||| ||||| ||||| |||||
571 TCCGGAACCG 580

seq_name: /cgnl_8/gcgsdata/geneseq/geneseqn/NA197.DAT: AAT93284
seq_documentation_block:
ID AAT93284 Standard; DNA; 1169 BP.
XX AAT93284:

```

```

XX XX 27-APR-1998 (first entry)
XX DT
XX DE Tomato mottle virus AC1 mutant TOMOV-AC1dim23 gene.
XX KW Geminivirus; TOMOV-AC1dim23; AC1 gene; transdominant mutation;
XX KW transgenic plant; disease resistance; ss; cyclic; circular.
XX OS Tomato mottle virus isolate Florida.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT CDS 44..1129
XX FT /*tag= a
XX PN MO9739110-A1.
XX PD 23-OCT-1997.
XX PF 15-APR-1997; 97WO-US06300.
XX PR 16-APR-1996; 96US-0015517.
XX PA (SEMI-) SEMINIS VEGETABLE SEEDS INC.
XX PA (WISC ) WISCONSIN ALUMNI RES FOUND.
XX PI Ahlquist PG, Hanson SF, Lou HT, Maxwell DP, Stout JT;
XX DR WPI: 1997-526447/48.
XX DR P-PSDB; AAW34326.
XX PT Transgenic plants expressing geminivirus AC1 and CI wild-type and
XX PT mutant genes - have increased resistance to geminivirus infection
XX PT e.g. tomato mottle virus, tomato yellow leaf curl virus or bean
XX PT golden mosaic geminivirus
XX PS Claim 11; Page 67-69; 132pp; English.
XX CC This DNA sequence comprises a transdominant lethal mutant,
XX CC designated TOMOV-AC1dim23, of the AC1 gene of tomato mottle virus
XX CC virus (TOMOV). It encodes an AC1 protein (see AAW34326) that carries
XX CC 2 mutations in an NTP-binding domain. The AC1 gene (see also
XX CC AAT93294) must be expressed for efficient replication of the two
XX CC genomic components, DNA-A and DNA-B, of the bipartite TOMOV genome.
XX CC The invention involves production of transgenic plants containing
XX CC DNA comprising geminivirus AC1 or CI wild-type or mutant sequences
XX CC that negatively interfere in trans with geminiviral replication
XX CC during infection. Such transgenic plants are resistant to viral
XX CC infection. The AC1/CI genes are especially from TOMOV, tomato
XX CC yellow leaf curl virus or bean golden mosaic geminivirus (see
XX CC AAT93282-93) and encode polypeptides (see AAW34324-35) that have
XX CC mutations in the highly conserved DNA-nicking and/or the NTP-binding
XX CC domains.
XX SQ Sequence 1169 BP; 364 A; 278 C; 257 G; 270 T; 0 other:

alignment_scores:
Quality: 220.00 Length: 70
Ratio: 3.729 Gaps: 0
Percent Similarity: 84.286 Percent Identity: 58.571

alignment_block:
US-09-289-346a-5 x AAT93284 ..

Align seg 1/1 to: AAT93284 from: 1 to: 1169

1 ThrleuValTTPGlyGluPheGlnValAspGlyArgSerAlaArgGlyG1 17
||||| ||||||| ||||||| ||||||| ||||||| |||||||
371 ACATTCGAATGGGAGATTCACATCGACGCGAGATCTGCCAGAGAGG 420
17 yCySGlnThSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerL 34
| ||||| ||||| ||||| ||||| ||||| |||||

```


CC viruses. The mutated viral nucleic acid is used for producing
 CC transgenic plants that are resistant to, or tolerant of, the native
 CC virus. The present sequence encodes a mutant form of the Rep (or CI)
 CC protein from the Sardinian isolate of tomato yellow leaf curl virus
 CC (STYLVCV) in which the wild-type Lys227 residue has been changed to an
 CC Ala residue; transgenic Nicotiana benthamiana plants generated by
 CC transformation with the mutated virus were found to be resistant to
 CC STYLVCV, i.e. the mutation results in a dominant negative phenotype.
 XX
 SO Sequence 1080 BP; 355 A; 248 C; 210 G; 267 T; 0 other;

alignment_scores: Length: 69
 Quality: 219.00
 Ratio: 3.842
 Gaps: 0
 Percent Similarity: 82.609 Percent Identity: 57.971

alignment_block:
 US-09-289-346a-5 x AAT12904 ..

Align seg 1/1 to: AAT12904 from: 1 to: 1080

```

2  LeuValTrpGlyGluPheGlnValAspGlyArgSerAlaArgGlyGlyC 18
   ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
331 CTTGAATGGGGTACTTCCAGATCGACGAGCATCTCTAGGCGAGACA 380
   ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
18  sGlnThrSerAsnAspAlaAlaGlnAlaLeuAsnAlaSerSerIysG 35
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
381 ACAGACAGCCACGACGCTTACGCAAGCAATTACCGCAAGGATTAAGT 430
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
35  lucGuaAlaLeuGlnIleIleArgGlnIysIleProAlaAlaAlaLeuPhe 51
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
431 CGCAGGCTCTTGATGTATTAACAAATTAGCCCTAGAGATTAGTCTCTA 480
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
52  GlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspIysThrPr 68
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
481 CATTTTCATATATATAATTAATTAATTAAGTTTCCAGGTGCTCC 530
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
68  oGluPro 70
   |||
531 GGCACCT 537
```

seq_name: /cgnl_8/gcgdata/geneseq/geneseqn/NA1996.DAT:AAT12905
 seq_documentation_block:
 ID AAT12905 standard; DNA; 1080 BP.

```

XX AC AAT12905;
XX AC AAT12905;
XX DT 07-NOV-1996 (first entry)
XX DE Sardinian tomato yellow leaf curl virus mutated CI gene (K227H).
XX XX
XX KM Nucleotide triphosphate binding site; DNA helicase; RNA helicase;
XX KM modification; mutation; viral replication; deficient; inhibition;
XX KM viral resistance; geminivirus; tomato yellow leaf curl virus;
XX KM Sardinian isolate; STYLVCV; transgenic plant; P-loop; CI gene;
XX KM Al1 gene; ss.
XX OS Sardinian tomato yellow leaf curl virus.
XX XX
XX FH Key
XX FT CDS
XX FT 1..1080
XX FT /tag= a
XX FT /product= Rep_(K227H)
XX FT /note= "encodes Rep protein in which wild-type Lys
XX FT at position 227, i.e. within the NTP-
XX binding site, is replaced by His"
XX PD 21-MAR-1996.
XX XX
```

PF 15-SEP-1995; 95WO-FR01192.
 XX
 PR 15-SEP-1994; 94FR-0011040.
 XX
 PA (CNRS) CENT NAT RECH SCI.
 XX
 PI Gronenborn B;
 XX
 DR WPI: 1996-179947/18.
 DR P-PSDB: AAR88871.
 XX

PT Prodn. of virus-resistant transgenic plants - using mutated genomic
 PT sequence from phytopathogenic DNA virus
 XX
 PS Disclosure; Fig 13; 93pp; French.
 XX

CC Mutation of consensus amino acids in the NTP-binding site of
 CC geminivirus Rep protein is used to produce replication deficient
 CC viruses. The mutated viral nucleic acid is used for producing
 CC transgenic plants that are resistant to, or tolerant of, the native
 CC virus. The present sequence encodes a mutant form of the Rep (or CI)
 CC protein from the Sardinian isolate of tomato yellow leaf curl virus
 CC (STYLVCV) in which the wild-type Lys227 residue has been changed to a
 CC His residue; transgenic Nicotiana benthamiana plants generated by
 CC transformation with the mutated virus were not resistant to STYLVCV.
 CC In contrast, plants transformed with a virus in which Lys227 had been
 CC replaced by Ala were found to be resistant.
 XX
 SO Sequence 1080 BP; 356 A; 248 C; 208 G; 268 T; 0 other;

alignment_scores: Length: 69
 Quality: 219.00
 Ratio: 3.842
 Gaps: 0
 Percent Similarity: 82.609 Percent Identity: 57.971

alignment_block:
 US-09-289-346a-5 x AAT12905 ..

Align seg 1/1 to: AAT12905 from: 1 to: 1080

```

2  LeuValTrpGlyGluPheGlnValAspGlyArgSerAlaArgGlyGlyC 18
   ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
331 CTTGAATGGGGTACTTCCAGATCGACGAGCATCTCTAGGCGAGACA 380
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
18  sGlnThrSerAsnAspAlaAlaGlnAlaLeuAsnAlaSerSerIysG 35
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
381 ACAGACAGCCACGACGCTTACGCAAGCAATTACCGCAAGGATTAAGT 430
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
35  lucGuaAlaLeuGlnIleIleArgGlnIysIleProAlaAlaAlaLeuPhe 51
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
431 CGCAGGCTCTTGATGTATTAACAAATTAGCCCTAGAGATTAGTCTCTA 480
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
52  GlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspIysThrPr 68
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
481 CATTTTCATATATATAATTAATTAATTAAGTTTCCAGGTGCTCC 530
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
68  oGluPro 70
   |||
531 GGCACCT 537
```

seq_name: /cgnl_8/gcgdata/geneseq/geneseqn/NA1996.DAT:AAT12906

seq_documentation_block:
 ID AAT12906 standard; DNA; 1080 BP.

```

XX AC AAT12906;
XX AC AAT12906;
XX DT 07-NOV-1996 (first entry)
XX DE Sardinian tomato yellow leaf curl virus mutated CI gene (K227R).
XX KM Nucleotide triphosphate binding site; DNA helicase; RNA helicase;
XX XX
```

modification; mutation; viral replication; deficient; inhibition;
KM viral resistance; geminivirus; tomato yellow leaf curl virus;
KM Sardinian isolate; STYLCV; transgenic plant; P-loop; C1 gene;
XX Alt gene; ss.
XX
OS Sardinian tomato yellow leaf curl virus.
XX
FH Key Location/Qualifiers
FT CDS 1..1080
FT /*tag= a
FT /product= Rep_(K227R)
FT /note= "encodes Rep protein in which wild-type Lys
FT at position 227, i.e. within the NTP-
FT binding site, is replaced by Arg"
XX
PN W09608573-A1.
XX
XX 21-MAR-1996.
PD
PF 15-SEP-1995: 95W0-FR01192.
PR 15-SEP-1994: 94FR-0011040.
PA (CNRS) CENT NAT RECH SCI.
PI Gronenborn B:
XX
XX WPI: 1996-179947/18.
DR P-PSDB: AAR88872.
XX
PT Prod. of virus-resistant transgenic plants - using mutated genomic
PT sequence from phytopathogenic DNA virus
XX
PS Disclosure; Fig 13; 93pp; French.
XX
CC Mutation of consensus amino acids in the NTP-binding site of
CC geminivirus Rep protein is used to produce replication deficient
CC viruses. The mutated viral nucleic acid is used for producing
CC transgenic plants that are resistant to, or tolerant of, the native
CC virus. The present sequence encodes a mutant form of the Rep (or C1)
CC protein from the Sardinian isolate of tomato yellow leaf curl virus
CC (STYLCV) in which the wild-type Lys227 residue has been changed to an
CC Arg residue: transgenic Nicotiana benthamiana plants generated by
CC transformation with the mutated virus were not resistant to STYLCV.
CC In contrast, plants transformed with a virus in which Lys227 had been
CC replaced by Ala were found to be resistant.
XX
SQ Sequence 1080 BP; 356 A; 247 C; 210 G; 267 T; 0 other;

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Percent Similarity:	82.609	Percent Identity:	57.971	

alignment_block:

US-09-289-346A-5 x AAT12906 ..

Align seg 1/1 to: AAT12906 from: 1 to: 1080

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          ||| ||||| |||||:::||||| ||||| |||||
    331 CTTGAATGGGTACTCTTCAGATCCACGCAGCAGCATCTGCTAGGGGAGACA 380
          |||||||serAsnASPalaIalagIuAlaleuasnIaserSergSG 35
          |||||||:::||||| ||||| ||||| ||||| |||||
    381 ACAGACAGGCCAACGACGCTTACGCCAAAGCAATTACCGCAGAGAAATAAGT 430
          |||||||leuGlnIleIleatrgCylsileProPalaIalaleuPhe 51
          ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
    431 CGAGAGCTCTTGATGTAATTAAGAATTAGAGCCCTAGAGATTACCTTCTTA 480
          |||
    52 GlupHeHisAsnIeAsnSerAsnLeuAsnParqIIepheaPlvsThPr 68
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      531 GGCACCT 537
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seq_documentation_block:
ID      AAQ84378 standard; DNA; 1695 BP.
AC
XX
XX      AAQ84378.
DT      19-AUG-1995 (first entry)
DE
XX      Tomato yellow leaf curl virus DNA sequence.
XX
XX      Tomato yellow leaf curl virus; plant disease:
KM      ribozyme target sequence; ds.
XX
XX      Tomato yellow leaf curl virus (S).
OS
XX
XX      Key      Location/Qualifiers
FH      misc_feature      405
FT      /*tag= a
FT      /note= "ribozyme cleavage site"
FT      1065
FT      /*tag= b
FT      /note= "ribozyme cleavage site"
FT      1286
FT      /*tag= c
FT      /note= "ribozyme cleavage site"
PN      WC9503404-A.
XX
XX      02-FEB-1995.
XX
XX      22-JUL-1993; 93WO-EP01946.
XX
XX      22-JUL-1993; 93AU-0047014.
PR      22-JUL-1993; 93WO-EP01946.
XX
XX      (BIOC-) BIOCEM SA.
PA      (CSIR } COMMONWEALTH SCI & IND RES ORG.
PA
PA      Baudino S, Comeau D, Dry IB, Gruber V, Lenee P;
PI      Mason J, Rezaian MA, Rigiden JE, Rezaian MA;
PI
XX      MPI: 1995-075232/10.
XX
XX      Synthetic DNA virus ribozyme(s) - reduce replication, infection
PT      and/or assembly of viruses by cleaving target virus sequence,
PT      useful for preparing resistant plants, esp tomatoes.
XX
XX      Disclosure; Fig 8; 90pp; English.
XX
XX      The sequence represents the complementary sense DNA strand of
CC      tomato yellow leaf curl virus-S strain. Ribozyme cleavage sites
CC      are indicated. Ribozymes against this sequence may be used in
CC      generation of transgenic tomato plants with disease-resistance.
XX
XX      Sequence 1695 BP; 568 A; 366 C; 308 G; 453 T; 0 other;
XX
alignment_scores:
      Quality: 219.00      Length: 69
      Ratio: 3.842      Gaps: 0
Percent Similarity: 82.609      Percent Identity: 57.971
alignment_block:
US-09-289-346A-5 x AAQ84378 ..

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Align seg 1/1 to: AA084378 from: 1 to: 1695

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487 CTTGAATGGGCTTCCAGTACGACGAGATCTGTAGGGAGACA 536
   ||| ||||| |||||:|||||:|||||:|||||:|||||
18 sGltThrSerAspAlaAlaGluAlaLeuAsnAlaSerSerIysG 35
   |||||:|||||:||||| |||||:|||||:|||||:|||||
537 ACACACAGCCACGACGCTTACGCAAGGCAATTACGACGAGTAAGT 586
   |||||:|||||:||||| |||||:|||||:|||||:|||||
35 IugIuaIaLeuGlnIleIleArgGluIuysIleProAlaAlaLeuPhe 51
   :|||||:|||||:||||| |||||:|||||:|||||:|||||
587 CCGAGGCTCTTGATGTATATTAACAATTAAGCCCTAGAGATTACGTTCTA 636
   :|||||:|||||:||||| |||||:|||||:|||||:|||||
52 GlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysThrPr 68
   :|||||:|||||:||||| |||||:|||||:|||||:|||||
637 CATTTTCATATATTAATTAATTAAGTTTTCAGGTCCTCC 686
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68 oGluPro 70
687 GGCACCT 693

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seq_name: /cgnl_8/gcgcdata/geneseq/geneseq/NA1997.DAT:AA193291

seq_documentation_block:

ID AAT93291 standard; DNA; 1062 BP.

XX AAT93291:

DT 27-APR-1998 (first entry)

XX Bean golden mosaic geminivirus CI mutant ORF BGAC221.

XX Geminivirus: BGMY: CI gene:: transdominant mutation:

KM transgenic plant; disease resistance; ss: cyclic; circular.

XX Bean golden mosaic virus type II isolate Guatemala.

OS WO9739110-A1.

PN 23-OCT-1997.

XX 15-APR-1997; 97WO-US06300.

XX 16-APR-1996; 96US-0015517.

XX (SEMI-) SEMINIS VEGETABLE SEEDS INC.

PA (WISC) WISCONSIN ALUMNI RES FOUND.

XX Ahlquist PG, Hanson SF, Luu HT, Maxwell DP, Stout JT;

PI MPI: 1997-526447/48.

XX P-PSDB; AAM34333.

DR Transgenic plants expressing geminivirus AC1 and CI wild-type and

XX mutant genes - have increased resistance to geminivirus infection

PT e.g. tomato mottle virus, tomato yellow leaf curl virus or bean

PT golden mosaic geminivirus

XX Claim 13: Page 107-109; 132pp; English.

PS This DNA sequence comprises construct BGAC221 that codes for a

CC transdominant lethal mutant (see AAM34333) of the CI protein (see

CC AAM34338) of bean golden mosaic virus (BGMY). It was obtained by

CC Kunkel mutagenesis of the wild-type CI gene (see AAT93314). CI is

CC required for replication. The invention involves production of

CC transgenic plants containing DNA comprising geminivirus CI or AC1

CC wild-type or mutant sequences that negatively interfere in trans

CC with geminiviral replication during infection. Such transgenic

CC plants are resistant to viral infection. The AC1/CI genes are

CC especially from BGMY, tomato mottle virus or tomato yellow leaf

CC curl virus (see AAT93282-93) and encode polypeptides (see AAM34324-35)

CC that have mutations in the highly conserved DNA-nicking and/or the

CC NTP-binding domains.

XX

SQ Sequence 1062 BP; 339 A; 245 C; 219 G; 259 T; 0 other;

alignment_scores:

Quality: 218.00

Ratio: 3.695

Percent Similarity: 84.286

Percent Identity: 60.000

alignment_block:

US-09-289-346A-5 x AAT93291 ..

Align seg 1/1 to: AAT93291 from: 1 to: 1062

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328 ACATCGAATGGGGACAATTCACAAGTCAGCCGCGATCTGCAAGAGGAGG 377
   |||||:|||||:||||| |||||:|||||:|||||:|||||
17 YcysGlnThrSerAspAlaAlaGluAlaLeuAsnAlaSerSerL 34
   |||||:|||||:||||| |||||:|||||:|||||:|||||
378 TCAGAGCTGTGCCACAGCACTCATATGCAAGGACAGACCAAGATTACGTC 427
   |||||:|||||:||||| |||||:|||||:|||||:|||||
428 TTGATCTGCCCTTGACAATATGCAAGGACAGACCAAGATTACGTC 477
   |||||:|||||:||||| |||||:|||||:|||||:|||||
34 YscIugIuaIaLeuGlnIleIleArgGluIuysIleProAlaAlaLeu 50
   |||||:|||||:||||| |||||:|||||:|||||:|||||
428 CTTCAACATCATCAACACATCGCTTCAATCTGCAAGGATCTGTCGTC 527
   |||||:|||||:||||| |||||:|||||:|||||:|||||
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
   :|||||:|||||:||||| |||||:|||||:|||||:|||||
478 CTTCAACATCATCAACACATCGCTTCAATCTGCAAGGATCTGTCGTC 527
   |||||:|||||:||||| |||||:|||||:|||||:|||||
67 rProGluPro 70
   :|||||
528 GCCGGAACCA 537

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OM of: US-09-289-346a-5 to: EST:* out_format: pfs
Date: Jan 3, 2002 6:15 PM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

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-O=/gn11/USP10_spool/US09289346/runat_03012002.153303.16354/app_query.fasta.1.1163  
-DB=EST -QFMT=fastap -SUPERX=p2n.rst -GAPOP=12.000 -GAPEXT=4.000  
-MINMATCH=0.100 -LOOPOI=0.000 -LOGEXT=0.000 -OGAPOP=4.500  
-OGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000  
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-DELEXT=7.000 -START=1 -MATRIX=blonum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR_SCORE=PCT -THR_MAX=100 -THR_MIN=0  
-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0  
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Search information block:

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Query length: 70
Database: EST:*
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Search time (sec): 8697.120000

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gb_gss:AO656777	-	72.50	8.93	570	! AO656777 Sheared DNA-27M23.TR S
gb_est1:BG473323	+	71.00	153.67	789	! BG473323 602513970F1 NIH.MGC.16
gb_est1:BF342302	+	69.00	150.82	646	! BF342302 602013083F1 NCI.CGAP.B
gb_est1:AT1731422	-	68.50	151.23	546	! AT1731422 BNLGH19563 SIX-Jday Cdt
gb_est1:BF293368	-	68.50	150.65	580	! BF293368 WHE2157_B02_D0325 Ttit
gb_est1:BG595046	-	68.50	148.44	732	! BG595046 EST493724 CSTS Solanum
gb_est1:BE964992	+	68.50	141.54	1512	! BE964992 601658769R1 NIH.MGC.6
gb_gss:AO950848	+	68.00	149.59	572	! AO950848 Sheared DNA-51M3.TF S
gb_gss:AO947513	+	68.00	147.35	587	! AO947513 Sheared DNA-49M17.TF S
gb_est1:AT533218	+	67.50	147.76	608	! AT533218 SD04968.5ptime SD Dros
gb_est1:BE977193	+	67.50	147.76	612	! BE977193 bs60911.y1 Drosophila
gb_est1:BI366217	-	67.50	144.71	645	! BI366217 RES1713.5ptime RE Dros
gb_est1:BF256735	-	67.00	144.71	844	! BF256735 HVSMEF0010N17E Hordeum
gb_gss:CN6058KF	-	67.00	141.26	1070	! AT351960 Tetradon nigroviridis
gb_est1:AM773300	+	66.50	141.50	921	! AM773300 EST00206 DT408uDBD Gal
gb_est1:AM206595	+	66.00	151.10	296	! AM206595 UI-R-B11-ato-e-05-0-UI
gb_est1:BE976954	-	66.00	144.09	619	! BE976954 bs58c02.y1 Drosophila
gb_est1:BG593614	-	65.50	143.15	603	! BG593614 EST492292 CSTS Solanum
gb_est1:AA950726	+	65.50	142.91	618	! AA950726 LD30829.5ptime LD Dros
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gb_est1:BG599652	-	65.50	141.45	721	! BG599652 EST04547 CSTS Solanum
gb_est1:BI406561	-	65.50	141.24	737	! BI406561 171B01 Mature tuber Id
gb_gss:AZ225957	+	65.00	151.76	215	! AZ225957 RPCT-23-78B10.TJ RPCT
gb_est1:BE223710	+	65.00	143.70	502	! BE223710 RPCT-23-365L15.TJ RPCT
gb_gss:AZ012319	+	65.00	142.39	576	! AZ012319 RPCT-23-365L15.TJ RPCT
gb_est1:AT1295401	+	65.00	142.13	592	! AT1295401 LP09019.3ptime LP Dros
gb_gss:AZ648984	-	65.00	141.36	642	! AZ648984 1M051823F Mouse.10Kb
gb_est1:BG635203	-	65.00	140.72	687	! BG635203 AT31714.5ptime AT Dros
gb_est1:BF501623	-	65.00	140.33	716	! BF501623 AT31999.5ptime AT Dros
gb_est1:BG477162	+	65.00	139.78	766	! BG477162 T62242492F1 NIH.MGC.20
gb_gss:CN6045Y5	+	65.00	137.71	943	! AT275990 Tetradon nigroviridis
gb_est1:AM521895	+	64.50	144.81	394	! AM521895 UI-R-B00-agu-e-10-0-UI
gb_est1:AT058491	+	64.50	144.12	424	! AT058491 UI-R-C1-Kv-a-06-0-UI
gb_est1:AT058495	+	64.50	144.09	425	! AT058495 UI-R-C1-Kv-b-04-0-UI
gb_est1:BI298579	+	64.50	143.66	445	! BI298579 UI-R-CV2-Ch1-8-12-0-UI
gb_est1:BG376082	+	64.50	143.55	450	! BG376082 UI-R-CV0-bum-e-09-0-UI
gb_est1:AT010158	+	64.50	142.88	483	! AT010158 EST07633 Normalized UI
gb_est1:AM532518	+	64.50	142.03	528	! AM532518 UI-R-B50-aml-I-08-0-UI

gb_est1:BE100608 + 64.50 141.91 96.86 535 ! BE100608 UI-R-BJ1-auk-d-05-0
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gb_est2:BG374197 + 64.50 141.56 101.30 555 ! BG374197 UI-R-CV1-bsm-e-07-0
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seq_documentation block:

LOCUS AJ273182 608 bp mRNA EST 29-DEC-1999
DEFINITION AJ273182 Metarhizium anisopliae ANSEF 2575 Metarhizium anisopliae
CDNA clone Ma#647, mRNA sequence.

ACCESSION AJ273182

VERSION AJ273182.1 GI:6432554

KEYWORDS EST.

SOURCE Metarhizium anisopliae.

ORGANISM Metarhizium anisopliae

REFERENCE 1 (bases 1 to 608)

AUTHORS Screen,S.E., Mathur,P. and St. Leger,R.J.

TITLE EST analysis of the Insect pathogenic Fungus Metarhizium anisopliae

JOURNAL Unpublished (1999)

COMMENT Contact: Screen SE

Entomology

University of Maryland

4112 Plant Sciences Building, College Park, MD 20742, USA.

FEATURES

source

1. 608

/organism="Metarhizium anisopliae"

/strain="ANSEF 2575"

/db_xref="taxon:5530"

/clone="Ma#647"

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/note="Vector: Unizap; Metarhizium anisopliae was grown on

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US-09-289-346a-5 x AJ273182 ..

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31AlaSerSerLysGluGluAlaLeuGlnIleLeuArgIuL 44

232 AAATTCGATGCGAGTCGCTCAAGATGCTAAATATCAACAATTCGAGAAG 281

44 yslleProAlaAlaLeuPheGlnPheHisAsnLeuAsnSer..... 58

282 ATTGGCGCGCGGCGACGGAATTCGCCGCCCAATCTTAACTCGATGANG 331

59AsnLeuAspArgIlePheAspLysThr 67

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seq_documentation_block: 623 bp mRNA EST 29-DEC-1999

LOCUS AJ272897

DEFINITION AJ272897 Metarhizium anisopliae ANSEF 2575 Metarhizium anisopliae

CDNA clone Ma#229, mRNA sequence.

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VERSION     AJ272897.1  GI:6432270
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SOURCE      Metarhizium anisopliae.
ORGANISM    Metarhizium anisopliae
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            Hypocreales; Clavicipitaceae; mitosporic Clavicipitaceae;
            Metarhizium.
REFERENCE   1 (bases 1 to 623)
AUTHORS     Screen,S.E., Mathur,P. and St. Leger,R.J.
TITLE       EST analysis of the insect pathogenic fungus Metarhizium anisopliae
JOURNAL     Unpublished (1999)
COMMENT     Contact: Screen SE
            Entomology
            University of Maryland
            4112 Plant Sciences Building, College Park, MD 20742, USA.
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175 CAAAGTGCGCCATTACAGCTCCAGAGATGCGCGCTCAACACCAATCA 224
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31  .....AlaSerSerLySGluAlaLeuGlnIleLeaArgGlu 44
    :::::::::::::::::::::
225 AAATTTCGATGCGCGATGCTCAGATGTAATAATCAAAATTCAGAAAG 274
    :::::::::::::::::::::
44  yslleProAlaAlaAlaLeuPheGlnPheHisAsnLeuAsnSer..... 58
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275 ATTGGCGCGCGCGCGAATATCTCGCGCCCAATCTTAACCTGATGAG 324
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59  .....AsnLeuAspArgIlePheAspLysThr 67
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325 GATCGAGGGGAAACCTGATGCGCTCGCAACACAGACC 363
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seq_documentation_block:
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DEFINITION   Sheared DNA-27M23-TR Sheared DNA Trypanosoma brucei genomic clone
ACCESSION   A0656777
VERSION     A0656777.1  GI:5164625
KEYWORDS
SOURCE      Trypanosoma brucei.
ORGANISM    Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1 (bases 1 to 570)
AUTHORS     El-Sayed,N., Zhao,S., Zhao,H., Gill,S., Suh,E., Malek,J., Fujil,C.,
            Gerrard,C., Leech,V., de Jong,P., Ullu,E., Melville,S., Doneison,J.,
            Fraser,C. and Adams,M.

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TITLE       Determination of clone end sequences from Trypanosoma brucei GUTat
JOURNAL     10.1 sheared DNA library
COMMENT     Unpublished (1999)
            Other-GSSs: Sheared DNA-27M23-TR
            Contact: Najib M. El-Sayed
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: nelsayed@tigr.org
            Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared
            DNA library constructed at TIGR. Clones will be available for
            distribution through ATCC. Sheared DNA end sequences search page:
            http://www.tigr.org/cdb/mdb/tbdb/.
            Seq primer: M13-Reverse
            Class: Shotgun.
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             /db_xref="taxon:5691"
             /clone="Sheared DNA-27M23"
             /clone_lib="Sheared DNA"
             /note="Vector: pUC18; Site1: SmaI; Constructed at The
             Institute for Genomic Research (TIGR), Rockville, MD.
             Genomic DNA isolated from a cloned population of
             Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically
             sheared to give a tight size distribution (approx 2 kb).
             The v + i method used for the library construction is
             described in detail in Smith, H.O. and Venter, J.C.
             (Making small insert libraries for whole genome shotgun
             sequencing projects. In Genome Sequencing: A Practical
             Approach, eds. M. Vaundin and B. Barrell, Oxford University
             Press, 1999)."
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alignment_block:
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    :::::::::::::::::::::
228 CAAGTGCTGTCGAAATATCAAAATTCAGCGGAGCGCGTCACAAACGCAAA 179
    :::::::::::::::::::::
22  n...AspAlaAlaAlaGluAlaLeuAsnAla.....SerSerLysG 35
    :::::::::::::::::::::
178 CAGCCAAAGCGCTACAGGCTGCTACTAAACGCATGTTCTTCAGCGCCCT 129
    :::::::::::::::::::::
35  lGluAlaLeuGlnIleLeaArgGluLysIleProAlaAlaAlaLeu... 50
    :::::::::::::::::::::
128 CAGTGCTGTCGAAATATCAAAACGCAACCGCGAGCATGATCAGCTACAGG 79
    :::::::::::::::::::::
51  PheGlnPheHisAsnLeuAsnSerAsnLeuAspArg 62
    :::::::::::::::::::::
78 ACAGCAACCCCACTTTTTCAGAGAGCAACGAAACAGAG 43
    :::::::::::::::::::::
seq_name: gb_est2: BG472323
seq_documentation_block:
LOCUS       BG472323      789 bp      mRNA      EST      21-MAR-2001
DEFINITION   602513970F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:4645793 5',
ACCESSION   BG472323
VERSION     BG472323.1  GI:13404598

```



```

SOURCE          human.
ORGANISM        Homo sapiens
REFERENCE       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS        Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE          1 (bases 1 to 789)
JOURNAL        NIH-MGC http://mgc.nci.nih.gov/
COMMENT        National Institutes of Health, Mammalian Gene Collection (MGC)
                Unpublished (1999)
                Contact: Robert Strausberg, Ph.D.
                Email: cgapds-remail.nih.gov
                Tissue Procurement: ATCC
                CDNA Library Preparation: Ling Hong/Rubin Laboratory
                CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
                DNA Sequencing by: Incyte Genomics, Inc.
                Clone distribution: MGC clone distribution information can be
                found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov
                Plate: LINC1419 row: 1 column: 18
                High quality sequence stop: 745.
                Location/Qualifiers
                1..789
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="IMAGE:4645793"
                /clone_1lb="NIH_MGC_16"
                /russue_type="retinoblastoma"
                /lab_host="DH10B (phage-resistant)"
                /note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2:
                EcoRI; cDNA made by oligo-dT priming. Directionally
                cloned into EcoRI/XhoI sites using the following 5'
                adaptor: GGCCAGAG(G). Library constructed by Ling Hong
                in the Laboratory of Gerald M. Rubin (University of
                California, Berkeley) using ZAP-CDNA synthesis kit
                (Stratagene) and Superscript II RT (Life Technologies)
                Note: this is a NIH_MGC library."
BASE COUNT      162 a      265 c      211 g      151 t
ORIGIN
alignment_scores:
    Quality:      71.00      Length:      78
    Ratio:        1.578      Gaps:      2
    Percent Similarity: 57.692      Percent Identity: 28.205
alignment_block:
US-09-289-346A-5 x BG472323 ..
Align seg 1/1 to: BG472323 from: 1 to: 789
1 ThrLeuValTrrpGlyGluPheGlnValAspGlyArgSerAlaArgGlyG1 17
||||| ||||||| :||| :||| :||| :||| :||| :||| :|||
480 ACCCTTGACACTGGGGGAGAACCCCGAATTGACCCGACGGCTTGAGGACG 529
17 ycyssglnThrSerAsnAspAlaAlaAlaGlnAlaLeuAsn..... 30
:||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
530 ACCGTACACGGGACGACACTTCGCCGCCGACCTTGACATGTCACATT 579
31 .....AlaSerSerIysGlnGlu 36
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
580 ATAACCTCAGACCTTTATCTCTGACGCCAGCAGCCAGCAGCAACAGTCAGNA 629
37 AlaLeuGlnIleIleIleArgGlnIlyIleProAlaAlaAlaIleuPheGlnph 53
:||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
630 GGCGTCGCGTGTCTCG.....GCTGTTCATTCATTCAGAT 661
53 ehtIsAsnLeuAsnSerAsnLeuAsnAlaPArgIlePhe 64
:||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
662 GGCGTCCTTCATTCGCTCATGACACAGGATCTTC 695
seq_name: gb_est2:BF342302
seq_documentation_block:
LOCUS          BF342302      646 bp      mRNA      EST      22-NOV-2000

```

```

DEFINITION      602013083F1 NCL_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4148757
ACCESSION       BF342302
VERSION         BF342302.1 GI:11289259
KEYWORDS        EST.
SOURCE          human.
ORGANISM        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE       1 (bases 1 to 646)
AUTHORS        NIH-MGC http://mgc.ncl.nih.gov/.
TITLE           National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL        Unpublished (1999)
COMMENT         Contact: Robert Strausberg, Ph.D.
                  Email: cgapbs-remail.nih.gov
                  Tissue Procurement: David N. Louis, M.D.
                  CDNA Library Preparation: Life Technologies, Inc.
                  CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
                  DNA Sequencing by: Incyte Genomics, Inc.
                  Clone distribution: MGC clone distribution information can be
                  found through the I.M.A.G.E. Consortium/LNML at:
                  http://image.llnl.gov
                  Plate: LLAM9409 row: f column: 22
                  High quality sequence stop: 613.
FEATURES        Location/Qualifiers
                 source          1..646
                                /organism="Homo sapiens"
                                /db_xref="taxon:9606"
                                /clone="IMAGE:4148757"
                                /clone_lib="NCL_CGAP_Brn64"
                                /lssue_type="gliblastoma with EGFR amplification"
                                /lab_host="DH10B (T1 phage-resistant)"
                                /note="Organ: brain; Vector: PCMV-SPOrt6; Site_1: Notif;
                                /Site_2: Salt; Cloned unidirectionally. Primer: Oligo dT.
                                Average insert size 1.57 kb. Constructed by Life
                                Technologies. Note: this is a NCL_CGAP Library."
BASE COUNT      150 a 158 c 197 g 141 t
ORIGIN
alignment_scores:
    Quality:     69.00      Length:   49
    Ratio:       2.156      Gaps:    3
    Percent Similarity: 65.306      Percent Identity: 40.816
Alignment Block:
US-09-289-346A-5 x BF342302 ..
Align seg 1/1 to: BF342302 from: 1 to: 646
3 ValTRGtGly...GlupheGlnValAspGIYArgSerAlaArGtIyGlycy 18
||||||| ||| ::::| | | | | | | | | | | | | | | | | | | |
202 GTGTGGGGGTAGAGCAGCGCTGCTGTGCAGGGGAGCGGGGGGATG 251
18 scInTrSerAshnASpAlaAlaIaGluAlaLeuAnAlaSerSerLyg 35
|::: ::::: ||| :::::| | | | | | | | | | | | | | | | |
252 TCACACTCGGGGACGGGGACCACCAAGAGGCTCAGGGGGGCCCAAACCTTG 301
35 luCluaIaleuGlnlleIleaRgtLuLys.....IlleRoAlaAla 48
||| | | | | | | | | | | | | | | | | | | | | | | | |
302 AA.....ATCCGTGAACAACGGGGGGGTCCCAAGAGCT 333
seq_name: gb_est1:A1731422
seq_documentation_block:
LOCUS      A1731422      546 bp      mRNA      EST      11-JUN-1999
DEFINITION BNHG19563 Six-day Cotton lfler Gosssystem hirsutum cDNA 5' similar
to mitochondrial processing peptidase (EC 3.4.99.41) alpha-II chain
precursor - potato gl1587562 (X80236) mitochondrial processing
peptidase [Solanium tuberosum], mRNA sequence.
ACCESSION   A1731422
VERSION     A1731422.1 GI:5050274
KEYWORDS    EST.

```

SOURCE	upland cotton.
ORGANISM	Gossypium hirsutum
REFERENCE	Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
AUTHORS	1 (bases 1 to 546)
TITLE	Blewitt, M., Matz, E. C., Davy, D. F. and Burr, B.
JOURNAL	ESTs from developing cotton fiber
COMMENT	Unpublished (1999) Contact: Ben Burr Biology Department Brookhaven National Laboratory Upton, NY 11973, USA Tel: 516-344-3396 Fax: 516-344-3407 Email: burr@nslu1.bnl.gov Seq primer: T3 primer. Location/Qualifiers 1..546 /organism="Gossypium hirsutum" /cultivar="Acala Maxxa" /db_xref="taxon:3635" /clone_lib="Six-day Cotton fiber" /tissue_type="Immature fiber" /dev_stage="Six days post anthesis" /lab_host="XL1-Blue" /note="Vector: pBluescript II KS+"
BASE COUNT	151 a 99 c 134 g 160 t 2 others
ORIGIN	
alignment_scores:	
Quality:	68.50 Length: 60
Ratio:	1.671 Gaps: 1
Percent Similarity:	68.333 Percent Identity: 33.333
alignment_block:	
US-09-289-346A-5 x AT731422/rev ..	
Align seg 1/1 to reverse of: AT731422 from: 1 to: 546	
11 GYARGSERAlaargGlyGlyCysGlnTyrSerAsnAspAlaAla.. 26	
469 GGAGAGTCGACAGAGAGTGGTTCTGCACAGATTAACAATTCCTCATGTTT 420	
27 .GluAlaLeuAsnAlaSerSerLysGlnGluAlaLeuGlnIleIleArg 43	
419 TACACCAAGTTGCTGCCAGTACCATCGAGAGACAGTAAATTTTGCAC 370	
43 IuLysIleProAlaIleAlaLeuPheGlnPheHisnLeuAsnSerAsn 59	
369 CAAAATCTCCAAAACTGACTGTTCAACATATTAATCACTGCAGATCTCGG 320	
60 LeuAspArgIlePheAspLysThrProGlu 69	
319 GCTAAAGAAGATTTCACATGCACACAGAA 290	
seq_name: gb_est2:BF2933368	
seq_documentation_block:	
LOCUS	BF2933368 580 bp mRNA EST 17-NOV-2000
DEFINITION	WH2157_B02.D03S5 Triticum turgidum L. var. durum (durum wheat)
ACCESSION	Whole plant cDNA library Triticum turgidum cDNA clone
VERSION	WH2157_B02.D03, mRNA sequence.
KEYWORDS	BF2933368 BF2933368.1 GI:11224528
SOURCE	EST.
ORGANISM	Triticum turgidum. Triticum turgidum. Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidaeae; Triticeae; Triticum.
REFERENCE	1 (bases 1 to 580)

TITLE

The structure and function of the expressed portion of the wheat genomes - Whole plant cDNA library from Triticum turgidum L. var. durum

JOURNAL COMMENT

unpublished (2000)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oanderson@pw.usda.gov
Sequence have been limited to remove vector sequence and low quality sequence with phred score less than 20
Seq primer: StrataGene SX primer.

FEATURES

Source location/Qualifiers

1..580

/organism="Triticum turgidum"
/cultivar="Langdon-16"
/db_xref="taxon:4571"
/clone="WHE2157.B02.D03"
/cclone.lib="Triticum turgidum L. var. durum (durum wheat) whole plant cDNA library"
/tissue_type="All tissues"
/dev_stage="Different growth stages"
/lab_host="E. coli SOLR"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid; Site 1: EcoRI; Site 2: XhoI; Plants were grown in a growth chamber at North Dakota State University (Kilian, Otto, Simons). Tissues collected from seven-day etiolated seedling leaf, stem, root and seed; leaf from plant at fourth leaf stage; spike from pre-anthesis through 20 days after anthesis; flag leaf; leaf and stem tissue from tillers and root. Total RNA and poly(A) RNA were prepared from each tissue and then pooled, a cDNA library was made, and the cDNA clones were in vivo excised to give pBluescript phagemids in the TJ Clouse lab (Akhunov, Chin, Choi, Clouse, Pentton, Kilian, Otto, Simons, Zhang) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

BASE COUNT

139 a 148 c 155 g 138 t

ORIGIN

alignment_scores:
Quality: 68.50 Length: 64
Ratio: 1.756 Gaps: 3
Percent Similarity: 60.938 Percent Identity: 37.500

Alignment_block:
US-09-289-346A-5 x BF293368/rev ..

Align seg 1/1 to reverse of: BF293368 from: 1 to: 580

5 GlycinephglnValaspGlyarserAlaargGlyglyCysglnthrse 21
|||||..... ||||| ||||| |||||
506 gggtccatcgatgcgtagatggccgcttcgccgctgatcatccacccaacaa 457
21 rasnasppalaalaaaglaaleuasnaIsaserterlys.....Glug 36
||||||:::|||:::|||
456 caac.....ACCAAGCTGTAAACCTCCCTTCCTTTAGCTGCC 416
36 laalaleugIntleileargluLytleproalaalaLeupeghn 52
|||||:::|||:::||| ::||| |||
415 ccctcctgcagctaccacgcgcgaagtaaccacgatgctccgcgaacca 366
53 phehisasnleuasn.Serasnleuasparqylepheasr 65
||||| |||:::||| |||:::|||
365 tgctcataaacctgaacctcatccttgaggagaacctccttgac 326

```

seq_name: gb_est2:BG595046
seq_documentation_block:
LOCUS BG595046 732 bp mRNA EST 12-APR-2001
DEFINITION EST93724 csts Solanum tuberosum cDNA clone csts9019 5' sequence,
mRNA sequence.
ACCESSION BG595046
VERSION BG595046.1 GI:13613186
KEYWORDS EST.
SOURCE potato.
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
REFERENCE
1 (bases 1 to 732)
Van der Hoeven,R., Bezzerides,J., Sun,H., Cho,J., Chiemlingo,A.,
Bougril,O., Buell,C.R., Ronning,C., Tanksley,S. and Baker,B.
Generations of ESTs from sprouting potato eyes
JOURNAL Unpublished (2000)
COMMENT
Contact: Cathy Ronning
The Institute for Genomic Research
For clone info: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com
Seq primer: M13F-R.
FEATURES
location/Qualifiers
1..732
/organism="Solanum tuberosum"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="csts9019"
/clone_lib="csts"
/tissue_type="sprouting eyes from tubers"
/dev_stage="12-14 weeks post harvest"
/lab_host="SOLE"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; Various sizes of sprouting eyes (2mm to 15mm) were
taken from tubers. The tubers were incubated at 26C in the
dark for 2-3 weeks prior to sprouting. The eyes were
frozen in liquid nitrogen immediately upon removal from
tubers."
BASE COUNT 198 a 154 c 164 g 216 t
ORIGIN
alignment_scores:
Quality: 68.50 Length: 54
Ratio: 1.903 Gaps: 3
Percent Similarity: 66.667 Percent Identity: 37.037
alignment_block:
US-09-289-346a-5 x BG595046/rev ..
Align seg 1/1 to reverse of: BG595046 from: 1 to: 732
11 GYARSerAlaIArgGlyGlyGlnThrSerAsnAsp.....AlaAl 25
|||||
408 GGAAGGTCGGCTCTACACATGCTAGACGAGTAATGGAATAGAGCTTG 339
|||||
25 aaIaGluAlaLeuAsnLaserSerLysGluAlaLeuGlnIleLea 42
|||||
358 TATTAGAACCAAAATATGCAAGACTCTTACAACTTATCCAAAGTTAGCA 309
|||||
42 rglLysIleProAlaAlaLeuPheGlnPheHisAsn...LeuAsn 57
|||||
308 AAATAAAATTT.....CTTCACTTGTTCAGATTCCCAATAGCCTCAAC 265
|||||
58 SerAsnLeuAsp 61
|||||
264 AACATATCAAC 253
seq_name: gb_est2:BE964992

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seq_documentation_block:
LOCUS BE964992 1512 bp mRNA EST 14-DEC-2000
DEFINITION 601658769R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886169 3',
mRNA sequence.
ACCESSION BE964992
VERSION BE964992.2 GI:11768902
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 1512)
NIH-MGC http://mgc.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT
On Oct 3, 2000 this sequence version replaced gi:10575697.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DRP/Gazdar
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1CM649 row: 1 column: 18
High quality sequence stop: 291.
FEATURES
location/Qualifiers
1..1512
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3886169"
/clone_lib="NIH_MGC_69"
/tissue_type="large cell carcinoma, undifferentiated"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pCMV-SPOrt6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.1 kb. Library constructed by Life
Technologies."
BASE COUNT 481 a 308 c 357 g 363 t 3 others
ORIGIN
alignment_scores:
Quality: 68.50 Length: 77
Ratio: 1.522 Gaps: 3
Percent Similarity: 58.442 Percent Identity: 29.870
alignment_block:
US-09-289-346a-5 x BE964992 ..
Align seg 1/1 to: BE964992 from: 1 to: 1512
4 TrpGlyClnPheGlnValAspGlyArgSerAlaArgGlyGlyGlnThr 20
|||||
944 TGGGGGGGCGACACACCGGGGGGTTCTCTACCGTGTGTGAAAC 993
|||||
20 rSerAsnAsp...AlaAlaIaGluAlaLeuAsnLaserSerLysGlu 35
|||||
994 CATCAACACCCCTTATATCAACACGAGGCTCTTCACATATAAAAAAGAGG 1043
|||||
36 ..GluAlaLeuGlnIleLe.....Arg 42
|||||
1044 CGGAAGGTATTAATATGCTGGCTGCCACAAAAGCGCGGGCGGCAAC 1093
|||||
43 GluLysIleProAlaAlaLeuPheGlnPheHisAsnLeuSerAs 59
|||||
1094 GAAAAACAACCTTTAAAGACATCCCTTATCCCTCACAGAAAGATTGTGA 1143
|||||
59 nLeuAspArgIlePheAspLysThrProGlu 69
|||||
1144 AGGCGATCGTGTGTTGCACAAACACACCTGTAC 1174

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seq_name: gb-gss:AQ950848

seq_documentation_block:

LOCUS AQ950848 572 bp DNA GSS 27-JAN-2000
DEFINITION Sheared DNA-51M3.TF Sheared DNA Trypanosoma brucei genomic clone

ACCESSION AQ950848

VERSION AQ950848.1 GI:6774113

KEYWORDS GSS.

SOURCE Trypanosoma brucei.
Trypanosoma brucei.
Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;

REFERENCE

1 (bases 1 to 572)
El-Sayed, N., Zhao, S., Zhao, H., Gill, S., Suh, E., Malek, J., Fujii, C.,
Gerrard, C., Leech, V., de Jong, P., Ullu, E., Melville, S., Donelson, J.,
Fraser, C. and Adams, M.Determination of clone end sequences from Trypanosoma brucei GUTat
10.1 sheared DNA library

Unpublished (1999)

Other GSSs: Sheared DNA-51M3.TF

Contact: Najib M. El-Sayed
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208

Email: nelsayed@tigr.org

Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared
DNA library constructed at TIGR. Clones will be available for
distribution through ATCC. Sheared DNA end sequences search page:
<http://www.tigr.org/tldb/mdb/tbdb/>.

Seq primer: M13-Forward

Class: Shotgun.

FEATURES
Location/Qualifiers

source

1..572
/organism="Trypanosoma brucei"
/strain="TREU927/4 GUTat 10.1"
/db_xref="taxon:5691"

/clone_11b="Sheared DNA-51M3"

/note="Vector: pUC18; Site: 1; SmaI; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically
sheared to give a tight size distribution (approx 2 kb).
The v + i method used for the library construction is
described in detail in Smith, H.O. and Venter, J.C.
(Making small insert libraries for whole genome shotgun
sequencing projects. In Genome Sequencing: A Practical
Approach, eds. M. Vaudin and B. Barrell, Oxford University
Press, 1999)."

BASE COUNT 115 a 118 c 180 g 159 t

ORIGIN

alignment_scores:
Quality: 68.00 Length: 31
Ratio: 2.519 Gaps: 0
Percent Similarity: 87.097 Percent Identity: 38.710

Percent Similarity:

Percent Identity:

Percent Identity:

Percent Identity:

Percent Identity:

Percent Identity:

Percent Identity:

Percent Identity:

Percent Identity:

Percent Identity:

Percent Identity:

Percent Identity:

seq_name: gb-gss:AQ947513

seq_documentation_block:

LOCUS AQ947513 587 bp DNA GSS 27-JAN-2000
DEFINITION Sheared DNA-49M17.TF Sheared DNA Trypanosoma brucei genomic clone

ACCESSION AQ947513

VERSION AQ947513.1 GI:6770778

KEYWORDS GSS.

SOURCE Trypanosoma brucei.
Trypanosoma brucei.
Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;

REFERENCE

1 (bases 1 to 587)
El-Sayed, N., Zhao, S., Zhao, H., Gill, S., Suh, E., Malek, J., Fujii, C.,
Gerrard, C., Leech, V., de Jong, P., Ullu, E., Melville, S., Donelson, J.,
Fraser, C. and Adams, M.Determination of clone end sequences from Trypanosoma brucei GUTat
10.1 sheared DNA library

Unpublished (1999)

Other GSSs: Sheared DNA-49M17.TF

Contact: Najib M. El-Sayed
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208

Email: nelsayed@tigr.org

Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared
DNA library constructed at TIGR. Clones will be available for
distribution through ATCC. Sheared DNA end sequences search page:
<http://www.tigr.org/tldb/mdb/tbdb/>.

Seq primer: M13-Forward

Class: Shotgun.

FEATURES
Location/Qualifiers

source

1..587
/organism="Trypanosoma brucei"
/strain="TREU927/4 GUTat 10.1"
/db_xref="taxon:5691"

/clone_11b="Sheared DNA-49M17"

/note="Vector: pUC18; Site: 1; SmaI; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically
sheared to give a tight size distribution (approx 2 kb).
The v + i method used for the library construction is
described in detail in Smith, H.O. and Venter, J.C.
(Making small insert libraries for whole genome shotgun
sequencing projects. In Genome Sequencing: A Practical
Approach, eds. M. Vaudin and B. Barrell, Oxford University
Press, 1999)."

BASE COUNT 176 a 175 c 128 g 108 t

ORIGIN

alignment_scores:
Quality: 68.00 Length: 31
Ratio: 2.519 Gaps: 0
Percent Similarity: 87.097 Percent Identity: 38.710

Percent Similarity:

Percent Identity:

Percent Identity:

Percent Identity:

Percent Identity:

Percent Identity:

Percent Identity:

Percent Identity:

Percent Identity:

Percent Identity:

Percent Identity:

Percent Identity:


```

17 ..... glycysglnthrserasnaplaalaalaglualeuasn 30  

    ||| ||| |||::: ::::::::::|||  

390 AGCTTGTGGCCTTCACATCTCCACCACAACACTGAGGCCCTC... 436  

31 AlaSerSerIsglUgluaLleugInLeIeIargGluyIsileProAl 47  

437 ..... CTACATTACTGCTCGCAAGAAGCCGCAGC 465  

47 aaLaLaLeuPhe.GlnPhenISAsnLeuSnsberAnLeuAspArgILe 63  

||||::::::::::||| :::::::::::|||  

466 GATCGCCCTTGCTGCTTCACACATCCAGCACCATAGATAAGCTC 515  

64 PheaSpLystrHrproGIUpRo 70  

:::::::::: |||  

516 CTGATGATGATCAACACCCCT 536  

seq_name: gb_est2.B1366217  

seq_documentation_block:  

LOCUS B1366217 645 bp mRNA EST 01-AUG-2001  

DEFINITION RE51713.Sprime RE Drosophila melanogaster normalized Embryo pflc-1  

Drosophila melanogaster cDNA clone RE51713 5 similar to CG1245;  

Fban001245; transcription factor binding' located on: 3R 83B7-83B  

.; 05/14/2001, mRNA sequence.  

ACCESSION B1366217  

VERSION B1366217.1 GI:15062245  

KEYWORDS EST.  

SOURCE fruit fly.  

ORGANISM Drosophila melanogaster  

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  

REFERENCE 1 (bases 1 to 645)  

Stapleton,M., Brockstein,P., Hong,L., Tyler,D., Berman,B., Carlson  

J., Champe,M., Chavez,C., Dorsett,V., Farfan,D., Frise,E., George  

,R., Gonzalez,M., Guarin,H., Harris,N., Li,P., Liao,G., Mistro,S.,  

Mungall,C.J., Nunoo,J., Patel,D.J., Parraga,Y., Park,S.,  

Phouamavong,S., Wan,K., Yu,C., Lewis,S.E., Celinker,S. and Rubin  

,G.M.  

BDGP/HIMI RE Drosophila EST Project  

Unpublished (2001)  

Contact: Stapleton, M.  

BDGP  

Lawrence Berkeley National Lab  

One Cyclotron Rd, Berkeley, CA 94720, USA  

Fax: 510 486. 6798  

Email: http://www.fruitfly.org/EST_est@fruitfly.berkeley.edu  

hit genomic AE003602: arm:3R [1267070..1564901]  

estimated-cyto:83A4-83C1: 05/14/2001  

Plate: RE.517 row: B column: 1  

High quality sequence stop: 608.  

Location/Qualifiers  

1. .645  

/oranism="Drosophila melanogaster"  

/db_xref="taxon:7227"  

/clone="RE51713"  

/cloned_lib="RE Drosophila melanogaster normalized Embryo  

pflc-1"  

/sex="male and female"  

/dev_stage="0-24 hours mixed stage embryonic".  

/note="Organ: DH5-alpha Yona"  

/library="Library was kindly generated by Piero Carninci at  

the RIKEN. The library was normalized and excised using  

Cre recombinase. Plasmid cDNA library."  

BASE COUNT 185 a 175 C 147 g 138 t  

ORIGIN
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Percent Similarity: 61.333 Percent Identity: 32.000

alignment_block:
US-09-289-346A-5 x BI366217 ..

Align seg 1/1 to: BI366217 from: 1 to: 645

1 ThrlleValTrrp.GlyluPhheglInValaspGlyArqSerAlarGlyL 16
||||| ||||||.....
339 ACCCTAGACTGGTTGAACAGCTACAATGGATGGACAAAGGTGCACGCCAC 388
17GlyCysglnThrSerAsnAspAlaIalagLuAlauasn 30
||| ||| |||... :|||....
389 AGCTTGTCGCGCTTCAACAATCTCCAACGACGACACACACGAGGGCTC... 435
31 AlaSerSeryGluGlualaleuglnlleIleArgGluylIleProAl 47
|||||... :|||....
436CTACATTACGCTCGCAGAAGCCGCACC 464
47 alalaIalaleupe.glnpheHisasnlLeuasnsenrslenuaspargile 63
|:::|:::: :::::::::::.....
465 GACTCGCCCTTCTGCTCTTCACAACAGCATCCAGCACCATATAAGCTC 514
64 pheasplysThrpProgLnro 70
::::::: |
515 CTGAGTAGATCATCACCCCCT 535

seq_name: qb_est2.BF256735

seq_documentation_block:
LOCUS BF256735 844 bp mRNA EST 23-FEB-2001
DEFINITION HYEMEF0010N17f Hordeum vulgare seedling root EST library HVCDNA0007
(clonated and unexpressed) Hordeum vulgare cDNA clone
HYMFE0010N17f, mRNA sequence.
ACCESSION BF256735
VERSION BF256735.2 GI:13118403
KEYWORDS EST.
SOURCE barley.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 844)
AUTHORS Wang,R., Close,T.J., Kleinhoofs,A., Wise,R., Begum,D., Fritsch,D., Yu,
Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo
T., Sasaki,C., Schwartzbeck,J., Simmons,J., Chol,D.W., Main,D. and
Wood,T.
Development of a genetically and physically anchored EST resource
for barley genomics
unpublished (2000)
On Nov 16, 2000 this sequence version replaced gi:11185848.
COMMENT Contact: Wing RA
Clemson University Genomics Institute
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: AATTAACCTTCACTAAGAAGCG
High quality sequence stop: 752.
Location/Qualifiers
. . 844

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alignment_scores:
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  Ratio: 1.467        Gaps: 4
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/note="Vector: lambdaZAP; site_1: EcoRI; site_2: XhoI; For more details on library preparation and sequence analysis see <http://www.genome.clemson.edu/projects/barley/> To

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order a clone see http://www.genome.clemson.edu/orders
BASE COUNT      209 a      181 c      240 g      214 t
ORIGIN

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BASE COUNT
ORIGIN

209 a 181 c 240 g

ORIGIN

alignment_scores:

Quality:	67.50
Patience:	2.109

Length: 55

Ratio:	2.109
Ratio:	59.193

Gaps: 2
Deaths: 39 193

Percent Similarity: 58.182

Percent Identity: 38.182

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alignment_block:
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US-09-289-346A-5 x BF256735/rev . .

Align seg 1/1 to reverse of: BF256735 from: 1 to: 844

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37 1aleuGlnllelearglulysileProalaAlaIaleuPheGlnPhe 53
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2166 CTTTAGCATATTAAGGAAAACTCCCTAAGATTATTATTTTCAATAT 2117
54 HisAsnLeuAsnSerAsnLeuAsnParGllePheAspLysThrPro 68
||||| ||||||| ||||||| ||||||| ||||||| |||||||
2116 CATATTTAAATGTAATTGATGATGATTTT.....ACACCT 2078
seq_name: /cgnl_7/ptodata/1/ina/6B_COMB.seq:US-08-838-151A-1

seq_documentation_block:
; Sequence 1, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing GeminiVirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; City: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1162 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Tomato Mottle Gemini Virus
; INDIVIDUAL ISOLATE: Florida
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 44..1127
; PUBLICATION INFORMATION:
; AUTHORS: Gilbertson, RL
; AUTHORS: Hidayat, SH
; AUTHORS: Padimatas, EJ
; AUTHORS: Rojas, MR
; AUTHORS: Hou, YM
; AUTHORS: Maxwell, DP
; TITLE: Pseudorecombination between the infectious
; TITLE: cloned DNA components of tomato mottle and bean
; TITLE: dwarf mosaic geminiviruses.
; JOURNAL: Jour. General Virol.

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; VOLUME: 74
; PAGES: 23-31
; DATE: 1993
; US-08-838-151A-1

alignment_scores:
; Quality: 220.00 Length: 70
; Ratio: 3.729 Gaps: 0
; Percent Similarity: 84.286 Percent Identity: 58.571

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371 ACAATCGAATGGGAGATTCAGATCGACGCGAGATCTCCAGAGAGG 420
17 yCysGlnThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerL 34
||||| ||||||| ||||||| ||||||| ||||||| |||||||
421 CCAGACTGCTGATATGATTCATATGCGAAGCGTTAATGCAAGTTCGG 470
34 ysglGluAlaLeuGlnllelearglulysileProalaAlaAlaLeu 50
||||| ||||||| ||||||| ||||||| ||||||| |||||||
471 TTCATATGCTTATGACAGTCTTAAGGAGACACCAAAAGATTGTGA 520
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAsnParGllePheAspLys 67
||||| ||||||| ||||||| ||||||| ||||||| |||||||
521 TTACAAATCATATACATCCCTTAACCTAAGACGATATTGCCAAAGCG 570
67 rProGluPro 70
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571 TCCGGAACCG 580

seq_name: /cgnl_7/ptodata/1/ina/6B_COMB.seq:US-08-838-151A-3

seq_documentation_block:
; Sequence 3, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing GeminiVirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; City: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460

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; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1169 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Tomato Mottle Gemini Virus
; STRAIN: Florida
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 44..1127
; PUBLICATION INFORMATION:
; AUTHORS: Gilbertson, RL et al.
; TITLE: Pseudorecombination between the infectious
; TITLE: cloned DNA components of tomato mottle and bean
; TITLE: dwarf mosaic geminivirus.
; JOURNAL: Journal of General Virology
; VOLUME: 74
; PAGES: 23-31
; DATE: 1993
; US-08-838-151A-3

alignment_scores:
    Quality: 220.00      Length: 70
    Ratio: 3.729        Gaps: 0
    Percent Similarity: 84.286    Percent Identity: 58.571

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    17 ycyGclThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerL 34
    | |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
421 CCACAGCTGCTGCTATGATTCATATGCGAAGCGCTTAATGCAAGTCGG 470
    34 ysgIguAlaLeuGlnIleIleArgGluIysIleProAlaAlaLeu 50
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471 TTCATCTGCTTACGAGTCTCTAGGAGAACACCAAAAGATTGTGTA 520
    51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspIysTh 67
    ::::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
521 TTACAAATCATATACATCGCTCTACCTAGCAAGCAATATTTCGCAAGGC 570
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seq_name: /cgnl_7/prodata/1/lna/6B_COMB.seq:us-08-838-151A-5
seq_documentation_block:
; Sequence 5, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocket, Milinow & Katz
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; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1169 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Tomato Mottle Gemini Virus
; STRAIN: Florida
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 44..1127
; US-08-838-151A-5

alignment_scores:
    Quality: 220.00      Length: 70
    Ratio: 3.729        Gaps: 0
    Percent Similarity: 84.286    Percent Identity: 58.571

alignment_block:
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    17 ycyGclThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerL 34
    | |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
421 CCACAGCTGCTGCTATGATTCATATGCGAAGCGCTTAATGCAAGTCGG 470
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    ::::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
471 TTCATCTGCTTACGAGTCTCTAGGAGAACACCAAAAGATTGTGTA 520
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521 TTACAAATCATATACATCGCTCTACCTAGCAAGCAATATTTCGCAAGGC 570
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571 TCCGGAACCG 580

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seq_documentation_block:
; Sequence 7, Application US/08838151A
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Patent No. 6291743
GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminitivirus
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESS: Dressler, Rockey, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ. ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1169 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Tomato Mottle Gemini Virus
STRAIN: Florida
FEATURE:
NAME/KEY: CDS
LOCATION: 44..1127
US-08-838-151A-7
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alignment_scores:
Quality: 220.00      Length: 70
Ratio: 3.729         Gaps: 0
Percent Similarity: 84.286      Percent Identity: 58.571
alignment_block:
US-09-289-346A-5 x US-08-838-151A-7
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Align seg 1/1 to: US-08-838-151A-7 from: 1 to: 1169

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17 yCysGlnThSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerL 34
|||||  |||||||  |||||||  |||||||  |||||||  |||||||
421 CCACAGCTCTCTAATGATCATATGCGAAGCGCTTAATGCAAGTTCGG 470
34 ySgUGluAlaLeuGlnLeuLeuArgGluysTlePrcAlaAlaAlaLeu 50
|||||  |||||||  |||||||  |||||||  |||||||  |||||||
471 TTCATCTGCTTAGCACTTCTAAGGAGAAACCAACCAAAAGATTTTGTA 520
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51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
|||||  |||||||  |||||||  |||||||  |||||||  |||||||
521 TTACAATAATCATACATCCGCTCTAACCTAGAACGATATTCCGAAGCC 570
67 rProGluPro 70
|||||  |||||||
571 TCCGGAACCG 580
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seq_documentation_block:

Sequence 17, Application US/08838151A

Patent No. 6291743

GENERAL INFORMATION:

APPLICANT: Stout, John T

APPLICANT: Luu, Hang T

APPLICANT: Maxwell, Douglas

APPLICANT: Ahlquist, Paul

TITLE OF INVENTION: Transgenic Plants Expressing Geminitivirus

NUMBER OF SEQUENCES: 63

CORRESPONDENCE ADDRESS:

ADDRESS: Dressler, Rockey, Milnamow & Katz

STREET: Two Prudential Plaza, Suite 4700

CITY: Chicago

STATE: Illinois

COUNTRY: U.S.A.

ZIP: 60601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/838,151A

FILING DATE:

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Mueller, Lisa V

REGISTRATION NUMBER: 38,978

REFERENCE/DOCKET NUMBER: SVS3801P0260

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-616-5400

TELEFAX: 312-616-5460

INFORMATION FOR SEQ. ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 2602 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ORIGINAL SOURCE:

ORGANISM: Tomato Mottle Geminitivirus

STRAIN: Florida

US-08-838-151A-17

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alignment_scores:
Quality: 220.00      Length: 70
Ratio: 3.729         Gaps: 0
Percent Similarity: 84.286      Percent Identity: 58.571
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alignment_block:

US-09-289-346A-5 x US-08-838-151A-17/rev

Align seg 1/1 to reverse of: US-08-838-151A-17 from: 1 to: 2602

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FEATURE:
NAME/KEY: CDS
LOCATION: 1..1077
US-08-809-103B-1

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Quality: 219.00      Length: 69
Ratio: 3.842         Gaps: 0
Percent Similarity: 82.609      Percent Identity: 57.971

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US-09-289-346A-5 x US-08-809-103B-1

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2  LeuValTrrpGlyGluPheGlnValAspGlyArgSerAlaArgGlyGlyC 18
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331 CTTGAATGGGCTGATGTAATTAAGACATTAGCGCTAGAGATTAGTTCTA 380
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
18  sGltThSerAsnAspAlaAlaAlaGluAlaLeuAsnAlaSerSerlysg 35
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
381 ACACACAGCCACGACGCTTACGCAAGGCATTAACGACGAGAGTAGT 430
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
35  LuGluAlaLeuGlnIleIleArgGluIysIleProAlaAlaAlaLeuPhe 51
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
431 CGCAGGCTCTGATGTAATTAAGACATTAGCGCTAGAGATTAGTTCTA 480
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
52  GlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspIysThrPr 68
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
481 CATTTTCATATATATTAATTAAGATTAGATTAGGTTTCCAGGTGCCCTCC 530
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
68  oGluPro 70
   |||
531 GGCACCT 537

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; Sequence 3, Application US/08809103B
; Patent No. 6133505
; GENERAL INFORMATION:
; APPLICANT: GROENENBORN, Bruno
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,103B
; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94.11040
; FILING DATE: 15-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR95/01192
; FILING DATE: 15-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: US894AL CNR TOM
; TELECOMMUNICATION INFORMATION:

```

```

; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 685-0573
; TELEX: 248425 EMBRON
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1150 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1077
; US-08-809-103B-3

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alignment_scores:
Quality: 219.00      Length: 69
Ratio: 3.842         Gaps: 0
Percent Similarity: 82.609      Percent Identity: 57.971

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alignment_block:
US-09-289-346A-5 x US-08-809-103B-3

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Align seg 1/1 to: US-08-809-103B-3 from: 1 to: 1150
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2  LeuValTrrpGlyGluPheGlnValAspGlyArgSerAlaArgGlyGlyC 18
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331 CTTGAATGGGCTGATGTAATTAAGACATTAGCGCTAGAGATTAGTTCTA 380
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
18  sGltThSerAsnAspAlaAlaAlaGluAlaLeuAsnAlaSerSerlysg 35
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
381 ACACACAGCCACGACGCTTACGCAAGGCATTAACGACGAGAGTAGT 430
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
35  LuGluAlaLeuGlnIleIleArgGluIysIleProAlaAlaAlaLeuPhe 51
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
431 CGCAGGCTCTGATGTAATTAAGACATTAGCGCTAGAGATTAGTTCTA 480
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
52  GlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspIysThrPr 68
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
481 CATTTTCATATATATTAATTAAGATTAGATTAGGTTTCCAGGTGCCCTCC 530
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
68  oGluPro 70
   |||
531 GGCACCT 537

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seq_documentation_block:
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; Sequence 5, Application US/08809103B
; Patent No. 6133505
; GENERAL INFORMATION:
; APPLICANT: GROENENBORN, Bruno
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,103B
; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:

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APPLICATION NUMBER: FR 94.11040
FILING DATE: 15-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR95/01192
FILING DATE: 15-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: PATCH, Andrew J.
REGISTRATION NUMBER: 32,925
REFERENCE/DOCKET NUMBER: US94AL CNR TOM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 521-2297
TELEFAX: (703) 685-0573
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1150 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1077
US-08-809-103B-5

alignment_scores:
Quality: 219.00 Length: 69
Ratio: 3.842 Gaps: 0
Percent Similarity: 82.609 Percent Identity: 57.971

alignment_block:
US-09-289-346a-5 x US-08-809-103B-5 ..

Align seq 1/1 to: US-08-809-103B-5 from: 1 to: 1150
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331 CTTGAATGGGGTACTTCCAGATCGACGACGATCTCTAGGGAGAGACA 380
18 sGlnTrpSerAsnAspAlaAlaIaGluAlaLeuAsnAlaSerSerLysG 35
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
381 ACAGACAGCCACGACGCTTACGCAAGCAATTACGACGAGAGTAGT 430
35 IuGluAlaLeuGlnIleIleArgGluLysIleProAlaAlaLeuPhe 51
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
431 CGCAGGCTCTGATGTAATTAAAGAAATTACGCGCTAGACATTACGTTCTA 480
52 GlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysThrPr 68
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
481 CATTTTCAATATATATAGTAATTTAGATTAAGGTTTCCAGGTGCTCC 530
68 oGluPro 70
I |||
531 GGCACCT 537

seq_name: /cgnl_7/ptodata/1/lna/6B_COMB.seq:US-08-838-151A-48

seq_documentation_block:
; Sequence 48, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Lou, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Gemnivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESSES:
; ADDRESS: Dressler, Rockey, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700

```

```

CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 1062 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bean Golden Mosaic Gemnivirus
STRAIN: Type II
INDIVIDUAL ISOLATE: Guatemala
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1059
US-08-838-151A-48

alignment_scores:
Quality: 218.00 Length: 70
Ratio: 3.695 Gaps: 0
Percent Similarity: 84.286 Percent Identity: 60.000

alignment_block:
US-09-289-346a-5 x US-08-838-151A-48 ..

Align seq 1/1 to: US-08-838-151A-48 from: 1 to: 1062
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17 yCySGlnTrpSerAsnAspAlaAlaIaGluAlaLeuAsnAlaSerL 34
I |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
378 TCAGACGTCTGCCAAGCATCTATGCAAGCATTTAAACGACATTCAA 427
428 TTGAACTCGCTTGACAAATATTGAAGAGACAAACGAAAGATTACGTC 477
34 ySGluAlaLeuGlnIleIleArgGluLysIleProAlaAlaLeu 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
478 CTTCAACATCACACACATCCCTTAATCTGAAACGATCTTCGTAAGT 527
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLys 67
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
478 CTTCAACATCACACACATCCCTTAATCTGAAACGATCTTCGTAAGT 527
67 rProGluPro 70
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528 CCCGAAACA 537

seq_name: /cgnl_7/ptodata/1/lna/6B_COMB.seq:US-08-838-151A-51

seq_documentation_block:
; Sequence 51, Application US/08838151A

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? Patent No. 6291743
? GENERAL INFORMATION:
? APPLICANT: Stout, John T
? APPLICANT: Luu, Hang T
? APPLICANT: Maxwell, Douglas
? APPLICANT: Ahlquist, Paul
? APPLICANT: Hanson, Steve
? TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
? NUMBER OF SEQUENCES: 63
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Dressler, Rockey, Milnamow & Katz
? STREET: Two Prudential Plaza, Suite 4700
? CITY: Chicago
? STATE: Illinois
? COUNTRY: U.S.A.
? ZIP: 60601
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/838,151A
? FILING DATE:
? CLASSIFICATION: 800
? ATTORNEY/AGENT INFORMATION:
? NAME: Mueller, Lisa V
? REGISTRATION NUMBER: 38,978
? REFERENCE/DOCKET NUMBER: SVS3801P0260
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 312-616-5400
? TELEFAX: 312-616-5460
? INFORMATION FOR SEQ ID NO: 51:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1062 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: circular
? MOLECULE TYPE: DNA (genomic)
? HYPOTHETICAL: NO
? ANTI-SENSE: NO
? ORIGINAL SOURCE:
? ORGANISM: Bean Golden Mosaic Geminivirus
? STRAIN: Type II
? INDIVIDUAL ISOLATE: Guatemala
? NAME/KEY: CDS
? LOCATION: 1..1059
? US-08-838-151A-51

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? Quality: 218.00 Length: 70
? Ratio: 3.695 Gaps: 0
? Percent Similarity: 84.286 Percent Identity: 60.000

alignment_block:
US-09-289-346a-5 x US-08-838-151A-51 ..
Align seq 1/1 to: US-08-838-151A-51 from: 1 to: 1062

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478 CTTCAACATCTGCACACATCCGTTTAAATCTGCACGCGATCTTCGCAAGT 527
67 rProGluPro 70
528 GCCGGAACCA 537

seq_name: /cgn1_7/prodata/1/lna/5B_COMB.seq:US-08-838-151A-54
seq_documentation_block:
? Sequence 54, Application US/08838151A
? Patent No. 6291743
? GENERAL INFORMATION:
? APPLICANT: Stout, John T
? APPLICANT: Luu, Hang T
? APPLICANT: Maxwell, Douglas
? APPLICANT: Ahlquist, Paul
? APPLICANT: Hanson, Steve
? TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
? NUMBER OF SEQUENCES: 63
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Dressler, Rockey, Milnamow & Katz
? STREET: Two Prudential Plaza, Suite 4700
? CITY: Chicago
? STATE: Illinois
? COUNTRY: U.S.A.
? ZIP: 60601
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/838,151A
? FILING DATE:
? CLASSIFICATION: 800
? ATTORNEY/AGENT INFORMATION:
? NAME: Mueller, Lisa V
? REGISTRATION NUMBER: 38,978
? REFERENCE/DOCKET NUMBER: SVS3801P0260
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 312-616-5400
? TELEFAX: 312-616-5460
? INFORMATION FOR SEQ ID NO: 54:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1062 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: circular
? MOLECULE TYPE: DNA (genomic)
? HYPOTHETICAL: NO
? ANTI-SENSE: NO
? ORIGINAL SOURCE:
? ORGANISM: Bean Golden Mosaic Geminivirus
? STRAIN: Type II
? INDIVIDUAL ISOLATE: Guatemala
? NAME/KEY: CDS
? LOCATION: 1..1059
? US-08-838-151A-54

alignment_scores:
? Quality: 218.00 Length: 70
? Ratio: 3.695 Gaps: 0
? Percent Similarity: 84.286 Percent Identity: 60.000

alignment_block:
US-09-289-346a-5 x US-08-838-151A-54 ..

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: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/838,151A
: FILING DATE:
: CLASSIFICATION: 800
: ATTORNEY/AGENT INFORMATION:
: NAME: Mueller, Lisa V
: REGISTRATION NUMBER: 38,978
: REFERENCE/DOCKET NUMBER: SVS3801P0260
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312-616-5400
: TELEFAX: 312-616-5460
: INFORMATION FOR SEQ ID NO: 45:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1183 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: circular
: MOLECULE TYPE: DNA (genomic)
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: ORIGINAL SOURCE:
: ORGANISM: Bean Golden Mosaic Geminiivirus
: STRAIN: Type II
: INDIVIDUAL ISOLATE: Guatemala
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..1059
: US-08-838-151A-45

alignment_scores:
      Quality: 218.00      Length: 70
      Ratio: 3.695      Gaps: 0
Percent Similarity: 84.286      Percent Identity: 60.000

alignment_block:
US-09-289-346a-5 x US-08-838-151A-45 ..

Align seg 1/1 to: US-08-838-151A-45 from: 1 to: 1183

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   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
17 YCYsGlnThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerL 34
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
378 TCAGCAGTCTGCCACAGCATCATATGCAAGGCGATTAAACGAGATTCMA 427
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
34 ysgIuGluAlaLeuGlnIleIleArgGluLysIleProAlaAlaAlaLeu 50
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
428 TTGAATCTGCTTACCAATATTGAAGAGAACCAACCAAGATTACGTC 477
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51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
   ::||| |||||:::|||||:::|||||:::|||||:::|||||:::
478 CTTCAACATCAACACATCGTTCTTAATCTGCAACGATCTTCGTCAAAGT 527
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67 rProGluPro 70
   ::||| |||||
528 GCCGGAACCA 537
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OM of: US-09-289-346a-6 to: GenEmbl:* out_format : pfs

Date: Jan 3, 2002 8:17 PM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

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-MODE=frame+ p2n.model -DEV=xlp  
-O=/cgn1/USPFO.spool/US09289346/runat_03012002_153304_15362/app-query.fasta.1.1163  
-DB=GenEmbl -QPM=fastap -SOFFIX=p2n.rge -GAPOP=12.000  
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPEL=0.000 -LOOPEXT=0.000  
-OGAPOP=4.500 -OGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500  
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500  
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=Diosum62  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct  
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs  
-NORR=ext -MINLEN=0 -MAXLEN=200000000  
-USER=US09289346_@CGN1.1.10412 -NCPU=6 -ICPU=3 -LONGLOG  
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Search information block:

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Query: US-09-289-346a-6  
Query length: 70  
Database: GenEmbl:*  
Database sequence: 1472140  
Search time (sec): 7316.720000
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Score list:

Sequence	Strd Orig	ZScore	EScore	Len	Documentation
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gb_v1:AY029750	-	291.00	638.51	2.7e-27	2588
gb_v1:AF291705	-	289.00	633.85	5.0e-27	2622
gb_v1:LM092532	-	272.00	601.76	3.1e-25	1193
gb_v1:AF131071	-	272.00	600.75	3.5e-25	1345
gb_v1:MBGARL	-	270.00	590.59	1.3e-24	2617
gb_v1:AF188708	-	268.00	591.51	1.1e-24	1365
gb_v1:AF288227	-	268.00	591.40	1.2e-24	1363
gb_v1:AF104036	-	268.00	585.38	1.5e-24	2828
gb_v1:SC067926	-	265.00	592.27	7.8e-24	554
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gb_v1:MGU75278	-	257.00	575.86	8.5e-24	447
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gb_v1:AF026553	-	251.00	554.13	1.4e-22	1165
gb_v1:AB001315	-	248.00	553.31	1.5e-22	570
gb_v1:AB001318	-	248.00	553.31	1.5e-22	570
gb_v1:AB001303	-	247.00	551.03	2.0e-22	570
gb_v1:AB001294	-	247.00	550.26	2.3e-22	625
gb_v1:AF350330	-	247.00	537.73	1.1e-21	2767
gb_v1:AB001296	-	245.00	545.70	4.0e-22	625
gb_v1:AB001297	-	245.00	545.70	4.0e-22	625
gb_v1:AB001298	-	243.00	541.15	7.3e-22	625
gb_v1:AB001319	-	242.00	539.06	5.5e-22	611
gb_v1:CLCVA1452	-	242.00	526.41	4.8e-21	2744
gb_v1:CLCVA4455	-	242.00	526.41	4.8e-21	2744
gb_v1:TPCTVCD	-	240.00	522.33	8.1e-21	2533
gb_v1:PYVVA	-	239.00	532.04	2.3e-21	625
gb_v1:AB001308	-	238.00	529.76	3.1e-21	625
gb_v1:AF307861	-	237.00	515.05	2.1e-20	2724
gb_v1:CVAM8363	-	235.00	518.80	1.3e-20	1020
gb_v1:CLCVA447	-	235.00	510.45	3.7e-20	2751
gb_v1:CLCVA458	-	235.00	510.45	3.7e-20	2751
gb_v1:AB001317	-	234.00	521.41	6.1e-21	570
gb_v1:CMVAJ3191	-	233.00	505.78	9.1e-20	2787
gb_v1:AB014347	-	232.00	503.50	9.1e-20	2787
gb_v1:AB014346	-	232.00	503.49	9.1e-20	2791
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gb_v1:AF105975	-	231.00	501.22	1.2e-19	2790
gb_v1:TYLCV12	-	231.00	501.22	1.2e-19	2790

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gb_v1:AB001304 - 230.00 512.81 2.9e-20 570 i AB001304 Tobacco leaf curl v  
gb_v1:AF155064 - 230.00 499.02 1.6e-19 2764 i AF155064 Okra enation virus  
gb_v1:CLE270867 - 229.00 505.98 6.6e-20 922 i AJ270867 cotton leaf curl vi
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seq_name: gb_v1:MTGA

seq_documentation_block: 2588 bp ss-DNA circular VRL 02-AUG-1993

LOCUS MTGA 2588 bp ss-DNA circular VRL 02-AUG-1993
DEFINITION Tomato golden mosaic virus, component A of complete genome.
ACCESSION K02029
VERSION K02029.1 GI:332213
KEYWORDS coat protein; complete genome; unidentified reading frame.
SOURCE TGMV cloned ds-DNA, clone PBH404.
ORGANISM tomato golden mosaic virus
VIRUSES: ssDNA viruses; Geminiviridae: Begomovirus.
REFERENCE 1 (bases 1 to 2588)
AUTHORS Hamilton,W.D. O., Stein,V.E., Coulters,R.H.A. and Buck,K.W.
TITLE Complete nucleotide sequence of the infectious cloned DNA components of tomato golden mosaic virus: Potential coding regions and regulatory sequences
EMBO J. 3, 2197-2205 (1984)

JOURNAL COMMENT
EMBO J. 3, 2197-2205 (1984)
Geminiviruses are characterized by twin isometric virions, major capsid polypeptides of about 28 kD, and ss-DNA genomes. The genomes of cassava latent virus (CLV) and tomato golden mosaic virus (TGMV) consist of two circular components, while that of maize streak virus (MSV) consists of a single circle.

[1] identifies the following additional open reading frames on the complementary strand that would code for proteins with >10 kD:
A11 -- 13-1543 (passing through origin)
A12 -- 1601-1212
A13 -- 1465-1067

The sequence at 1-235 is highly homologous to an equivalent region on component B; it doesn't appear to code for protein and has the potential to form a stable hairpin [1]. An analogous region is found in CSV.
The virion-sense (+) strand is shown below.

FEATURES

source . location/Qualifiers

1..2588
/organism="tomato golden mosaic virus"
/db_xref="taxon:10831"
327..1070
/note="coat protein (AR1)"
/codon_start=1
/protein_id="AAA46582.1"
/db_xref="GI:332214"

translation="MPKRDAPWRLAGTSKVSRSANYSFPGSLPKRDADVNRPRKRP
RYSRLAGDVPKCGCEPKQVSQYGRDHSILGVYMCISDVTGNGITHRGKRRPV
KSVYTIKTMDENTKIKRHTNSVFMILVRDRRPGCTPMDPGVNMEDNPESTAPVK
NDLRPFQVTHFRFAKVGCGYASNEQALVRRFMKNNNNVYNNHDEAGKYEMNTENAL
LLVMCTHASNVVATKIRIYFQYSTIN"

BASE COUNT 672 a 513 c 605 g 798 t
ORIGIN 140 bp upstream of HpaII site; beginning of A-B homology region.

alignment_scores:
Quality: 340.00 Length: 70
Ratio: 5.075 Gaps: 0
Percent Similarity: 95.714 Percent Identity: 95.714

alignment block:

US-09-289-346a-6 x MTGA/rev ..
Align seg 1/1 to reverse of: MTGA from: 1 to: 2588

```
1 Thireuvalrtpgylgylupneglnvalaspjlyarvserlaaaglygl 17  
|||||  
2271 ACTCTTGATGAGGAGAAATTCAGGTGACGCTGAAGTCTTAAGAGAGC 2222  
17 ycyysglnThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerL 34  
|||||  
2221 TTGCGAACAACATCTAACGACGCTGACGAGAGGCGTTAAATGCTTCTTCA 2172
```

```

34 ysglgluaialaueglnlleiearglulysllleproglulysfyrleu 50
|||||
2171 AAGAAAGAGCCCTGCAGATATTAGAGAAAGAAACCCAGAAATATTTA 2122
51 Phealaphaealaaleuasnsersanleuaspargillepheasplysth 67
|||||
2121 TTTCAGTTCACACATCTAATAGCAATTGATAGCATATTGTATAGAC 2072
67 rProgluPro 70
|||||
2071 TCCGAGACCA 2062

seq_name: gb_v1:AY029750
LOCUS AY029750 2588 bp DNA circular VRL 08-MAY-2001
DEFINITION Tomato severe rugose virus DNA-A, complete sequence.
ACCESSION AY029750
VERSION AY029750.1 GI:14009278
KEYWORDS
SOURCE Tomato severe rugose virus.
ORGANISM Tomato severe rugose virus.
REFERENCE 1 (bases 1 to 2588)
AUTHORS Resende,W.L., Goulart,L.R., Parreira,K.S. and Figueiredo,J.E.F.
TITLE The full-length DNA-A nucleotide sequence of a novel
JOURNAL tomato-infecting begomovirus, Tomato severe rugose virus, in Brazil
2 (bases 1 to 2588)
UNPUBLISHED
AUTHORS Resende,W.L., Goulart,L.R., Parreira,K.S. and Figueiredo,J.E.F.
TITLE Direct Submission
JOURNAL Submitted (03-APR-2001) Instituto de Genetica e Biologia,
Universidade Federal de Uberlandia, Av. Amazonas s/n, Bloco 2E,
Sala 24, Campus Umuarama, Uberlandia, Minas Gerais 38.400-000,
Brazil

FEATURES
source 1. 2588
Location/Qualifiers
/organism="Tomato severe rugose virus"
/strain="Minas Gerais"
/db_xref="taxon:158463"
/country="Brazil"
/note="segment: DNA-A"
305..1060
/gene="AV1"
305..1060
/gene="AV1"
305..1060
/gene="AV1"
/codon_start=1
/product="coat protein"
/protein_id="AAK50360.1"
/db_xref="GI:14009282"
/translation="MPKRDAPWRLMAGTSKVSRSANYSRAGYGPXYKKAEMVRRPM
YRKPRITRLRGPDVPRGCEGPKVOSTESRHDSHVGCVCISVDTGNGITHRVGK
RVCVSLYLKGVMEDESKLNHTNSVFMVLRPRPGTPMDGQVFNMDNPSPT
AVAKNDLRDQVHMFFAKYVGQYASNEQALVRFKVNKNVNVYNHQEGKYENHT
ENALLLYMACTASNPYATKIRIFYFDSITN"
complement(1057..1455)
/gene="AC3"
complement(1057..1455)
/gene="AC3"
/codon_start=1
/product="enhancer protein"
/protein_id="AAK50358.1"
/db_xref="GI:14009280"
/translation="WDSRTGGLITARQAEKNGVYIWEISNPLEYKINRVEDPMYTSRV
YHVQIRFNHNLRLALHLKHSFINQIWTSTLASGFTYLNREKYLVLVLDRLGVISI
NNVIRAVFPADTKSYVNAVLENNHLIKFFKY"
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/gene="AC2"
complement(1202..1591)
/gene="AC2"
/codon_start=1
/product="trfap"

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/protein_id="AAK50361.1"
/db_xref="GI:14009283"
/translation="MRNSSLTPPSIKYOHRAAKRGITRRRRIDIECCGSTYVHIGCR
GHGFTNRHTICTSGREWRILGDIRSLFDQKSGSGSVNHEQSLPRPNTVQPOPEE
SIASPOELHQLPMDPDFDSFWDIFK"
complement(1533..2588)
/gene="AC1"
complement(1533..2588)
/gene="AC1"
/codon_start=1
/product="rep protein"
/protein_id="AAK50357.1"
/db_xref="GI:14009279"
/translation="MPSATKRPOIKAKNYFLTPKSGSKREALSQKKLTPTNNKT
IKVCRELHENGEPHLVILQFEGNCRONQFFEDLVSTFRSTHFPNIOAKSSDVK
SYVKDGDGTIEWGEFQIDGRSARGCQTDNDAEALNAPSKDVALQIIRKLPKFL
FOFINLNSNLDRIFAFAPEWAPFPLPSSNPVREMDMADDFRGCAARPERPISI
IEGDSPTGKTMMARAFCAHNYLSGHLDFNFRVYSNHYENVIDDIAPHYLYLKHKKE
LLGAKQDMQSNCKYKGPVOIKGICIEICLPGDEASVKKVPRKKNASLNNTKHKNA
KFVPLNPLRYOGTTQSC"
complement(2171..2434)
/gene="AC4"
complement(2171..2434)
/gene="AC4"
/codon_start=1
/product="AC4 protein"
/protein_id="AAK50359.1"
/db_xref="GI:14009281"
/translation="MKMSGLSTCFENSKAITAAKINDSTWSPQOGHISIRFREL
NHRPTSSPMSTRTLEILNSGANSKSTAEVLEAVARQITMLPKRP"
join(2583..2588.1..304)
/note="common region"

rep_origin
BASE COUNT 660 a 525 c 598 g 805 t
ORIGIN

alignment_scores:
Quality: 291.00 Length: 70
Ratio: 4.619 Gaps: 0
Percent Similarity: 90.000 Percent Identity: 78.571

alignment_block:
US-09-289-346a-6 x AY029750/rev ..
Align seg 1/1 to reverse of: AY029750 from: 1 to: 2588

1 ThleuValtrpqlgylupheglnvalaspllyargseralaarglgl 17
|||||
2258 ACTATCGAATGGGGCGCAATTCCAAATCCAGCCAGCAAGTCTAGAGCGG 2209
17 YCYGlnThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerL 34
|||||
2208 TTGCGAGACGACGCTACGATGCTGCCGAGAAAGCTTGACAGCACTTCCA 2159
34 ysglgluaialaueglnlleiearglulysllleproglulysfyrleu 50
|||||
2158 AAGACGCGCGCTGCAGATATCCGGAGAGAGCTACCGGAAAGCTTTT 2109
51 Phealaphaealaaleuasnsersanleuaspargillepheasplysth 67
|||||
2108 TTTCAGTTCACACATCTAATAGCAATTGATAGCATATTGTCAAGGCG 2059
67 rProgluPro 70
|||||
2058 TCCGAGACCA 2049

seq_name: gb_v1:AF291705
LOCUS AF291705 2622 bp DNA circular VRL 25-SEP-2000
DEFINITION Tomato rugose mosaic virus DNA-A, complete sequence.
ACCESSION AF291705
VERSION AF291705.1 GI:10281644

```

KEYWORDS Tomato rugose mosaic virus.

SOURCE Tomato rugose mosaic virus.

ORGANISM Viruses: ssDNA viruses; Geminiviridae; Begomovirus.

REFERENCE 1 (bases 1 to 2622)

AUTHORS Fernandes,J.J., Fontes,E.P.B., Broomonschenkel,S.H., Carvalho,M.G., Zambolim,E.M. and Zerbini,F.M.

TITLE Molecular Cloning and Characterization of Tomato rugose mosaic virus (TRMV), a Begomovirus isolated from Tomatoes at Triangulo Mineiro, Minas Gerais, Brazil

JOURNAL unpublished

REFERENCE 2 (bases 1 to 2622)

AUTHORS Fernandes,J.J. and Zerbini,F.M.

TITLE Direct Submission

JOURNAL Submitted (31-JUN-2000) Dept. de Fitopatologia, Universidade Federal de Viçosa, Av. P.H. Rolfs, s/n - Centro, Viçosa, MG 36571-000, Brazil

FEATURES

source Location=Qualifiers

1..2622

/organism="Tomato rugose mosaic virus"

/viroon

/db_xref="taxon:134599"

/country="Brazil: Uberlandia, Triangulo Mineiro, Mians Gerais"

/note="previously referred to as Tomato geminivirus TRMV"

rep_origin 1..227

/note="common region"

/complement(240..992)

/gene="AC4"

/complement(240..992)

CDS

/gene="AC4"

/codon_start=1

/product="putative AC4 protein"

/protein_id="AAG15549.1"

/db_xref="GI:10281649"

/translation="MILVESSFLAVVDMDIVDLPRLDKRLVACVLSQDLSIELHM DLKTTTEIVFHSRGRLVYFHYKHLAKYRGITSTVDPQPHGVRYVLOLDVILHP YLTONIRHLNTELTHTYCNVTYTCGIDAHHLNMSGIVILFKRLDPTWATTTWNTI GGSHIPYILGLVHGPVYVSGLVGWPNSCWRIINAPNLRCTSHVAPGIALRHFF ELKLTYYRLILYSRYATWALSSSKYLSSSNAS"

342..1097

/gene="AV1"

342..1097

/gene="AV1"

/note="Cp"

/codon_start=1

/product="capsid protein"

/protein_id="AAG15545.1"

/db_xref="GI:10281645"

/translation="MPKRDAPRMHASTSKISRGVNSPRAGVGRSKAKDWDVRPM YRPKIVRMVRRPDVPRGEGCKVQSFQRHDIHSHTCKVMCVSDVTGNGITTHRVGK RFCKVSVYLIGKIMDENIKLKNHTNSAMFWLVRDRRYGTGPMDFGVNMDNEPST ATVKNDLRDRQVHMKFYAKVTGGQYASNEQALYRFKVVNNVVYNNHQEAGKYENHT ENALLIYACHTASNPVYATLKIRIFYDSITN"

complement(1094..1492)

/gene="AC3"

complement(1094..1492)

CDS

/gene="AC3"

/note="REN"

/codon_start=1

/product="replication-enhancer protein"

/protein_id="AAG15548.1"

/db_xref="GI:10281648"

/translation="MDSRTGELITAHQAENGVTWEISNPLYFKMYNVEDILYTRTRV YHVQIRFHNLRVYLGHLKAYLNFQIWTTSLSASGTYLNRFKYLLMLYIDLGVISV NNVIRAFPAFDROGVNAVLEHNSIKYIT"

complement(1239..1628)

/gene="AC2"

complement(1239..1628)

CDS

/gene="AC2"

/note="TirAP"

/codon_start=1

/product="trans-activation protein"

/protein_id="AAG15547.1"

/db_xref="GI:10281647"

/translation="MHNSSSTPPSIKVOHRAKRRATRRRIDLQCCSIFVHIDCA GHGFYRGTHHTSGREWRVYIGNTKSPFDVQRGHTTHEDSLPRNTPVQPOPE STGSPQGLSQLPNLDIDIESFWDDIFK"

complement(join(1570..2622,1..6))

/gene="AC1"

complement(join(1570..2622,1..6))

/gene="AC1"

/note="Rep"

/codon_start=1

/product="replication-associated protein"

/protein_id="AAG15546.1"

/db_xref="GI:10281646"

/translation="MPSATRRPOIKAKNPLYTPKCSISKEBALSOLKNLPTPKKF IKVCRELHENGEPHLVLLQEGNCCONRFEDLVSPTRSTHFPHNIDRAKSSDVK SYVDKDGDTIEWGEFQIDGRSARCCGCTAFDAALNALNSKDIALQITIREKPEFL FOFHNLNSNLDRIEFARAPENAPAPTPPLSSFTNPRMDMADYFGRGAAPERPDIS IITIEDSRCKTMARALCAHNYLSGHLDFNPRVYSNHYEVVIDIAPHYIKLHKMK ELIGKORDMOSCKTKGKPVQIKGILPCIVLCNPGGASTKCTLDKEENSALSSWTKH AQIFLNSPLYQSSSTG"

BASE COUNT 684 a 562 c 600 g 776 t

ORIGIN

alignment_scores:

quality: 289.00 length: 70

ratio: 4.587 gaps: 0

percent similarity: 90.000 percent identity: 78.571

alignment_block:

US-09-289-346A-6 x AF291705/rev ..

Align seg 1/1 to reverse of: AF291705 from: 1 to: 2622

1 ThrleuValTrrpglygluphegluValAspGLVArgserlaArGlygl 17

2298 ACTATCGAATGGGGGGAATTCGAATCGAGCGCGAAGTGTGAGGCGG 2249

17 yCYGlnFThrSerAnspAlaAlaGluAlaAlaAsnAlaSerSerL 34

2248 TTGCGACAGACGCTAACGACGCTGCCGAGAAAGCTTGAACGACCTTCCA 2199

34 ysgluGluAlaLeuGlnIleleargGluysIleProGluysTyrleu 50

2198 AAGACATCGCCTTCAGATATATCCGCGAAGATGCCGAAAGTCTCTTA 2149

51 PheAlaPheAlaAlaLeuAnserAsnLeuAspArgIlePheAspIysTh 67

2148 TTYCAGTTTCACAACTTAATTAATTAGATGATGATTTGCCAAGGCC 2099

67 rProGluPro 70

2098 TCCGAGACCA 2089

seq_name: gb_v1:LM092532

seq_documentation_block:

locus LM092532 1193 bp DNA VRL 01-APR-1997

DEFINITION Leonurus mosaic virus Rep protein (rep) and coat protein (cp)

ACCESSION U92532

VERSION U92532

KEYWORDS genes, partial cds.

ORGANISM Leonurus mosaic virus.

SOURCE Viruses: ssDNA viruses; Geminiviridae; Begomovirus.

REFERENCE 1 (bases 1 to 1193)

AUTHORS Farla,C.C. and Maxwell,D.P.

TITLE Variability in geminivirus associated with Phaseolus vulgaris in Brazil

```

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1193)
AUTHORS Faria,J.C. and Maxwell,I.D.P.
TITLE Direct Submission
JOURNAL Submitted (08-MAR-1997) Plant Pathology, University of Wisconsin, 1630 Linden Dr, Madison, WI 53706-1598, USA
FEATURES
Source location/qualifiers
1..1193
/organism="Leonurus mosaic virus"
/strain="Lemv- Brazil 1"
/db_xref="taxon:58177"
complement(1..678)
/gene="rep"
complement(<1..678)
/gene="rep"
/note="AC1: replication associated protein"
/codon_start=1
/product="Rep protein"
/protein_id="AAB51157.1"
/db_xref="GI:1916345"
/translation="MPSKPRFRVQAKNIFLTYPQCTLTKREALSQAIALQPSNKRRIKIRLEHDDQPHLHVLLQLEGVQITNNLFLPLVSTTSAAHPHPNIOGAKSSSDVWASYIKDGDPTVMGEFQVDRSSRGQGVNDAAEALNAPKRALDIKKELEPKYVIFQFNLINLDIRFAKAPPEWPPPLSSFTINVDENQMADEFGRSSARPLRPLNSLIVGCSR"
LIVGCSR"
676..797
/note="Origin of replication; common region"
1039..1193
/gene="cp"
1039..>1193
/gene="cp"
/note="AV1"
/codon_start=1
/product="coat protein"
/protein_id="AAB51158.1"
/db_xref="GI:1916346"
/translation="MPKRDPSMRPMVGTSKISRTSNFSRPGICGPKFNKASQWYKKRPPYCSKKPNS"
YCSKKPNS"

BASE COUNT 295 a 269 c 276 g 353 t
ORIGIN

alignment_scores:
Quality: 272.00 Length: 70
Ratio: 4.459 Gaps: 0
Percent Similarity: 87.143 Percent Identity: 77.143

alignment_block:
US-09-289-346A-6 x LMU92532/rev ..

Align seg 1/1 to reverse of: LMU92532 from: 1 to: 1193

1 ThleuValTroglyglupheginValAspGlyArgSerAlaIargLyl 17
||||| ||||||| ||||||| ||||||| ||||||| |||||||
348 ACAgTTCaATGGGGGTGAATTCACAGTCGACGGGAGAGATTCTAGACGAG 299
17 yCysGInThrSerAsnAspAlaAlaIaGluAlaLeuAsnAlaSerSer 34
1 ||||| ||||||| ||||||| ||||||| ||||||| |||||||
298 CCAACGACAGACAGTTAATGACGCTGCACACTGAGCGCTTAATGCTCCACATA 249
34 ySgIuGluAlaLeuGInIleIleArgGluLysIleProGluLysTyrLeu 50
||||| ||||||| ||||||| ||||||| ||||||| |||||||
248 AACGACGCGCTCTTCAATAATTAACGACGAAATTCGCCGAGAAATATCTT 199
51 PheAlaPheAlaAlaLeuAsnSerAsnLeuAsnAspArgIlePheAspLysTh 67
1 ||||| ||||| ||||||| ||||||| ||||||| |||||||
198 TTTTCATTTCTATTAATTTAAATTCCTAATTTGGATAGAAATTTCCGCAAGGC 149
67 rProGluPro 70
:|||||||
148 TCCGAGAGCCA 139

seq_name: gb_v1:AF131071

```

seq documentation block:				LOCUS	AF131071	1345 bp	DNA	VRL	17-JUN-1999
DEFINITION	Tomato mild mottle geminivirus segment A replication-associated protein (rep) and coat protein (cp) genes, partial cds.								
ACCESSION	AF131071								
VERSION	AF131071.1								
KEYWORDS									
SOURCE									
ORGANISM	tomato mild mottle geminivirus.								
REFERENCE	Viruses: ssDNA viruses: Geminiviridae; Unclassified Geminiviridae.								
AUTHORS	1 (bases 1 to 1345)								
TITLE	Nakhla,M.K., Mejia,L., Ramirez,P., Karkashian,J.P., Doyle,M.M. and Maxwell,D.P.								
JOURNAL	Molecular characterization and DNA-based detection methods for vegetable-infecting geminiviruses in Central America								
AUTHORS	Unpublished								
TITLE	2 (bases 1 to 1345)								
JOURNAL	Nakhla,M.K., Welland,G., Kamal,S. and Maxwell,D.P.								
FEATURES	Submitted (25-FEB-1999) Plant Pathology, University of Wisconsin-Madison, 1630 Linden Dr., Madison, WI 53706-1598, USA								
source	Location/Qualifiers								
	1..1345								
	/organism="tomato mild mottle geminivirus"								
	/isolate="HN96-H5Kw"								
	/specimen_voucher="H5"								
	/db_xref="taxon:92943"								
	/chromosome="segment A"								
	/clone="PHNH5akw"								
	/country="Honduras: Comayagua Valley"								
	/note="obtained from a tomato plant collected in Dec. 1996 by M.K. Nakhla and D.P. Maxwell"]								
	complement(<1..678)								
gene	/gene="rep"								
	/note="ac1"								
	complement(<1..678)								
CDS	/gene="rep"								
	/note="rep protein"								
	/codon_start=1								
	/product="replication-associated protein"								
	/protein_id="AAD33471.1"								
	/db_xref="GI:4928324"								
	/translation="MPLPKKFLINSKNYFLTPHGSLSKETLEQLRLPTTPNKRYIKIRLEHDEGHHVLIQPEGKFTQNCFFPLVSTRTHPHVWGAKSSTDYKSYVNDKDPFTIMGEFQIDGRARCGCOTANAAEALNASKEPAMRLTEKLEPFLFYHNLSSNLDRIFAKADPEWPVPPPLSFTNVDEQEMWTDITFGVAVARPERPISITIEGDSR"								
rep_origin	676..832								
	/note="ori"								
	1001..>1345								
gene	/gene="cp"								
	/note="av1"								
	1001..>1345								
CDS	/gene="cp"								
	/note="capsid protein"								
	/codon_start=1								
	/product="coat protein"								
	/protein_id="AAD33472.1"								
	/db_xref="GI:4928325"								
	/translation="MPKRDAPWRLMSATPKVSRSSNYVPDGLGRKFDKSSAAMNRPWYRKPRITYRSADVPRGCEGPCKIQSPEDQHHDSHGKVMCISDYTRNGITTHRVGKRYRFCVKSYYTLGKV"								
BASE COUNT	329 a 289 c 313 g 414 t								
ORIGIN									
alignment_scores:	Quality:	272.00	Length:	70					
	Ratio:	4.250	Gaps:	0					
Percent Similarity:	91.429	Percent Identity:	72.857						


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CDS      complement(815..1072)
         /gene="AC4"
         /note="A14"
         /codon_start=1
         /product="AC4"
         /protein_id="AAG01007.1"
         /db_xref="GI:9858127"
         /translation="MGNTSMCKSSKANSASQIADSSIMSHRTDRITFTPTSRRLN
         APMSPTSIKIRGIRSPGVNSKSTADILEASRLTLTPORL"

BASE COUNT      359 a      296 c      327 g      401 t
ORIGIN

alignment_scores:
      Quality: 268.00      Length: 68
      Ratio: 4.467      Gaps: 0
      Percent Similarity: 88.235      Percent Identity: 79.412

alignment_block:
US-09-289-346a-6 x AF288227/rev ..

Align seg 1/1 to reverse of: AF288227 from: 1 to: 1383

      1  ThrLeuValTrpGlyGluupheGlnValAspGlyArgSerAlaArgGlyG1 17
          |||:::|||||
      902  ACCATCACCCTGGGGCTGATTCCAGTCGACGCGACGATCTCTAGAGAGG 853
          |||
      17  yCysGlnThrSerAsnAspAlaAlaGlnAlaLeuAsnAlaSerSer1 34
          |||
      852  CCAGCAGACTGCTAACGACGCGCAGAGGCTTAACGCGAGTTCTA 803
          |||
      34  ysgGluAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeu 50
          |||
      802  AGGAACCTCGTTGCAATATATCATGAGGAAACTCCCTGAAATATATTA 753
          |||
      51  PheAlaPheAlaAlaLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
          |||
      752  TTTCATTTTCATATATTAGTTAGTAATTAGATGATTTTTCCTCTCC 703
          |||
      67  rPro 68
          |||
      702  ACCT 699

seq_name: gb_v1:AF104036

seq_documentation_block:
LOCUS      AF104036      2828 bp      DNA      circular      VRL      05-AUG-1999
DEFINITION Sweet potato leaf curl virus DNA A, complete sequence.
ACCESSION  AF104036
VERSION    AF104036.1 GI:5702158
KEYWORDS
SOURCE
ORGANISM   Sweet potato leaf curl virus.
            Sweet potato leaf curl virus
            Viruses: ssDNA viruses; Geminiviridae; Begomovirus.
            1 (bases 1 to 2828)
REFERENCE  Lotrakul,P., Valverde,R.A., Clark,C.A., Sim,J. and De la Torre,R.
TITLE      Detection of a geminivirus infecting sweet potato in the United
            States
JOURNAL    Plant Dis. 82, 1253-1257 (1998)
REFERENCE  Lotrakul,P. and Valverde,R.A.
AUTHORS    Cloning of a DNA-A-like genomic component of sweet potato leaf curl
            virus: nucleotide sequence and phylogenetic relationships
            http://www.bspg.org.uk/mpopol/1999/042210trakul/
REMARK     3 (bases 1 to 2828)
AUTHORS    Lotrakul,P. and Valverde,R.A.
TITLE      Direct Submission
JOURNAL    Submitted (02-NOV-1998) Plant Pathology and Crop Physiology,
            Louisiana State University, 302 Life Sciences Bldg., LSU, Baton
            Rouge, LA 70803, USA
FEATURES
SOURCE      Location/Qualifiers
            1..2828

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gene      /organism="Sweet potato leaf curl virus"
CDS      /db_xref="taxon:100755"
         /chromosome="DNA A"
         /country="USA"
         /gene="AV2"
         132..476
         /gene="AV2"
         132..476
         /note="AV2"
         /codon_start=1
         /product="precoat protein AV2"
         /protein_id="AAD47169.1"
         /db_xref="GI:5702159"
         /translation="MAELMDPLONPLPTLIGFGRCLSVKYLOSILKKRPGTGFEL
         CSELIRIRVROYDRANARFAEISSIMGETGTAELELDSTRALHMECCPNCCPALCP
         GFKRRPDEKES"
         301..1065
         /gene="AV1"
         301..1065
         /gene="AV1"
         /note="AV1"
         /codon_start=1
         /product="coat protein AV1"
         /protein_id="AAD47170.1"
         /db_xref="GI:5702160"
         /translation="MTGRNVSRRFHYGGRVBRRLNFEALIVPTGNAPVARSY
         VPSVSGVSMKRGRDRIPKGVGPKVDDEKMDVPHTGTVCYSDFTRGTLTRL
         GKRVCVKSMDIGKVMDDNNAKRQHTNITWYLIRDRPNKDPUNFQDIFPMYNEP
         ITAKIRMDLRDMQVLKRESVYSGPYSHKEQALIRFEKGLYNHVVYNNKEEAKYE
         NOLENAIMLYSSSHASNPNVYQTLRCRAVFYDSHNN"
         /complement(1081..1515)
         /gene="AC3"
         /complement(1081..1515)
         /gene="AC3"
         /note="AC3"
         /codon_start=1
         /product="AC3"
         /protein_id="AAD47171.1"
         /db_xref="GI:5702161"
         /translation="MDSRTGESISHAOTTRAVEFPTNPMSVGRAPAFRLIMYHEST
         OGRTILKFOLRVNVREEROLGFHKIFLQFRLITRLTGAIHSMWTGILERTLKRICNEL
         ANLGFFSLVNLFEVIRYLRVCSWIDELDTVCNDVDKVLVY"
         /complement(1232..1678)
         /gene="AC2"
         /complement(1232..1678)
         /gene="AC2"
         /note="AC2"
         /codon_start=1
         /product="transactivator protein AC2"
         /protein_id="AAD47172.1"
         /db_xref="GI:5702162"
         /translation="MSNPLSGYKRCPIOEPLHTFAKKAKRKRVPEQRIRIVKGGCCS
         AFITTCXVGHGFTIRGINKSCSDYESSIRIQPIVCGSDVPSQNNVCPREHGEN
         HQIPAGFLOKKEATGIPDLPPIPDLDPPSNMVCYSQLDWVFGRP"
         /complement(1587..2681)
         /gene="AC1"
         /complement(1587..2681)
         /gene="AC1"
         /note="AC1"
         /codon_start=1
         /product="replication initiation protein AC1"
         /protein_id="AAD47173.1"
         /db_xref="GI:5702163"
         /translation="MAPPRKFIQAKNFITYPRCSLSKEDCIAQLINLTPSNKKYI
         HVARLHEDEPHLIVLVOFEKFPCTNRFPDVLPNSNHFHPHIGAKSSDYKS
         VYDKDGDITNGEFOVODGSRAGGQOTNDAAEALNMGSKFAALQIIREKLPERYLF
         OPHNLVSNLDRIFSPSPSYSSPSSSSFNNAVDPDISMAENWMSARPRPSIV
         IEGPSRIKTVARSLGPHNYLGHLDLSPKAYSNSANVINVIDVNPOTLAKRFREMG
         AOKDMQSNCKYKGPVIRKIGIPITLFCNGEBSSEKVLWDKEQGLAKWAVANALFC
         DVQSPFWQVEEVSHGATAHRCBOQESS"
         /complement(2267..2524)
         /gene="AC4"
         /complement(2267..2524)

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/gene="AC4"
/notes="AC4"
/codon_start=1
/product="AC4"
/protein_id="AAD47174.1"
/db_xref="GI:5702164"
/translation="MGNLTSMCMWSSKANSNAQDSSIMSHRTDRITFTPTSRRLNP
APMSPSTIRCTGIPSPGVNSRSTADLEASRLTTPORL"
BASE COUNT      741 a      606 c      675 g      806 t
ORIGIN

alignment_scores:
  Quality: 268.00      Length: 68
  Ratio: 4.467      Gaps: 0
Percent Similarity: 88.235      Percent Identity: 79.412

alignment_block:
US-09-289-346a-6 x AF104036/rev ..

Align seg 1/1 to reverse of: AF104036 from: 1 to: 2828

1   ThrLeuValTrpGlyIupheGlnValAspGlyArgSerAlaArgGlyI 17
    |||:::|||||
2354  ACCATCACTGGGGTGAATTCACAGTCGACGGCAGATCTGTACAGGAGC 2305
    17  YCysGlnThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerL 34
    |||:::|||||
2304  CCACGACACTGCTACGACAGCCGCGAGAGCTCTTAACGCGAGTTCTA 2255
    34  YsgGluAlaAlaLeuGlnIleIleArgGluIuysIleProGluIuysTyLeu 50
    |||:::|||||
2254  AAGAACCTGGCTTCAATATATCAGGAGAACTCCCTGAATAATATTTA 2205
    51  PheAlaIheAlaAlaLeuAsnSerAsnLeuAspArgIlePheAspIysTh 67
    |||:::|||||
2204  TTTCAAATTTCATATTAGTTAGTAATTTAGATGATTTTCTCCTCC 2155
    67  rPro 68
    |||
2154  ACCT 2151

seq_name: gb_v1:SG067926

seq_documentation_block:
LOCUS      SG067926      554 bp      DNA      VRL      28-JAN-1998
DEFINITION Side golden mosaic geminivirus Rep protein (AC1) gene, partial cds.
ACCESSION  U67926
VERSION    U67926.1  GI:1546801
KEYWORDS   .
SOURCE     .
  ORGANISM .
    sida golden mosaic virus.
  sida golden mosaic virus.
  Viruses: ssDNA viruses; Geminiviridae; Begomovirus.
  1 (bases 1 to 554)
  Roye,M.E., McLaughlin,W.A., Nakhla,N.K. and Maxwell,D.P.
  Genetic Diversity among geminiviruses associated with the weed
  species Sida spp. Macroptilium lachnoides, and Mispadula
  amplessima from Jamaica
  Plant Dis. 81, 1251-1258 (1997)
  2 (bases 1 to 554)
  Roye,M.E., McLaughlin,W.A. and Maxwell,D.P.
  Direct Submission
  Submitted (23-AUG-1996) Plant Pathology, University of Wisconsin,
  1630 Linden Drive, Madison, WI 53706-1598, USA
  Location/Qualifiers
    1..554
    /organism="Sida golden mosaic virus"
    /strain="Jamaica"
    /isolate="Jamaica, May 1993"
    /db_xref="taxon:51034"
    /note="DNA A component"
    complement(1..554)
    /gene="AC1"
gene
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complement(<1..554)
/gene="AC1"
/notes="replication-associated protein"
/codon_start=1
/product="Rep protein"
/protein_id="AAB97865.1"
/db_xref="GI:1546802"
/translation="SISKREALSOLQTLTPYNNKKEIKICRELHNGEPHLVLIOFE
GKYNCTNNRFPDLVSPTRSVHHPNIOGAKSSSDSVKEDQNTIEMCVFOIDGSA
RGGQOTANDNAAEALNSGKEDALKIIRKLEPRYLFOYHNLSSNIDRLFSRPPRMS
HPFLPSFTYVPGOMQEWADGTFGR"
BASE COUNT      121 a      127 c      139 g      167 t
ORIGIN

alignment_scores:
  Quality: 265.00      Length: 70
  Ratio: 4.206      Gaps: 0
Percent Similarity: 90.000      Percent Identity: 70.000

alignment_block:
US-09-289-346a-6 x SG067926/rev ..

Align seg 1/1 to reverse of: SG067926 from: 1 to: 554

1   ThrLeuValTrpGlyIupheGlnValAspGlyArgSerAlaArgGlyI 17
    |||:::|||||
290  ACCATCAATGGGGGTGTTCCAGATGACCGAAGAACTGCTGCGAGC 241
    17  YCysGlnThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerL 34
    |||:::|||||
240  TCACCAACACAGCTACGACAGCCGCGGAGCATGTAATCTGGAACAA 191
    34  YsgGluAlaAlaLeuGlnIleIleArgGluIuysIleProGluIuysTyLeu 50
    |||:::|||||
190  AGGAGGATGCGACGAAATCATCAGACAGAACTTACGAAAGTATCTC 141
    51  PheAlaIheAlaAlaLeuAsnSerAsnLeuAspArgIlePheAspIysTh 67
    |||:::|||||
140  TTTCAGTATCAGACACTATCCAGTAATATCGATGATTTTCAGTAAGC 91
    67  rProGluPro 70
    |||
90  TCAGAACCG 81

seq_name: gb_v1:IYEL32548

seq_documentation_block:
LOCUS      IYEL32548      2763 bp      DNA      circular VRL      01-FEB-1999
DEFINITION Ipomoea yellow vein virus V2, V1, C3 and C2 genes.
ACCESSION  AJ132548
VERSION    AJ132548.1  GI:4210720
KEYWORDS   C2 gene; C2 protein; C3 gene; C3 protein; coat protein; V1 gene; V2
  gene; V2 protein.
SOURCE     Ipomoea yellow vein virus.
  Ipomoea yellow vein virus.
  Viruses: ssDNA viruses; Geminiviridae; Begomovirus.
  1 (bases 1 to 2763)
  Banks,G.K.
  Direct Submission
  Submitted (26-JAN-1999) Banks G.K., Virus Research, John Innes
  Centre, Norwich Research Park, Colney Lane, Norwich, NR4 6JL, UK
  2 (bases 1 to 2763)
  Banks,G.K., Bedford,I.D., Beitia,F.J., Cerezo,E.R. and Markham,P.G.
  A novel geminivirus of Ipomoea indica (Convolvulaceae) from southern
  Spain
  JOURNAL      Unpublished
  FEATURES
    source
    Location/Qualifiers
      1..2763
      /organism="Ipomoea yellow vein virus"
      /viroon
      /specific_host="Ipomoea indica"
      /db_xref="taxon:87832"
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gene      995..1390
/gene="V2"
CDS       995..1390
          /gene="V2"
          /codon_start=1
          /product="V2 protein"
          /protein_id="CA10695.1"
          /db_xref="GI:4210721"
          /translation="MTLLYKQSDSCRAMCPSTAMPDLPNLPDPTLYGPRCMLSVKY
          LOGILKYEPTGTGFLCSFLIRFRROYDRANSRAELISSLNGETGKTESELRDSY
          RALHMECCPNCPCPLCPGFKRRPDEKEG"
gene      1215..1979
/gene="V1"
CDS       1215..1979
          /gene="V1"
          /codon_start=1
          /product="coat protein"
          /protein_id="CA10696.1"
          /db_xref="GI:4210722"
          /translation="MTGRIRVSPREHPHYGGROVRSNLLETAIVPYGNAPVARSY
          VPSRGVRRMRRRGDRIPKSCYGPCKTODEYFKKDYPTGTFCVSDPFRGTGTHRL
          GKRYCIKSNIDCKWMDVNAKDHNTIITWILIRPRPKDPLNFGQLFTMYDNEP
          TTAKIRMDLDRMQVLKRFSTVYSGPYSHKEQALIRKFRCLYNHVTYNHKEBAKYE
          NOLENALMLYSASSHSNPYQTLRCRAFYDSHK"
gene      complement(1976..2413)
CDS       complement(1976..2413)
          /gene="C3"
          /complement(1976..2413)
          /gene="C3"
          /codon_start=1
          /product="C3 protein"
          /protein_id="CA10697.1"
          /db_xref="GI:4210723"
          /translation="MDSRTGESLSHAQITRAEFPNNPMSGQAPPHILRLMYHTNN
          LDSFTTKMKVQVQVHNHNRKREIGFQKITFLQETIIFRLIGALPNNVTGTSNRLKRICNS
          LASIGYFSLNLYVIRHLRPOQCLMVEBVDVLDCKDIKVLKY"
gene      complement(2127..2576)
CDS       complement(2127..2576)
          /gene="C2"
          /complement(2127..2576)
          /gene="C2"
          /codon_start=1
          /product="C2 protein"
          /protein_id="CA10698.1"
          /db_xref="GI:4210724"
          /translation="MSTAPSGYKRRKCPAOPETIAAARKROKTPPEPRRIYKGGCCS
          AFTINDCKFOHGTFRKGVTKSCDYESRILQSHVCGSDCTIPSTIDVCYKOPRLK
          DDHESAASSQPPEDGWNWIPEDLPPIPDHNASDMWYSQLDWYFQSP"
BASE COUNT 734 a 570 c 671 g 788 t
ORIGIN
alignment_scores:
  Quality: 264.00      Length: 68
  Ratio: 4.475        Gaps: 0
  Percent Similarity: 86.765  Percent Identity: 76.471
Percent Similarity: 86.765  Percent Identity: 76.471
alignment_block:
US-09-289-346a-6 x IYEL32548/rev ..
Align seg 1/1 to reverse of: IYEL32548 from: 1 to: 2763
1 ThrlEuValTrpGlyGluPheGlnValAspGlyArgSerAlaArgGlyG 17
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
469 ACCCTCATATGAGGGGTAATTCAGATCGACGCGCATCTGCTAGAGAGG 420
17 yCysGlnThrSerAsnAspAlaAlaIaGluAlaLeuAsnAlaSerSer 34
1 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
419 TCAGCAGGTCTGCTAACGACGACGCGCAGAGGGCTAAACGCTATGTC 370
34 ySGluGluAlaLeuGlnIleIleArgGluIulSerProGluIulSerTy 50
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
369 AAGAACTCGCTTGCAAAATATCAGGAGAACTCCCTGAAAAATATTTTA 320
51 PheAlaPheAlaIaLeuAsnSerAsnLeuAspArgIlePheAspLysTr 67

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|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
319 TTTCATATCATATATTTAGTATAGTAATTTAGATAGCATTTTCTCTCC 270
67 rPro 68
|||||
269 TCCT 266
seq_name: gb_v1:MGU75278
seq_documentation_block:
LOCUS      MGU75278          447 bp      DNA          27-NOV-1996
DEFINITION Macropitillium golden mosaic geminivirus replication-associated
protein (AC1) gene, partial cds.
ACCESSION  U75278
VERSION    U75278.1
KEYWORDS   GI:1688188
SOURCE     Macropitillium golden mosaic geminivirus.
ORGANISM   Macropitillium golden mosaic geminivirus
Viruses: ssDNA viruses; Geminiviridae; Begomovirus.
REFERENCE  1 (bases 1 to 447)
AUTHORS   Royle,M.E.
TITLE     Diversity and phylogeny of whitefly-transmitted geminiviruses from
Jamaica
JOURNAL    Thesis (1996)
REFERENCE  2 (bases 1 to 447)
AUTHORS   Royle,M.E., McLaughlin,W.A. and Maxwell,D.P.
TITLE     Three distinct geminiviruses infecting M. jathyroides from Jamaica
but not BCMV
JOURNAL    Unpublished (1996)
REFERENCE  3 (bases 1 to 447)
AUTHORS   Royle,M.E., McLaughlin,W.A. and Maxwell,D.P.
TITLE     Direct Submission
JOURNAL    Submitted (17-OCT-1996) Biochemistry, University of the West
Indies, Mona, Kingston 7, Jamaica
FEATURES   Location/Qualifiers
source     1..447
            /organism="Macropitillium golden mosaic geminivirus"
            /strain="Jamaican"
            /isolate="2"
            /db_xref="taxon:51676"
            /clone="pmcJA2"
            /complement(1..447)
            /gene="AC1"
            /complement(<1..>447)
            /gene="AC1"
            /codon_start=1
            /product="replication-associated protein"
            /protein_id="AAB36919.1"
            /db_xref="GI:1688189"
            /translation="HVLIQFOGKFNCTNNRFLDLYVSPSRSAHFHPIQAGAKSSDYKS
            YVERKGDITENGWFOIDGRSARGGQOTSDAAEAALNSGTAEAAIRIVKEKIPKFLF
            QYHNLSNMDRITFMKDPPEPMAPEPLASSFTNVDPDEMAWNTYFGRG"
BASE COUNT 97 a 112 c 110 g 128 t
ORIGIN
alignment_scores:
  Quality: 257.00      Length: 70
  Ratio: 4.213        Gaps: 0
  Percent Similarity: 87.143  Percent Identity: 68.571
Percent Similarity: 87.143  Percent Identity: 68.571
alignment_block:
US-09-289-346a-6 x MGU75278/rev ..
Align seg 1/1 to reverse of: MGU75278 from: 1 to: 447
1 ThrlEuValTrpGlyGluPheGlnValAspGlyArgSerAlaArgGly 17
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
294 ACCATCAATGAGGAGGTCTCCAGATCGACGAGAAAGTCTGAGGCGG 245
17 yCysGlnThrSerAsnAspAlaAlaIaGluAlaLeuAsnAlaSerSer 34
1 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
244 TCAGCAAACTCTACGATGACGCCCGCAAGCATTTAAATTTCGAACAA 195

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/protein_id="AAB82606.1"
/db_xref="GI:2583075"
/translation="MPKRDAWPMWMACTSKVSRNANYSPPSGIGPRLKAAEWVRPM
YRKCST"
464..>1165
/note="replication-associated protein"
/product="AC1"
/codon_start=1
/protein_id="AAB82605.1"
/db_xref="GI:2583074"
/translation="MPKGSFSTAKKVFELTYPOCSLSEKEDALSOIONLTTPVKKFI
KICRELHNEGPHLVLIQEKGKPCNNRLLDVSPTSTHFPNIGAKSSDVKS
YKENDGPTIEWGLFQIDGRSARGCOGTANDAAALNSGTKEAMKIKELPERFLP
QYHNLSSDLRIFMKAPNPMAPPPPLSFTNVPHMGWMSHDYFGRSAARGETTSII
IEGDSPTGKTMACRC"
BASE COUNT      350 a      264 c      256 g      295 t
ORIGIN

alignment_scores:
  Quality: 251.00      Length: 70
  Ratio: 3.984      Gaps: 0
  Percent Similarity: 90.000      Percent Identity: 67.143

alignment_block:
US-09-289-346a-6 x AF026553 ..
Align seg 1/1 to: AF026553 from: 1 to: 1165

1 ThrLeuValTrrpGlyGluPhgInValAspGlyArgSerAlaArgGly1 17
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
791 ACCATGCAATGGGGATTGTTCCGATTGACCGAAGAGTCTCGAGSTGG 840

17 yCysGlnThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSer1 34
| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
841 CCACAGACCGCAACGACGACGACGACGACGACGACGACGACGACGACG 890

34 ysgGluGluAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeu 50
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
891 AGCAAGAACGATGAAATCATATAAGACAGAGTTCGCGAAGAGTTTCTT 940

51 pheAlaPheAlaAlaLeuAsnSerAsnLeuAspArgIlePheAspLysThr 67
||| :||| ||||| ||||| ||||| ||||| ||||| |||||
941 TTTCAGTATCATCACTATCCAGTACGACGACGATTTTCATGAAGCC 990

67 rProGluPro 70
:|||||
991 TCCAAATCCG 1000

seq_name: gb_v1:AB001315

seq_documentation_block:
LOCUS      AB001315      570 bp      DNA      VRL      13-FEB-1999
DEFINITION Tobacco leaf curl virus C1 and C4 genes, clone YOKOHAMA3-1, partial
and complete cds.
ACCESSION  AB001315
VERSION    AB001315.1 GI:3798714
KEYWORDS
SOURCE
ORIGINISM  1 (bases 1 to 570)
            tobacco leaf curl virus (isolate:YOKOHAMA3,
            specific_host:Eupatorium makinoi) DNA, clone:YOKOHAMA3-1,
            tobacco leaf curl virus
            Viruses: ssDNA viruses; Geminiviridae; Begomovirus.
REFERENCE  1 (bases 1 to 570)
AUTHORS   Ooi,K.
TITLE     Direct Submission
JOURNAL   Submitted (19-FEB-1997) to the DBJ/EMBL/GenBank databases.
            Kazuyuki Ooi, Kyushu University, Department of Biology, 6-10-1
            Hakozaki Higashi-ku, Fukuoka, Fukuoka 812, Japan
            (E-mail:kooisch@box.nc.kyushu-u.ac.jp, Tel:+81-92-642-2624,
            Fax:+81-92-642-2645)
2 (bases 1 to 570)
AUTHORS   Ooi,K., Ohshita,S., Ishii,T. and Yahara,T.
TITLE     Molecular phylogeny of geminivirus infecting wild plants in Japan

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JOURNAL      J. Plant Res. 110, 247-257 (1997)
FEATURES
source
location/Qualifiers
1..570
/organism="tobacco leaf curl virus"
/isolate="YOKOHAMA3"
/specific_host="Eupatorium makinoi"
/db_xref="taxon:67762"
/clone="YOKOHAMA3-1"
/complement(1..570)
/gene="C1"
/complement(<1..>570)
/gene="C1"
/codon_start=1
/protein_id="BAA34033.1"
/db_xref="GI:4426541"
/translation="EEALSQIONITPINKLYIKICRELHNEGSPHLVLIQEPKIK
CONNRFDPVSPTSAHFHPNIGAKSSSDVKSVDYDKGDPTLEWGTFOIDGSARGG
ONANDACAEALNASSKAEALAIIREKLPKDFIYOYHNINLSNDRIFAPPLFVFCPT
ASSFDQVPEELEENWASENVMSGARPMRPM"
complement(231..488)
/gene="C4"
/complement(231..488)
/gene="C4"
/codon_start=1
/protein_id="BAA34034.1"
/db_xref="GI:3798715"
/translation="MEALISMCFCSKANTNAKITDSSRWYPOPDHISIRFRELNP
AFTSPSTRIEIRNSGHSRSTEEVLEAAHMLTHVQR"
BASE COUNT      141 a      121 c      126 g      182 t
ORIGIN

alignment_scores:
  Quality: 248.00      Length: 85
  Ratio: 4.066      Gaps: 1
  Percent Similarity: 71.765      Percent Identity: 58.824

alignment_block:
US-09-289-346a-6 x AB001315/rev ..
Align seg 1/1 to reverse of: AB001315 from: 1 to: 570

1 ThrLeuValTrrpGlyGluPhgInValAspGlyArgSerAlaArgGly1 17
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
318 ACGCTCCAAATGGGACACATTCAGATCGACGAGAGAGTGTAGAGGAG 269

17 yCysGlnThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSer1 34
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
268 CTGCCAGAAATGCTAACGACGACGACGACGACGACGACGACGACGAC 219

34 ysgGluGluAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeu 50
||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
218 AGGCAAGAACGATTAAGCAATTAATAGGAGAAAGCTCCATAAGATTATA 169

51 pheAlaPheAlaAlaLeuAsnSerAsnLeuAspArgIlePheAspLysThr 63
||| :||| ||||| ||||| ||||| ||||| ||||| |||||
168 TTTCATATCATATTAATTAATAGTAATTTAGATTTTGTCTCTCC 119

64 .....PheAspLysThrP 68
118 GTTCAGAGTTTGTGTTGTCCTTCACAGCCTCATCTTGTATCAAGTTC 69

68 rGluu 69
|||||
68 CAGAA 64

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2216 AGCTAATGATGCTCCGAGAGCCCTTAATGAGTTTCACTGACAG 2167
37 1aleuGlnIleIleArgGluIysIleProGluIysTyrlleuPheAlaPhe 53
2166 CTTTAGCAATATTAGGAGAAACTCCCTAAGATTATTATTCAATAT 2117
54 Ala1aleuAsnSerAsnleuAspArgIlePheAspIysThrPro 68
2116 CATAAATTTAAATGTAAATTAGATGATTTT.....ACACCT 2078
seq_name: /cgnl_8/gcgdata/geneseq/geneseqn/NA1995.DAT:AA084371
seq_documentation_block:
ID AA084371 standard; DNA; 434 BP.
XX
AC AA084371;
XX
DT 19-AUG-1995 (first entry)
XX
DE Gemini virus-specific polyribozyme-E target sequence.
XX
KW ribozyme target sequence; polyribozyme-E;
KM tomato leaf curl virus; RNA cleavage; tomato transgenic plant;
KW virus disease-resistance; ss.
XX
OS Tomato leaf curl virus.
XX
FH Key Location/Qualifiers
FT misc_feature 13..43
FT /tag= a
FT /note= "ribozyme R1 target sequence"
FT misc_feature 26..28
FT /tag= b
FT /note= "ribozyme R1 cleavage site"
FT misc_feature 312..342
FT /tag= c
FT /note= "ribozyme R2 target sequence"
FT misc_feature 325..327
FT /tag= d
FT /note= "ribozyme R2 cleavage site"
FT misc_feature 384..414
FT /tag= e
FT /note= "ribozyme R3 target sequence"
FT misc_feature 397..399
FT /tag= C
FT /note= "ribozyme R3 cleavage site"
XX
PN WO9503404-A.
XX
PD 02-FEB-1995.
XX
PF 22-JUL-1993; 93WO-EP01946.
XX
PR 22-JUL-1993; 93AU-0047014.
PR 22-JUL-1993; 93WO-EP01946.
XX
PA (BIOC-) BIOCEM SA.
PA (CSTR) COMMONWEALTH SCI & IND RES ORG.
XX
PI Baudino S, Comeau D, Dry IB, Gruber V, Lenee P;
PI Mason J, Rezaiian MA, Rliden JE, Rezanan MA;
XX
DR MPI: 1995-075232/10.
XX
PT Synthetic DNA virus ribozyme(s) - reduce replication, infection
PT and/or assembly of viruses by cleaving target virus sequence,
PT useful for preparing resistant plants, esp tomatoes.
XX
PS Example 10; Fig 11b; 90pp; English.
XX
CC The sequence is a tomato leaf curl virus target sequence for
CC polyribozyme-E, which hybridizes to and cleaves the sequence and
CC thereby reduces replication, infection and/or assembly of the virus

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CC substantially. The ribozyme may be expressed in a transgenic plant,
CC e.g. tomato, to confer virus disease-resistance.
XX
SQ Sequence 434 BP; 126 A; 86 C; 91 G; 131 T; 0 other;

alignment_scores:
Quality: 220.00 Length: 85
Ratio: 3.667 Gaps: 1
Percent Similarity: 70.588 Percent Identity: 52.941

alignment_block:
US-09-289-346a-6 x AA084371 ..
Align seg 1/1 to: AA084371 from: 1 to: 434

1 ThrleuValTrpGlyGluPheGlnValAspGlyArgSerAlaArgGlyG1 17
||||| |||||||||.....:|||||
95 ACCCTCGAATGCGAGAGATTTCAGATCGATGACGATCTGCCAAGCGGG 144
17 yCysGlnThrsAsnAspAlaAlaGluAlaAlaAsnAlaSerSerL 34
1 |||:||||| |||:||||| |||:|||||
145 ACAACAAATCACCACCAATGACGCTTACGCCAGCCGCTTAACCTGAAGTA 194
34 ySGlGluAlaLeuGlnIleIleArgGluIysIleProGluIysTyrlleu 50
|||:||||| |||:||||| |||:|||||
195 AGTCAGAGGCTTTACGCTCTTAGGGAATTAGCCCTAAGATTATAGTT 244
51 PheAlaPheAlaAlaLeuAsnSerAsnleuAspArgIle..... 63
::: ||| ||||||||| |||||||||
245 TTACAAATTTTCATTAATTAAATAGTAATTAGATAGATTTTTACACCTCC 294
64 .....PheAspIysThrP 68
295 GTTGGAGGTTTATGTTCTCCTTTTATATCTTCTTGTGATGAGATTC 344
68 roGlu 69
|||||
345 CAGAA 349

seq_name: /cgnl_8/gcgdata/geneseq/geneseqn/NA1995.DAT:AA084372
seq_documentation_block:
ID AA084372 standard; DNA; 479 BP.
XX
AC AA084372;
XX
DT 19-AUG-1995 (first entry)
XX
DE Gemini virus-specific polyribozyme-F target sequence.
XX
KW ribozyme target sequence; polyribozyme-F;
KM tomato leaf curl virus; RNA cleavage; tomato transgenic plant;
KM virus disease-resistance; ss.
XX
OS Tomato leaf curl virus.
XX
FH Key Location/Qualifiers
FT misc_feature 46..96
FT /tag= a
FT /note= "ribozyme R4-R5 target sequence"
FT misc_feature 58..60
FT /tag= b
FT /note= "ribozyme R4 cleavage site"
FT misc_feature 81..83
FT /tag= c
FT /note= "ribozyme R5 cleavage site"
FT misc_feature 356..386
FT /tag= d
FT /note= "ribozyme R2 target sequence"
FT misc_feature 370..372
FT /tag= C
FT /note= "ribozyme R2 cleavage site"

```



```

FT misc_feature 429..459
FT /*tag= e
FT /note= "ribozyme R3 target sequence"
FT misc_feature 442..444
FT /*tag= d
FT /note= "ribozyme R3 cleavage site"
XX
XX WO9503404-A.
XX
XX 02-FEB-1995.
XX
XX 22-JUL-1993; 93WO-EP01946.
XX
XX 22-JUL-1993; 93AU-0047014.
XX
XX 22-JUL-1993; 93WO-EP01946.
XX
XX (BIOC-) BIOCEM SA.
XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX
XX Baudino S, Comeau D, Dry IB, Gruber V, Lenee P;
XX Mason J, Rezalan MA, Rigden JE, Rezanan MA;
XX
XX WPI: 1995-075232/10.
XX
XX Synthetic DNA virus ribozyme(s) - reduce replication, infection
XX and/or assembly of viruses by cleaving target virus sequence,
XX useful for preparing resistant plants, esp tomatoes.
XX
XX Example 10; Fig 11c; 90pp; English.
XX
XX The sequence is a tomato leaf curl virus target sequence for
XX polyribozyme-F, which hybridizes to and cleaves the sequence and
XX thereby reduces replication, infection and/or assembly of the virus
XX substantially. The ribozyme may be expressed in a transgenic plant,
XX e.g. tomato, to confer virus disease-resistance.
XX
XX Sequence 479 BP; 145 A; 95 C; 97 G; 142 T; 0 other;

alignment_scores:
Quality: 220.00 Length: 85
Ratio: 3.667 Gaps: 1
Percent Similarity: 70.588 Percent Identity: 52.941

alignment_block:
US-09-289-346a-6 x AA084372 ..
Align seg 1/1 to: AA084372 from: 1 to: 479

1 ThleuValTrpGlyGluPheGlnValAspGlyArgSerAlaArgGly 17
||||| ||||||||| ||||||||| ||||||||| |||||||||
140 ACCCTCGAATGGGGAGAGTTTCAGATCGATGAGATCTCCAGAGCGGG 189
17 yCysGlnThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSer 34
| ||||| ||||| ||||| ||||| ||||| ||||| |||||
190 ACAACATCATGACCAATGACGCTTACGCCGCGCTTAACACTGGAAGTA 239
34 yScGluAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeu 50
| ||||| ||||| ||||| ||||| ||||| ||||| |||||
240 AGTCAGAGCGCTCTTAACGCTCTTACGCGAATTAGCCCTAAGATTAATGTT 289
51 PheAlaPheAlaAlaLeuAsnSerAsnLeuAspArgIle..... 63
::: ||| ||||||||| ||||||||| |||||||||
290 TTACAATTTCATTAATTAAATAGTAATTAGATTTTATACACCTCC 339
64 .....PheAspLysThrP 68
||||| :|||:|
340 GTTGAGAGTTATGTTCTTCTTTTATCTTCTTCTTTGATCGAGTTC 389
68 roGlu 69
|||||
390 CAGAA 394

```

```

seq_name: /cgnl_8/gcdata/geneseq/geneseqn/NA1995.DAT:AA084375
seq_documentation_block:
ID AA084375 standard; DNA; 550 BP.
XX
XX AA084375;
XX
XX 19-AUG-1995 (first entry)
XX
XX Tomato leaf curl virus Australian strain DNA sequence.
XX
XX Tomato leaf curl virus; Australia strain; plant disease; ds.
XX
XX OS Tomato leaf curl virus (Australia).
XX
XX PN WO9503404-A.
XX
XX PD 02-FEB-1995.
XX
XX PF 22-JUL-1993; 93WO-EP01946.
XX
XX PR 22-JUL-1993; 93AU-0047014.
XX
XX 22-JUL-1993; 93WO-EP01946.
XX
XX (BIOC-) BIOCEM SA.
XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX
XX Baudino S, Comeau D, Dry IB, Gruber V, Lenee P;
XX Mason J, Rezalan MA, Rigden JE, Rezanan MA;
XX
XX WPI: 1995-075232/10.
XX
XX Synthetic DNA virus ribozyme(s) - reduce replication, infection
XX and/or assembly of viruses by cleaving target virus sequence,
XX useful for preparing resistant plants, esp tomatoes.
XX
XX Disclosure; Fig 1; 90pp; English.
XX
XX The sequence represents the complementary sense DNA strand of an
XX Australian strain of tomato leaf curl virus. Ribozymes specific
XX for this sequence may be used in generation of transgenic plants
XX with disease-resistance.
XX
XX Sequence 550 BP; 148 A; 120 C; 134 G; 142 T; 6 other;

alignment_scores:
Quality: 219.50 Length: 86
Ratio: 3.658 Gaps: 1
Percent Similarity: 69.767 Percent Identity: 52.326

alignment_block:
US-09-289-346a-6 x AA084375 ..
Align seg 1/1 to: AA084375 from: 1 to: 550

1 ThleuValTrpGlyGluPheGlnValAspGlyArgSerAlaArgGly 17
||||| ||||||||| ||||||||| ||||||||| |||||||||
201 ACCCTCGAATGGGGAGAGTTTCAGATCGATGAGATCTCCAGAGCGGG 250
17 yCysGlnThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSer 34
| ||||| ||||| ||||| ||||| ||||| ||||| |||||
251 ACAACATCATGACCAATGACGCTTACGCCGCGCTTAACACTGGAAGTA 300
34 yScGluAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeu 50
| ||||| ||||| ||||| ||||| ||||| ||||| |||||
301 AGTCAGAGCGCTCTTAACGCTCTTACGCGAATTAGCCCTAAGATTAATGTT 350
51 PheAlaPheAlaAlaLeuAsnSerAsnLeuAspArgIle..... 63
::: ||| ||||||||| ||||||||| |||||||||
351 TTACAATTTCATTAATTAAATAGTAATTAGATTTTNNNTACACC 400
64 .....PheAspLysT 67

```

```

401 TCCGTTGAGCTTATGTCTCTCTTTTATGCTTCTTTGATCGAG 450
67 hrProGlu 69
:::|||||
451 TTCACGAA 458
seq_name: /cgnl_8/gcgdata/geneseq/geneseqn/NA1996.DAT:AA12904
seq_documentation_block:
ID AA12904 standard; DNA; 1080 BP.
XX
AC AA12904;
XX
DE 07-NOV-1996 (first entry)
XX
DE Sardinian tomato yellow leaf curl virus mutated C1 gene (K227A).
XX
KW Nucleotide triphosphate binding site; DNA helicase; RNA helicase;
KW modification; mutation; viral replication; deficient; inhibition;
KW viral resistance; geminivirus; tomato yellow leaf curl virus;
KW Sardinian isolate; STYLCV; transgenic plant; P-loop; C1 gene;
KW A11 gene; dominant negative phenotype; ss.
XX
OS Sardinian tomato yellow leaf curl virus.
XX
FH Key Location/Qualifiers
FT CDS 1..1080
FT /*tag= a
FT /product= Rep_(K227A)
FT /note= "encodes Rep protein in which wild-type Lys
FT at position 227, i.e. within the NTP-
FT binding site, is replaced by Ala"
XX
PN WO9608573-A1.
XX
PD 21-MAR-1996.
XX
PF 15-SEP-1995; 95MO-FR01192.
XX
PR 15-SEP-1994; 94FR-0011040.
XX
PA (CNRS ) CENT NAT RECH SCI.
XX
PI Gronenborn B;
XX
DR WPI: 1996-179947/18.
DR P-PSDB: AAR88870.
XX
PT Prodn. of virus-resistant transgenic plants - using mutated genomic
PT sequence from phytopathogenic DNA virus
XX
PS Disclosure: Fig 13; 93pp; French.
XX
CC Mutation of consensus amino acids in the NTP-binding site of
CC geminivirus Rep protein is used to produce replication deficient
CC viruses. The mutated viral nucleic acid is used for producing
CC transgenic plants that are resistant to, or tolerant of, the native
CC virus. The present sequence encodes a mutant form of the Rep (or C1)
CC protein from the Sardinian isolate of tomato yellow leaf curl virus
CC (STYLCV) in which the wild-type Lys227 residue has been changed to an
CC Ala residue; transgenic Nicotiana benthamiana plants generated by
CC transformation with the mutated virus were found to be resistant to
CC STYLCV, i.e the mutation results in a dominant negative phenotype.
XX
SQ Sequence 1080 BP; 355 A; 248 C; 210 G; 267 T; 0 other:

```

```

alignment_scores:
Quality: 210.00 Length: 69
Ratio: 3.750 Gaps: 0
Percent Similarity: 81.159 Percent Identity: 56.522

```

```

alignment_block:
US-09-289-346a-6 x AA12904
Align seq 1/1 to: AA12904 from: 1 to: 1080
2 LeuValTTPGlyGluPheGlnValAspGlyArgSerAlaArgGlyGly 18
||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
331 CTTGAATGCGGTACTTTCAGATCGACGACGATCTCTAGGAGGACCA 380
18 sGlnThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerIys 35
||||| ||||| ||||| ||||| ||||| ||||| |||||
381 ACAGACAGCCACGACGACCTTACGCAAGCAATTACGACGAGTAAGT 430
35 LucAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeuPhe 51
||||| ||||| ||||| ||||| ||||| ||||| |||||
431 CGCAGGCTTGATGATGATTAAGCAATTAGCGCTACGATTCGTTCTA 480
52 AlaPheAlaAlaLeuAsnSerAsnLeuAspArgIlePheAspLysThrPr 68
||| ||||| ||||| ||||| ||||| ||||| |||||
481 CATTTTCATATATATAATAGTAATTAGATTAGCTTTCCAGTCCGCC 530
68 oGluPro 70
| |||
531 GGCACCT 537
seq_name: /cgnl_8/gcgdata/geneseq/geneseqn/NA1996.DAT:AA12905
seq_documentation_block:
ID AA12905 standard; DNA; 1080 BP.
XX
AC AA12905;
XX
DE 07-NOV-1996 (first entry)
XX
DE Sardinian tomato yellow leaf curl virus mutated C1 gene (K227H).
XX
KW Nucleotide triphosphate binding site; DNA helicase; RNA helicase;
KW modification; mutation; viral replication; deficient; inhibition;
KW viral resistance; geminivirus; tomato yellow leaf curl virus;
KW Sardinian isolate; STYLCV; transgenic plant; P-loop; C1 gene;
KW A11 gene; ss.
XX
OS Sardinian tomato yellow leaf curl virus.
XX
FH Key Location/Qualifiers
FT CDS 1..1080
FT /*tag= a
FT /product= Rep_(K227H)
FT /note= "encodes Rep protein in which wild-type Lys
FT at position 227, i.e. within the NTP-
FT binding site, is replaced by His"
XX
PN WO9608573-A1.
XX
PD 21-MAR-1996.
XX
PF 15-SEP-1995; 95MO-FR01192.
XX
PR 15-SEP-1994; 94FR-0011040.
XX
PA (CNRS ) CENT NAT RECH SCI.
XX
PI Gronenborn B;
XX
DR WPI: 1996-179947/18.
DR P-PSDB: AAR88871.
XX
PT Prodn. of virus-resistant transgenic plants - using mutated genomic
PT sequence from phytopathogenic DNA virus
XX
PS Disclosure: Fig 13; 93pp; French.
XX
CC Mutation of consensus amino acids in the NTP-binding site of

```

CC geminivirus Rep protein is used to produce replication deficient
CC viruses. The mutated viral nucleic acid is used for producing
CC transgenic plants that are resistant to, or tolerant of, the native
CC virus. The present sequence encodes a mutant form of the Rep (or C1)
CC protein from the Sardinian isolate of tomato yellow leaf curl virus
CC (STYLCV) in which the wild-type Lys227 residue has been changed to a
CC His residue; transgenic Nicotiana benthamiana plants generated by
CC transformation with the mutated virus were not resistant to STYLCV.
CC In contrast, plants transformed with a virus in which Lys227 had been
CC replaced by Ala were found to be resistant.

XX Sequence 1080 BP; 356 A; 248 C; 208 G; 268 T; 0 other;

alignment_scores:
Quality: 210.00 Length: 69
Ratio: 3.750 Gaps: 0
Percent Similarity: 81.159 Percent Identity: 56.522

alignment_block:

US-09-289-346a-6 x AAT12905 ..

Align seg 1/1 to: AAT12905 from: 1 to: 1080

```
2 LeuValTrrpGlyGluPheGlnValAspGlyArgSerAlaArgGlyGlyC 18
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
331 CTTGAATGGGGTACTTCCAGATCGACGACGATCTGTAGGGAGAGACA 380
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
18 sGlnThrSerAsnAspAlaAlaGlnAlaLeuAsnAlaSerSerIysG 35
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
381 ACAGACAGCGCAACGACGCTTACGCAAGCAATTACGACGAACTAAGT 430
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
35 InGlnAlaLeuGlnIleIleArgGluLysIleProGluIysTyrLeuPhe 51
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
431 CGCAGGCTCTTGAATTAAGAAATTAAGCGCTTACGATTAAGTTCTTA 480
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
52 AlaPheAlaAlaLeuAsnSerAsnLeuAspArgIlePheAspIysThrPr 68
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
481 CATTTTCATATAATTAATAGTAATTAGTAAGCTTTTCCAGGTGCTCC 530
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
68 oGluPro 70
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
531 GGCACCT 537
```

seq_name: /cgn1_8/gcdata/geneseq/geneseq/NA11996.DAT: AAT12906

seq_documentation_block:

ID AAT12906 standard; DNA; 1080 BP.

XX AAT12906;

DT 07-NOV-1996 (first entry)

XX Sardinian tomato yellow leaf curl virus mutated C1 gene (K227R).

XX Nucleotide triphosphate binding site; DNA helicase; RNA helicase;
KW modification; mutation; viral replication; deficient; inhibition;
KW viral resistance; geminivirus; tomato yellow leaf curl virus;
KW Sardinian isolate; STYLCV; transgenic plant; P-loop; C1 gene;
KW All gene; ss.

OS Sardinian tomato yellow leaf curl virus.

XX Key Location/Qualifiers

FT CDS 1..1080

FT /tag= a

FT /product= Rep (K227R)

FT /note= "encodes Rep protein in which wild-type Lys

FT at position 227, i.e. within the NTP-

FT binding site, is replaced by Arg"

XX MO9608573-A1.

PD 21-MAR-1996.

XX 15-SEP-1995; 95WO-FR01192.

XX 15-SEP-1994; 94PR-0011040.

XX (CNRS) CENT NAT RECH SCI.

XX Gronenborn B;

XX WPI: 1996-179947/18.

XX P-PSDB; AAR88872.

XX Prodn. of virus-resistant transgenic plants - using mutated genomic

XX sequence from phytopathogenic DNA virus

XX Disclosure: Fig 13; 93pp: French.

CC Mutation of consensus amino acids in the NTP-binding site of
CC geminivirus Rep protein is used to produce replication deficient
CC viruses. The mutated viral nucleic acid is used for producing
CC transgenic plants that are resistant to, or tolerant of, the native
CC virus. The present sequence encodes a mutant form of the Rep (or C1)
CC protein from the Sardinian isolate of tomato yellow leaf curl virus
CC (STYLCV) in which the wild-type Lys227 residue has been changed to an
CC Arg residue; transgenic Nicotiana benthamiana plants generated by
CC transformation with the mutated virus were not resistant to STYLCV.
CC In contrast, plants transformed with a virus in which Lys227 had been
CC replaced by Ala were found to be resistant.

XX Sequence 1080 BP; 356 A; 247 C; 210 G; 267 T; 0 other;

alignment_scores:
Quality: 210.00 Length: 69
Ratio: 3.750 Gaps: 0
Percent Similarity: 81.159 Percent Identity: 56.522

alignment_block:

US-09-289-346a-6 x AAT12906 ..

Align seg 1/1 to: AAT12906 from: 1 to: 1080

```
2 LeuValTrrpGlyGluPheGlnValAspGlyArgSerAlaArgGlyGlyC 18
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
331 CTTGAATGGGGTACTTCCAGATCGACGACGATCTGTAGGGAGAGACA 380
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
18 sGlnThrSerAsnAspAlaAlaGlnAlaLeuAsnAlaSerSerIysG 35
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
381 ACAGACAGCGCAACGACGCTTACGCAAGCAATTACGACGAACTAAGT 430
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
35 InGlnAlaLeuGlnIleIleArgGluLysIleProGluIysTyrLeuPhe 51
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
431 CGCAGGCTCTTGAATTAAGAAATTAAGCGCTTACGATTAAGTTCTTA 480
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
52 AlaPheAlaAlaLeuAsnSerAsnLeuAspArgIlePheAspIysThrPr 68
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
481 CATTTTCATATAATTAATAGTAATTAGTAAGCTTTTCCAGGTGCTCC 530
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
68 oGluPro 70
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
531 GGCACCT 537
```

seq_name: /cgn1_8/gcdata/geneseq/geneseq/NA11995.DAT: AA084378

seq_documentation_block:

ID AA084378 standard; DNA; 1695 BP.

XX AA084378;

DT 19-AUG-1995 (first entry)

XX Tomato yellow leaf curl virus DNA sequence.

```

XX  Tomato yellow leaf curl virus; plant disease:
KM  ribozyme target sequence: ds.
XX
XX  Tomato yellow leaf curl virus (S).
OS
XX  Key      Location/Qualifiers
FH  misc_feature 405
FT  /tag= a
FT  /note= "ribozyme cleavage site"
FT  1065
FT  misc_feature /tag= b
FT  /note= "ribozyme cleavage site"
FT  1286
FT  misc_feature /tag= c
FT  /note= "ribozyme cleavage site"
XX
XX  WO9503404-A.
PN
XX
XX  -02-FEB-1995.
PD
XX
XX  22-JUL-1993; 93MO-EP01946.
PF
XX  22-JUL-1993; 93AU-0047014.
PR
XX  22-JUL-1993; 93MO-EP01946.
PR
XX
XX  (BIOC-) BIOCEM SA.
PA  (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX
XX  Baudino S, Comeau D, Dry IB, Gruber V, Lenee P;
PI  Mason J, Rezaian MA, Rigden JE, Rezaian MA;
XX
XX  WPI; 1995-075232/10.
DR
XX
XX  Synthetic DNA virus ribozyme(s) - reduce replication, infection
PT  and/or assembly of viruses by cleaving target virus sequence,
PT  useful for preparing resistant plants, esp tomatoes.
XX
XX  Disclosure: Fig 8; 90pp; English.
XX
XX  The sequence represents the complementary sense DNA strand of
CC  tomato yellow leaf curl virus-S strain. Ribozyme cleavage sites
CC  are indicated. Ribozymes against this sequence may be used in
CC  generation of transgenic tomato plants with disease-resistance.
XX
XX  Sequence 1695 BP; 568 A; 366 C; 308 G; 453 T; 0 other:
SQ

```

alignment_scores: Quality: 210.00 length: 69
Ratio: 3.750 Gaps: 0
Percent Similarity: 81.159 Percent Identity: 56.522

alignment_block:
US-09-289-346A-6 x AA084378 ..

Align seg 1/1 to: AA084378 from: 1 to: 1695

```

2  LeuValTrpGlyGluPheGlnValAspGlyArgSerAlaArgGlyGly 18
   ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
487 CTGGAATGGGCTTCTCCAGATCGACGAGCATCTCTAGCGAGACA 536
   ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
18 sGlnThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerlySG 35
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
537 ACAGACAGCCACGACGCTTACGCAAGCAATTAAACGAGAAATAGT 586
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
35 lUGlUAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeuPhe 51
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
587 CGAGGCTCTTGATGTAATTAAAGAAATTACGCTACGATTCTCTA 636
   ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
52 AlaPheAlaAlaLeuAsnSerAsnLeuAspArgIlePheAspLysThrPr 68
   ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
637 CAATTTCATATATATAATACTAATTAGATACGTTTCCAGAGTGCCTCC 686

```

```

68 oGluPro 70
   | |||
687 GGCACCT 693

```

seq_name: /cgnl_8/gcdata/geneseq/geneseqn/NA1998.DAT:AAV29761

seq_documentation_block:
ID AAV29761 standard; DNA; 2766 BP.
XX
XX AAV29761;
AC
XX
XX 11-AUG-1998 (first entry)
DT
XX
XX Tobacco leaf curling virus gene.
DE
XX
XX Tobacco leaf curling virus gene; TLCV; promoter; ds.
XX
XX Tobacco leaf curling virus.
XX
XX JPI0070982-A.
PN
XX
XX 17-MAR-1998.
PD
XX
XX 30-AUG-1996; 96JP-0230394.
PF
XX
XX 30-AUG-1996; 96JP-0230394.
PR
XX
XX (NORO) NORINSUISANSHO KYUSHU NOGYO SHIKENJYO.
PA
XX
XX WPI; 1998-233630/21.
DR
XX
XX Tobacco leaf curling virus gene - useful for inserting into vectors
PT for expression in, e.g. tomato plants
PT
XX
XX Claim 1: Figs 1-3; 9pp; Japanese.
XX
XX This sequence represents the tobacco leaf curling virus (TLCV) gene of
CC the invention. TLCV gene or its promoter can be inserted into a vector
CC for expression in plants, e.g. tobacco and tomato. This sequence is
CC believed to encode the TLCV proteins shown in AAW56493-W56498.
XX
XX Sequence 2766 BP; 722 A; 576 C; 609 G; 859 T; 0 other:
SQ

alignment_scores: Quality: 210.00 length: 84
Ratio: 3.500 Gaps: 1
Percent Similarity: 71.429 Percent Identity: 52.381

alignment_block:
US-09-289-346A-6 x AAV29761/rev ..

Align seg 1/1 to reverse of: AAV29761 from: 1 to: 2766

```

2  LeuValTrpGlyGluPheGlnValAspGlyArgSerAlaArgGlyGly 18
   ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2436 CTGATTTGGAGTTTCCAAAGTCGATGGAAGATCAGCTAGGGAGGTG 2387
   ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
18 sGlnThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerlySG 35
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2386 CCAATCTGCCACACGCCCATATGCGGAGCAATCACTCAGATCAAGT 2337
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
35 lUGlUAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeuPhe 51
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2336 CATCGGCACTCAATATATTAAAGGAGAAAGCTCCCAAGATTGTGTTTA 2287
   ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
52 AlaPheAlaAlaLeuAsnSerAsnLeuAspArgIle..... 63
   ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2286 CAATTTCATATATTAATTAATTAAGATGAGATTTTTCCTCCTCAT 2237
   ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
64 .....PheAspLysThrProG 69
   ||||| ||||| |||||

```


PA (SEMI-) SEMINIS VEGETABLE SEEDS INC.
 PA (MISC) WISCONSIN ALUMNI RES FOUND.
 XX
 PI Ahlquist PG, Hanson SF, Luu HT, Maxwell DP, Stout JT:
 XX WPI; 1997-526447/48.
 DR P-PSDB; AAW34338.
 XX
 PT Transgenic plants expressing geminivirus AC1 and CI wild-type and
 PT mutant genes - have increased resistance to geminivirus infection
 PT e.g. tomato mottle virus, tomato yellow leaf curl virus or bean
 PT golden mosaic geminivirus
 XX
 PS Example 5; Page 100-102; 132pp; English.
 XX
 CC This genomic DNA sequence includes the open reading frame (ORF) of
 CC the wild-type CI gene of bean golden mosaic virus (BGMV), a
 CC geminivirus that has a monopartite genome. The CI protein (see
 CC AAW34338) is required for replication. The wild-type CI ORF was
 CC subjected to Kunkel mutagenesis (see AAT93290-93). The invention
 CC involves production of transgenic plants containing DNA comprising
 CC CI or AC1 wild-type or mutant sequences that negatively interfere
 CC in trans with geminiviral replication during infection. Such
 CC transgenic plants are resistant to viral infection. The AC1/CI
 CC genes are especially from BGWV, tomato mottle virus or tomato
 CC yellow leaf curl virus (see AAT93282-93) and encode polypeptides
 CC (see AAW34324-35) that have mutations in the highly conserved
 CC DNA-nicking domain and/or the NTP-binding domains.
 XX
 SQ Sequence 1183 BP; 372 A; 276 C; 248 G; 287 T; 0 other;

alignment_scores:
 Quality: 206.00 Length: 70
 Ratio: 3.352 Gaps: 0
 Percent Similarity: 82.857 Percent Identity: 57.143

alignment_block:
 US-09-289-346A-6 x AAT93314 ..

Align seg 1/1 to: AAT93314 from: 1 to: 1183

```

1   ThrLeuValTrpGlyGluPheGlnValAspGlyArgSerAlaArgGlyG1 17
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
328 ACATCGAATGGGACAAATTCGAAGTCGACGCGCATCTGCAAGAGAGG 377
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
17  yCysGlnThSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSer1 34
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
378 TCAGCACTGTCCCAACGACATCATGCAAGCGCATTAACGCGCATTCAA 427
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
34  ySGluGluAlaLeuGlnIleLeargLysIleProGluLysTyrLeu 50
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
428 TTGAATCTGCTTGACAAATATGGAAGAGAACCGAAAGATTACGTC 477
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
51  PheAlaPheAlaAlaLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
478 CTTCAACATCAACAATCCGCTTCTAATCTGCAACGATCTTCGCAAGT 527
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
67  rProGluPro 70
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
528 GCCGGAACCA 537
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
seq_name: /cgnl_8/gcgdata/geneseq/geneseqn/NA1997.DAT: AAT93290
seq_documentation_block:
ID AAT93290 standard; DNA; 1183 BP.
XX
AC AAT93290;
XX
DT 27-APR-1998 (first entry)
XX
DE Bean golden mosaic geminivirus CI mutant gene.
XX
```

KW Geminivirus: BGWV, CI gene; transdominant mutation;
 KW transgenic plant; disease resistance; ss; cyclic; circular.
 XX
 OS Bean golden mosaic virus type II isolate Guatemala.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1062
 FT /*tag= a
 XX
 PN W09739110-A1.
 XX
 PD 23-OCT-1997.
 PD
 PF 15-APR-1997; 97WO-US06300.
 XX
 PR 16-APR-1996; 96US-0015517.
 XX
 PA (SEMI-) SEMINIS VEGETABLE SEEDS INC.
 PA (MISC) WISCONSIN ALUMNI RES FOUND.
 XX
 PI Ahlquist PG, Hanson SF, Luu HT, Maxwell DP, Stout JT:
 XX WPI; 1997-526447/48.
 DR P-PSDB; AAW34332.
 XX
 PT Transgenic plants expressing geminivirus AC1 and CI wild-type and
 PT mutant genes - have increased resistance to geminivirus infection
 PT e.g. tomato mottle virus, tomato yellow leaf curl virus or bean
 PT golden mosaic geminivirus
 XX
 PS Claim 13; Page 103-105; 132pp; English.
 XX
 CC This DNA sequence comprises construct BGAC190 that codes for a
 CC control mutant (see AAW34332) of the CI protein (see AAW34338) of bean
 CC golden mosaic virus (BGWV). It was obtained by Kunkel mutagenesis
 CC of the wild-type CI gene (see AAT93314). CI is required for
 CC replication. The invention involves production of transgenic
 CC plants containing DNA comprising geminivirus CI or AC1 wild-type or
 CC mutant sequences that negatively interfere in trans with
 CC geminiviral replication during infection. Such transgenic plants
 CC are resistant to viral infection. The AC1/CI genes are especially
 CC from BGWV, tomato mottle virus or tomato yellow leaf curl virus (see
 CC AAT93282-93) and encode polypeptides (see AAW34324-35) that have
 CC mutations in the highly conserved DNA-nicking and/or the NTP-binding
 CC domains.
 XX
 SQ Sequence 1183 BP; 371 A; 277 C; 249 G; 286 T; 0 other;

alignment_scores:
 Quality: 206.00 Length: 70
 Ratio: 3.352 Gaps: 0
 Percent Similarity: 82.857 Percent Identity: 57.143

alignment_block:
 US-09-289-346A-6 x AAT93290 ..

Align seg 1/1 to: AAT93290 from: 1 to: 1183

```

1   ThrLeuValTrpGlyGluPheGlnValAspGlyArgSerAlaArgGlyG1 17
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
328 ACATCGAATGGGACAAATTCGAAGTCGACGCGCATCTGCAAGAGAGG 377
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
378 TCAGCACTGTCCCAACGACATCATGCAAGCGCATTAACGCGCATTCAA 427
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
34  ySGluGluAlaLeuGlnIleLeargLysIleProGluLysTyrLeu 50
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
428 TTGAATCTGCTTGACAAATATGGAAGAGAACCGAAAGATTACGTC 477
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
51  PheAlaPheAlaAlaLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
51  PheAlaPheAlaAlaLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

478 CTTCAACATCAACACATCCGTTCTAATCTCGAACGATCTTGTCAAAAGT 527
 67 rProGluPro 70
 :|||||||
 528 GCCGGAACCA 537

seq_name: /cgnl_8/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA94700

seq_documentation_block:
 ID AAA94700 strand: DNA; 1651 BP.

AC AAA94700:
 XX
 DT 15-JAN-2001 (first entry)
 XX
 DE PMRG 2288 35S-rep gene cassette.

XX Geminiivirus: DNA-A: geminivirus replication inhibitor; ac3 gene;
 KW transgenic plant; antiviral; gene therapy; bean golden mosaic virus;
 KW BGWV; alfalfa mosaic virus; AMV; cauliflower mosaic virus; CaMV; ds.

XX Bean golden mosaic virus.
 OS Cauliflower mosaic virus.
 OS Alfalfa mosaic virus.
 OS Synthetic.

XX US6118048-A.

PD 12-SEP-2000.

XX 24-APR-1998: 980S-0065999.

XX 25-APR-1997: 970S-0044925.

XX (WISC) WISCONSIN ALUMNI RES FOUND.

DR WPI: 2000-610861/58.

XX Genetic construct comprising a mutant geminiviral rep gene, useful for
 PT producing a plant resistant to geminiviral infection -

XX Example: Column 15-16; 14pp; English.

XX The present sequence is a 35S-rep gene cassette comprising the rep gene
 CC of bean golden mosaic virus (BGWV)-GA cloned downstream of the CaMV
 CC 35S promoter and an alfalfa mosaic virus (AMV) leader sequence. The
 CC sequence was integrated into pBSII-KS+ to produce a rep gene expression
 CC vector. DNA-nicking domain mutations may be incorporated into rep gene
 CC to produce a genetic construct that acts as a trans-dominant inhibitor
 CC of geminiviral replication. When expressed in a plant cell, this
 CC inhibitor is able to dramatically reduce replication of geminivirus.
 CC Genetic constructs that include sequences containing a portion of the
 CC ac3 gene in addition to the trans-dominant inhibitor exhibit increased
 CC efficiency and broadened specificity of inhibition of geminiviral
 CC replication. Geminiviruses are one of the greatest constraints on
 CC production of important crops, including cassava, beans, cowpeas,
 CC peppers, tomatoes and cotton. The effects of the virus can be overcome
 CC by using the genetic construct.

XX Sequence 1651 BP; 517 A; 393 C; 342 G; 399 T; 0 other:

alignment_scores:

Quality:	206.00	Length:	70
Ratio:	3.552	Gaps:	0
Percent Similarity:	82.857	Percent Identity:	57.143

alignment_block:

US-09-289-346A-6 x AAA94700 ..

Align seg 1/1 to: AAA94700 from: 1 to: 1651

1 ThrleuValTrpGlyGluPheGlnValAspGlyArgSerAlaArgGlyG1 17

796 ACATCGAATGGGACAAATTCAGTGCAGCGCAGATCTGCAAGAGCAG 845
 17 YCysGlnThrSerAsnAspAlaAlaIagAlaLeuAsnAlaSerSerL 34
 846 TCAGAGTCTGCGCAGACGACTCATATGCAAGGCAATTAAACGAGATTCAA 895
 34 YsgIguAlaLeuGlnIleIleArgGluLysIleProGluLysTryIeu 50
 896 TTGAATCTGCCCTTGACAAATATTCAGAGCAGACACGCAAAAGATTACGTC 945
 51 PheAlaPheAlaLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
 946 CTTCAACATCAACACATCCGTTCTAATCTCGAACGATCTTGTCAAAAGT 995
 67 rProGluPro 70
 996 GCCGGAACCA 1005

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embryonic shield stage (5.6 h) libraries. Fingerprint data were used to computationally cluster cDNAs, and a single cDNA from each cluster was chosen for sequencing. In some cases multiple members of the same cluster were sequenced to assess clustering parameters or single clones were sequenced additional times to assess quality control."

BASE COUNT 141 a 130 c 161 g 128 t
ORIGIN

alignment_scores:
Quality: 73.00 Length: 61
Ratio: 2.028 Gaps: 2
Percent Similarity: 59.016 Percent Identity: 31.148

alignment_block:
US-09-289-346A-6 x A1959235 ..

Align seg 1/1 to: A1959235 from: 1 to: 560

```
1 ThleuValTtpGlytupheGlnValAspGlyArgSerAlaArgIyl 17
||||| |||||
22 ACATGTGCTGCGGGG.....GGGGGTGTGGCGG 50
17 ycyGlnTThSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSert 34
||||| |||||
51 GTGTGACCCCTCTCCCTCCACGCGTCCGCCACGCGTCCGACGCGATC 100
34 yscGluAlaLeuGlnIleIleArgGlyIulysIleProGlyIulysTyrLeu 50
||||| |||||
101 AACATGCTCTCTC.....GTCAATGCCAGAGAAAGTTTCAG 135
51 PheAlaPheAlaAlaLeuAsnSerAsnLeuAsp 61
||||| |||||
136 CACATCTCTGTCCTCCACACGACGACATGAT 168
```

seq_name: gb_est1:AV742525

seq_documentation_block:
LOCUS AV742525 439 bp mRNA EST 17-OCT-2000
DEFINITION AV742525 CB Homo sapiens cDNA clone CBMAJ012 5', mRNA sequence.
ACCESSION AV742525
VERSION AV742525.1 GI:10860106
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 439)
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Zhang, Q., Ye, M., Wu, X., Gu, J., Huang, Q., Zhou, J., Shen, Y., Han, Z.,
Chen, S., Mao, M., and Chen, Z.
Homo sapiens CB library cDNA clones
Unpublished (2000)
CONTACT: Zhu Chen
Shanghai Institute of Hematology, Rui-Jin Hospital
197 Rui-Jin II Road, Shanghai 200025, P. R. China
Tel: 86-21-64740490
Fax: 86-21-64743206
Email: mbs@shim.su.sh.cn
This clone is available at Shanghai Hematology Institute in
Shanghai.
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong.
Location/Qualifiers

FEATURES
SOURCE

1..439
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CBMAJ012"
/clone_lib="CB"
/tissue_type="cord blood"
/cell_type="CD34+ hematopoietic stem/progenitor cell"
/lab_host="BM25.8"

/note="Vector: pBluescript; Site 1: EcoRI; The insert is cloned randomly with the EcoRI digestion"
BASE COUNT 117 a 108 c 131 g 83 t
ORIGIN

alignment_scores:
Quality: 71.00 Length: 53
Ratio: 1.919 Gaps: 2
Percent Similarity: 69.811 Percent Identity: 32.075

alignment_block:
US-09-289-346A-6 x AV742525 ..

Align seg 1/1 to: AV742525 from: 1 to: 439

```
10 AspGlyArgSerAlaArgGlyGlyCysGln...ThSerAsnAspAla 25
||||| |||||
1 AATTCGGCGCCGCGCTCGACACGGGCTGGAGAGACGACAGAGGGGCTTC 50
25 aAlaGluAlaLeuAsnAlaSerSerIylsGluGluAlaLeuGlnIleLea 42
||||| |||||
51 CACAGAGAGGCGCTACACGCCCTTGTGCTGCACGACCATGCTCTAGTG. 99
42 rgGlyIulysIleProGlyIulysTyrLeuPheAlaPheAlaAlaLeuAsnSer 58
||||| |||||
100 .....ATCCCTGAAAGTTCACGACATATTTTGGAGTACTCAACACC 141
59 AsnLeuAsp 61
||||| |||||
142 AACATCGAT 150
```

seq_name: gb_est1:AV744255

seq_documentation_block:
LOCUS AV744255 514 bp mRNA EST 17-OCT-2000
DEFINITION AV744255 CB Homo sapiens cDNA clone CBMAJ03 5', mRNA sequence.
ACCESSION AV744255
VERSION AV744255.1 GI:10861836
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 514)
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Zhang, Q., Ye, M., Wu, X., Gu, J., Huang, Q., Zhou, J., Shen, Y., Han, Z.,
Chen, S., Mao, M., and Chen, Z.
Homo sapiens CB library cDNA clones
Unpublished (2000)
CONTACT: Zhu Chen
Shanghai Institute of Hematology, Rui-Jin Hospital
197 Rui-Jin II Road, Shanghai 200025, P. R. China
Tel: 86-21-64740490
Fax: 86-21-64743206
Email: mbs@shim.su.sh.cn
This clone is available at Shanghai Hematology Institute in
Shanghai.
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong.
Location/Qualifiers

FEATURES
SOURCE

1..514
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CBMAJ03"
/clone_lib="CB"
/tissue_type="cord blood"
/cell_type="CD34+ hematopoietic stem/progenitor cell"
/lab_host="BM25.8"
/note="Vector: pBluescript; Site 1: EcoRI; The insert is cloned randomly with the EcoRI digestion"
BASE COUNT 127 a 135 c 154 g 96 t
ORIGIN

alignment_scores:
 Quality: 71.00 Length: 53
 Ratio: 1.919 Gaps: 2
 Percent Similarity: 69.811 Percent Identity: 32.075

alignment_block:

US-09-289-346A-6 x AV744255 ..

Align seg 1/1 to: AV744255 from: 1 to: 514

```

10 AspGlyArgSerAlaArgGlyGlyCysGln...ThrsrAsnAspAlaAl 25
   :::::|||||  |||  |||||:::  ||:::  ||:::
1  AATTCGGCGCCGCTCGACAGCGCTCGCAGAGAAGCAGAGAGGCGCTTC 50
   :::::  :::::  :::::  :::::  :::::  :::::
25 aAlaGluAlaLeuAsnAlaSerSerLysGluGluAlaLeuGlnIleIleA 42
   :::::  :::::  :::::  :::::  |||  :::::  :::::
51 CACAGAGAGCGCTACAGCCGCCGCTGTGCTGCAGCATGCTCTAGTG. 99
   |||||  |||||  |||||  |||||  |||||  |||||
42 rgGluLysIleProGluLysTyrIleuPheAlaPheAlaAlaLeuAsnSer 58
   |||||  |||||  |||||  |||||  |||||  |||||
100 .....ATCCCTGAAAGTTCCAGCATATTTTGGCAGTACTCAACACC 141
   ||:::  ||:::  ||:::  ||:::  ||:::  ||:::
59 AsnLeuAsp 61
   ||:::  ||:::
142 AACATCGAT 150

```

seq_name: gb_est1:AV737185

seq_documentation_block:

LOCUS AV737185 585 bp mRNA EST 17-OCT-2000
 DEFINITION AV737185 CB Homo sapiens cDNA clone CBMARG03 5', mRNA sequence.
 ACCESSION AV737185
 VERSION AV737185.1 GI:10854766
 KEYWORDS EST.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 585)

AUTHORS

Zhang, Q., Ye, M., Wu, X., Gu, J., Huang, Q., Zhou, J., Shen, Y., Han, Z.,

TITLE

Human sapiens CB library cDNA clones

JOURNAL

Unpublished (2000)

COMMENT

Contact: Zhu Chen

Shanghai Institute of Hematology, Rui-Jin Hospital

197 Rui-Jin II Road, Shanghai 200025, P. R. China

Tel: 86-21-64740490

Fax: 86-21-64743206

Email: mbs@shims.stn.sh.cn

This clone is available at Shanghai Hematology Institute in

Shanghai.

Chinese National Human Genome Center at Shanghai

351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong.

Location/Qualifiers

1. 585

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="CBMARG03"

/clone_1lb="CB"

/tissue_type="cord blood"

/cell_type="CD34+ hematopoietic stem/progenitor cell"

/lab_host="BM25.8"

/note="Vector: pBluescript; Site_1: EcoRI. The insert is

cloned randomly with the EcoRI digestion"

BASE COUNT 162 a 140 c 166 g 115 t 2 others

ORIGIN

alignment_scores:

Quality: 71.00 Length: 53

Ratio: 1.919 Gaps: 2

Percent Similarity: 69.811 Percent Identity: 32.075

alignment_block:
 US-09-289-346A-6 x AV737185 ..

alignment_block:

US-09-289-346A-6 x AV737185 ..

Align seg 1/1 to: AV737185 from: 1 to: 585

```

10 AspGlyArgSerAlaArgGlyGlyCysGln...ThrsrAsnAspAlaAl 25
   :::::|||||  |||  |||||:::  ||:::  ||:::
1  AATTCGGCGCCGCTCGACAGCGCTCGCAGAGAAGCAGAGAGGCGCTTC 50
   :::::  :::::  :::::  :::::  :::::  :::::
25 aAlaGluAlaLeuAsnAlaSerSerLysGluGluAlaLeuGlnIleIleA 42
   :::::  :::::  :::::  :::::  |||  :::::  :::::
51 CACAGAGAGCGCTACAGCCGCCGCTGTGCTGCAGCATGCTCTAGTG. 99
   |||||  |||||  |||||  |||||  |||||  |||||
42 rgGluLysIleProGluLysTyrIleuPheAlaPheAlaAlaLeuAsnSer 58
   |||||  |||||  |||||  |||||  |||||  |||||
100 .....ATCCCTGAAAGTTCCAGCATATTTTGGCAGTACTCAACACC 141
   ||:::  ||:::  ||:::  ||:::  ||:::  ||:::
59 AsnLeuAsp 61
   ||:::  ||:::
142 AACATCGAT 150

```

seq_name: gb_est1:AV736552

seq_documentation_block:

LOCUS AV736552 586 bp mRNA EST 17-OCT-2000
 DEFINITION AV736552 CB Homo sapiens cDNA clone CBNAUE10 5', mRNA sequence.
 ACCESSION AV736552
 VERSION AV736552.1 GI:10854133
 KEYWORDS EST.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 586)

AUTHORS

Zhang, Q., Ye, M., Wu, X., Gu, J., Huang, Q., Zhou, J., Shen, Y., Han, Z.,

TITLE

Human sapiens CB library cDNA clones

JOURNAL

Unpublished (2000)

COMMENT

Contact: Zhu Chen

Shanghai Institute of Hematology, Rui-Jin Hospital

197 Rui-Jin II Road, Shanghai 200025, P. R. China

Tel: 86-21-64740490

Fax: 86-21-64743206

Email: mbs@shims.stn.sh.cn

This clone is available at Shanghai Hematology Institute in

Shanghai.

Chinese National Human Genome Center at Shanghai

351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong.

Location/Qualifiers

1. 586

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="CBNAUE10"

/clone_1lb="CB"

/tissue_type="cord blood"

/cell_type="CD34+ hematopoietic stem/progenitor cell"

/lab_host="BM25.8"

/note="Vector: pBluescript; Site_1: EcoRI. The insert is

cloned randomly with the EcoRI digestion"

BASE COUNT 158 a 142 c 168 g 116 t 2 others

ORIGIN

alignment_scores:

Quality: 71.00 Length: 53

Ratio: 1.919 Gaps: 2

Percent Similarity: 69.811 Percent Identity: 32.075

US-09-289-346A-6 x AV736552 ..

Align seg 1/1 to: AV736552 from: 1 to: 586

10 AspGlyArgSerAlaArgGlyCysGln...ThSerAsnAspAlaI 25
 :::::||| || | |||||::: ||::: ||:::
 1 AATTCCGCGCGGTCGACACGCGCTCTCGAAGACACACAGAGGCGCTTC 50

1 AATTCCGGCGCGGCTGCACACGCGCTCGAATAACACACAGAGGGCTTC 5
25 aa|ag|ua|a|a|e|u|s|a|l|a|s|e|r|y|s|c|u|a|l|a|l|e|u|n|l|e|a 42

25 aalacgualaleuasnalaSerSertylsgluclualaleuglinIleIlea 42
::: ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|
51 CACAGAGGCCCTCACACGCGCGCTTGTCTGCAGSCCAITCTCATTG. 99
42 rgGlulysIleProglulysTyTrtleuphealaIaphelaIaleuanSer 58


```

LOCUS      AI731422          546 bp     mRNA                      EST           11-JUN-1999
DEFINITION BNHG19563 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar
            to mitochondrial processing peptidase (EC 3.4.99.41) alpha-II chain
            precursor - potato g11587562 (X80236) mitochondrial processing
            peptidase [Solanum tuberosum], mRNA sequence.
ACCESSION   AI731422
VERSION     AI731422.1 GI:5050274
KEYWORDS    EST.
SOURCE      upland cotton.
ORGANISM    Gossypium hirsutum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
REFERENCE   1 (bases 1 to 546)
AUTHORS     Blewitt,M., Matz,E.C., Davy,D.F. and Burr,B.
TITLE       ESTs from developing cotton fiber
JOURNAL     Unpublished (1999)
COMMENT     Contact: Ben Burr
            Biology Department
            Brookhaven National Laboratory
            Upton, NY 11973, USA
            Tel.: 516-344-3396
            Fax: 516-344-3407
            Email: burr@nsluxl.bnl.gov
            Seq primer: T3 primer.
FEATURES
             source
               1..546
                /organism="Gossypium hirsutum"
                /cultivar="Acala Maxxa"
                /db_xref="taxon:3635"
                /clone_lib="Six-day Cotton fiber"
                /tissue_type="Immature fiber"
                /dev_stage="Six days post anthesis"
                /lab_host="XL1-Blue"
                /note="Vector: pBluescript II KS+"
BASE COUNT   151 a         99 c        134 g        160 t        2 others
ORIGIN
alignment_scores:
              Quality: 68.50      Length: 60
              Ratio: 1.756        Gaps: 1
Percent Similarity: 65.000      Percent Identity: 33.333
Alignment_block:
US-09-289-346A-x AI731422/rev ..
Align seg 1/1 to reverse of: AI731422 from: 1 to: 546
11 G1YARSerAlaArgIgyLcysGIInhrSerAsnASPAlAlAla.. 26
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
469 GGAAGATCTGCACAGAAGTGTCTCGACAAGATMACAAATTCTTCATGTTT 420
27 .GUUAlAlaLeuASnAlaSerSerLySLuGLuAlAlaLuGlnIIleIleArg 43
::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
419 TACACCAGTGCTGCCAGTACCATCCGAAAGCAGATAAAAATTTTGGCA 370
43 LuLySLleProGIuLySTyLeuPheAlAPheAlAlaLeuASnSerAsn 59
||| |:: ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
369 CAAAAATCTCCAAACTGTACTGTTTAACATATTAATGACGATGCTTGGG 320
60 LeuASPArgIIlePheASPlySThrProGIu 69
||| ||| :::: |||||
319 GCTAAAGAAGAGATTGCGCATGACACAGAA 290
seq_name: gb_gss:AQ950848
seq_documentation_block:
LOCUS      AQ950848          572 bp     DNA                      GSS           27-JAN-2000
DEFINITION Shared DNA-SIM3.TF Shared DNA Trypanosoma brucei genomic clone
Shared DNA-SIM3, DNA sequence.
ACCESSION   AQ950848
VERSION     AQ950848.1 GI:6774113

```

```

KEYWORDS      GSS.
SOURCE        Trypanosoma brucei.
ORGANISM      Trypanosoma brucei
              Eukaryota; Euzlenozoa; Kinetoplastida; Trypanosomatidae;
REFERENCE     1 (bases 1 to 572)
AUTHORS       El-Sayed, N., Zhao, S., Zhao, H., Gill, S., Suh, E., Malek, J., Fujii, C.,
              Gerrard, C., Leech, V., de Jong, P., Ullin, E., Melville, S., Donelson, D.,
              Fraser, C. and Adams, M.
              Determination of clone end sequences from Trypanosoma brucei GUTat
              10.1 sheared DNA library
              Unpublished (1999)
JOURNAL       Other_GSSs: Sheared DNA-51M3.TR
COMMENT       Contact: Najib M. El-Sayed
              Department of Eukaryotic Genomics
              The Institute for Genomic Research
              9712 Medical Center Dr., Rockville, MD 20850, USA
              Tel: 301 838 0200
              Fax: 301 838 0208
              Email: nelsayed@ligr.org
              Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared
              DNA library constructed at TIGR. Clones will be available for
              distribution through ATCC. Sheared DNA end sequences search page:
              http://www.tigr.org/tdb/mbd/tbdb/.
              Seq primer: M13-Forward
              Class: Shotgun.
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                /note="Vector: pUC18; Site 1: SmaI; Constructed at The
                Institute for Genomic Research (TIGR), Rockville, MD.
                Genomic DNA isolated from a cloned population of
                Trypanosoma brucei (TRE0927/4 GUTat 10.1) was mechanically
                sheared to give a tight size distribution (approx 2 kb).
                The v + i method used for the library construction is
                described in detail in Smith, H.O. and Venter, J.C.
                (Making small insert libraries for whole genome shotgun
                sequencing projects. In Genome Sequencing: A Practical
                Approach, eds. M. Vaudin and B. Barrell, Oxford University
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BASE COUNT   115 a      118 c      180 g      159 t
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      27 uAlaLeuAsnAlaSerSerLyScLuGluAlaLeuGlnIleIle 41
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seq_documentation_block:
LOCUS      AQ947513      587 bp      DNA      GSS      27-JAN-2000
DEFINITION Sheared DNA-49M17.TF Sheared DNA Trypanosoma brucei genomic clone
            Sheared DNA-49M17, DNA sequence.
ACCESSION  AQ947513

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VERSION      A0947513.1   GI:6770778
KEYWORDS     GSS.
SOURCE       Trypanosoma brucei.
ORGANISM     Eukaryota; Elenozoa; Kinetoplastida; trypanosomatidae;
              Trypanosoma.
REFERENCE    1 (bases 1 to 587)
AUTHORS      El-Sayed,N., Zhou,S., Zhao,H., Gill,S., Sub,E., Malek,J., Fujit,C.,
              Gerrard,C., Leech,V., de Jong,P., Ullu,E., Melville,S., Donelson,J.,
              Fraser,C. and Adams,M.
TITLE        Determination of clone end sequences from Trypanosoma brucei GUTat
              10.1 sheared DNA library
JOURNAL      Unpublished (1999)
COMMENT      Other.GSSS: Sheared DNA-49M17.TR
              Contact: Najib M. El-Sayed
              Department of Eukaryotic Genomics
              The Institute for Genomic Research
              9712 Medical Center Dr., Rockville, MD 20850, USA
              Tel: 301 838 0200
              Fax: 301 838 0208
              Email: nelsayed@tifgr.org
              Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared
              DNA library constructed at TIGR. Clones will be available for
              distribution through ATCC. Sheared DNA end sequences. search page:
              http://www.tigr.org/tdb/mdb/tbdb/.
              Seq primer: M13-Forward
              Class: shotgun.
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             Location/Qualifiers
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                           /organism="Trypanosoma brucei"
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                           Institute for Genomic Research (TIGR), Rockville, MD.
                           Genomic DNA isolated from a cloned population of
                           Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically
                           sheared to give a tight size distribution (approx 2 kb).
                           The v + i method used for the library construction is
                           described in detail in Smith, H.O. and Venter, J.C.
                           (Making small insert libraries for whole genome shotgun
                           sequencing projects. In Genome Sequencing: A Practical
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            Ratio:          2.519           Gaps:              0
Percent Similarity: 87.097      Percent Identity: 38.710
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27 uAlaLeuAsnAlaSerSerLyScLuLuLaLeuGlnIlelle 41
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DEFINITION 602013083F1 NCL_CGAP_Brn64 Homo sapiens cdNA clone IMAGE:4148757
5', mRNA sequence.

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ACCESSION      BF342302
VERSION        BF342302.1
KEYWORDS       EST.
SOURCE         human.
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE      NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS        National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE          Unpublished (1999)
JOURNAL        Contact: Robert Strausberg, Ph.D.
COMMENT        Email: cgapbs-r@mail.nih.gov
                Tissue Procurement: David N. Louis, M.D.
                CDNA Library Preparation: Life Technologies, Inc.
                DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                DNA Sequencing by: Incyte Genomics, Inc.
                Clone distribution: MGC clone distribution information can be
                found through the I.M.A.G.E. Consortium/LLNL at:
                http://image.llnl.gov
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                     /note="Organ: brain; Vector: pCMV-Sport6; Site_1: NCI;
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                     Average insert size 1.57 kb. Constructed by Life
                     Technologies. Note: this is a NCI CGAP Library."

BASE COUNT      150 a      158 c      197 g      141 t

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Percent Similarity: 69.048      Percent Identity: 42.857

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US-09-289-346A-6 x BF342302 ..

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252 TGAATCGGGGACGGGACGCCACAAGGCGTCACAGGGGCGCCAAACCCTTG 301
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302 AA.....ATCCGTGAA 312

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Align seg 1/1 to: BF342302 from: 1 to: 646

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2166 CTTTACCATAATTTAGGGAATACTCCCTCCATAAGCATTTTATTTTTCAATAT 2117
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seq_name: /cgnl7/ptodata/1/ina/6A_COMB.seq:US-08-809-103B-7

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Sequence 7, Application US/08809103B
Patent No. 6133505
GENERAL INFORMATION:
APPLICANT: GRONENBORN, Bruno
TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS FOR OBTAINING SAME
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: YOUNG & THOMPSON
STREET: 745 South 23rd Street
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,103B
FILING DATE: 17-MAR-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94.11040
FILING DATE: 15-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR95/01192
FILING DATE: 15-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: PATCH, Andrew J.
REGISTRATION NUMBER: 32,925
REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 521-2297
TELEFAX: (703) 685-0573
TELEX: 248425 EMBON
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1145 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1077
US-08-809-103B-7

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Ratio: 3.750 Gaps: 0
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; Patent No. 6133505
; GENERAL INFORMATION:
; APPLICANT: GROENENBORN, Bruno
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
; TITLE OF INVENTION: TRANSENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; APPLICATION NUMBER: US/08/809,103B
; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94,11040
; FILING DATE: 15-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR95/01192
; FILING DATE: 15-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 685-0573
; TELEX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1148 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
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; NAME/KEY: CDS
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; US-08-809-103B-1

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; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
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; APPLICATION NUMBER: US/08/809,103B
; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94.11040
; FILING DATE: 15-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR95/01192
; FILING DATE: 15-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 685-0573
; TELEX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1150 base pairs
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; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
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; NAME/KEY: CDS
; LOCATION: 1..1077
; US-08-809-103B-3

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; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR95/01192
; FILING DATE: 15-SEP-1995
; ATTORNEY/AGENT INFORMATION:
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APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Gemlinivirus
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESS: Dressler, Rockey, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5460
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 1062 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bean Golden Mosaic Gemlinivirus
STRAIN: Type II
INDIVIDUAL ISOLATE: Guatemala
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1059
US-08-838-151A-51

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Percent Similarity: 82.857 Percent Identity: 57.143

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34 YsGluAlaLeuGlnIleAlaArgGluIysTleProGluTyrLeu 50
|||||
428 TTGAATCTGCTTGACATATGTAAGAGAGACCAAGCAAGATTACGTC 477
51 PheAlaIleAlaLeuAsnSerAsnLeuAspArgIlePheAspTyr 67
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67 rProGluPro 70
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; Sequence 54, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Scout, John T
; APPLICANT: Lau, Hong T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Gemlinivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESS: Dressler, Rockey, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5460
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 1062 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bean Golden Mosaic Gemlinivirus
STRAIN: Type II
INDIVIDUAL ISOLATE: Guatemala
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1059
US-08-838-151A-54

alignment_scores:
Quality: 206.00 Length: 70
Ratio: 3.552 Gaps: 0
Percent Similarity: 82.857 Percent Identity: 57.143

alignment_block:
US-09-289-346A-6 x US-08-838-151A-54 ..
Align seg 1/1 to: US-08-838-151A-54 from: 1 to: 1062

1 ThleuValTrpGluPheGlnValAspGlyArgSerAlaArgGly 17
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328 ACAATCGAATGGGACAAATTCGAAGTCCGACGAGATCTCGAAGAGG 377
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17 YCysGlnThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerL 34
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
378 TCAGACGTCGCCAACGACGATCATATGCAAGCATTAAAGCAGATTCAA 427
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
34 ysglgluAlaLeuGlnIleIleArgGluLysIleProGluLysTyrIeu 50
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428 TTGAATCTGCCCTTGACATATTGAAGAGAACCAACGAAAGATTACGTC 477
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
51 PheAlaPheAlaAlaLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
478 CTTCAACATCTCAACATCCGTTCTAATCTCGAACGATCTTCGTCAAAGT 527
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
528 GCCGGAACCA 537
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seq_name: /cgnl_7/ptodata/1/lna/5B_COMB.seq:US-08-838-151A-43

seq_documentation_block:
; Sequence 43, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Gemminivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1183 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bean Golden Mosaic Gemminivirus
; STRAIN: Type II Isolates
; INDIVIDUAL ISOLATE: Guatemala
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1059
; PUBLICATION INFORMATION:
; AUTHORS: Faria, JC
; AUTHORS: Gilbertson, RL
; AUTHORS: Hanson, SF

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;
; AUTHORS: Morales, FJ
; AUTHORS: Ahlquist, P
; AUTHORS: Loniello, AO
;
; AUTHORS: Maxwell, D
;
; TITLE: Bean Golden Mosaic Gemminivirus Type II
; TITLE: Isolates from the Dominican Republic and
; TITLE: Guatemala: Nucleotide Sequences, Infectious
; TITLE: Pseudorecombinants, and Phylogenetic Relationships
; JOURNAL: Phytopathology
;
; VOLUME: 84
; ISSUE: 3
; PAGES: 321-329
; DATE: 1994
; US-08-838-151A-43

alignment_scores:
; Quality: 206.00 Length: 70
; Ratio: 3.552 Gaps: 0
; Percent Similarity: 82.857 Percent Identity: 57.143

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328 ACAATCGAATGCGGCAATTCGAAGTCGACGCGACATCTCGCAAGAGAG 377
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17 YCysGlnThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerL 34
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378 TCAGACGTCGCCAACGACGATCATATGCAAGCATTAAAGCAGATTCAA 427
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34 ysglgluAlaLeuGlnIleIleArgGluLysIleProGluLysTyrIeu 50
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
428 TTGAATCTGCCCTTGACATATTGAAGAGAACCAACGAAAGATTACGTC 477
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
51 PheAlaPheAlaAlaLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
478 CTTCAACATCTCAACATCCGTTCTAATCTCGAACGATCTTCGTCAAAGT 527
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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seq_name: /cgnl_7/ptodata/1/lna/5B_COMB.seq:US-08-838-151A-45

seq_documentation_block:
; Sequence 45, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Gemminivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

```

STREET: One South Plinckney Street

ADDRESSEE: Quarles & Brady

ADDRESS: Onaries & Brady
STREET: One South Pinckney Street
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ver1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/065, 999
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 960296.9475
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1894 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

alignment_scores:	
Quality:	Length:
Ratio:	Gaps:
206.00	70
3.552	0

alignment_block:

[illegible]

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seq_documentation_block:
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: Sequence 7, Application US/09065999

; Patent No. 6118048

; GENERAL INFORMATION:

APPLICANT: Hanson, Stephen F.

APPLICANT: Maxwell, Douglas P.

10 TITLE OF INVENTION: TRANS-DOMINANT INHIBITION OF GEMINIVIRAL

TITLE OF INVENTION: DN

```

CORRESPONDENCE ADDRESS:
ADDRESS: Quarles & Brady
STREET: One South Plinckney Street
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/065,999
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 960296.94754
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2072 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-065-999-7

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alignment_scores:
Quality: 206.00      Length: 70
Ratio: 3.552         Gaps: 0
Percent Similarity: 82.857   Percent Identity: 57.143

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alignment_block:
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Align seg 1/1 to: US-09-065-999-7 from: 1 to: 2072

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796 ACATTCGAATGGGAGGACATTCACAGTCGACGCGCATCTGCAAGAGG 845
17 YCYSGLnThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerL 34
| |||:|||||:|||||:|||||:|||||:|||||:|||||:
846 TCAGCACTCGCCACAGCATCATTCGAAGGCGATTAAAGCGCATTCMA 895
34 ysgtGluAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeu 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
896 TTGATCTGCGCTTGACATATTTGAAGAGAACCAACGAAAGATTACGTC 945
51 PheAlaPheAlaAlaLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:
946 CTTCAACATCAACAACATCGCTTGAATCTGCAACGATCTTCGCAAGT 995

seq_name: /cgnl_7/ptodata/1/lna/6B_COMB.seq:US-08-838-151A-1
seq_documentation_block:
: Sequence 1, Application US/08838151A
: Patent No. 6291743
: GENERAL INFORMATION:
: APPLICANT: Strout, John T
: APPLICANT: Liu, Hang T
: APPLICANT: Maxwell, Douglas
: APPLICANT: Ahlquist, Paul

```

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APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminiiviruses
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESS: Dressler, Rockey, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1162 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Tomato Mottle Gemini Virus
INDIVIDUAL ISOLATE: Florida
FEATURE:
NAME/KEY: CDS
LOCATION: 44..1127
PUBLICATION INFORMATION:
AUTHORS: Gilbertson, RL
AUTHORS: Hidayat, SH
AUTHORS: Papliomas, EJ
AUTHORS: Rojas, MR
AUTHORS: Hou, YM
AUTHORS: Maxwell, DP
TITLE: Pseudorecombination between the infectious
TITLE: cloned DNA components of tomato mottle and bean
TITLE: dwarf mosaic geminiviruses.
JOURNAL: Jour. General Virol.
VOLUME: 74
PAGES: 23-31
DATE: 1993
US-08-838-151A-1

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Quality: 204.00      Length: 70
Ratio: 3.517         Gaps: 0
Percent Similarity: 82.857   Percent Identity: 54.286

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alignment_block:
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Align seg 1/1 to: US-08-838-151A-1 from: 1 to: 1162

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```

```

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471 TTCATCTGCCCTTGCAGTTCTAAGGAGAGAACCAACCAAAAGATTTCGA 520
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67 rProGluPro 70
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571 TCCGGAACCG 580

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OM of: US-09-289-346a-7 to: GenBank: * out_format: pfs
Date: Jan 3, 2002 8:17 PM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

-MODE=frame+2.pn.model -PRV=xlp
-Q=/genl1/USPTO.spool/US09289346/runat_03012002_153304_16362/app_query.fasta_1.1163
-DB=GenBank -QFMT=fastap -SUFFIX=p2n.rge -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPEXT=0.000
-GAPOP=4.500 -GAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -START=1 -MARRIX=blosome62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
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-NORM=ext -MINLEN=0 -MAXLEN=200000000
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-NO_XLPHY -WAIT -THREADS=1

Search information block:

Query: US-09-289-346a-7
Query length: 70
Database: GenBank: *
Database sequences: 1472140
Database length: -341344837
Search time (sec): 7316.720000

score list:

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gb_v1:MTGA	-	342.00	776.65	5.5e-35	2588	K02029 Tomato golden mosaic virus
gb_v1:AF0729150	-	293.00	661.57	1.4e-28	2588	AY029750 Tomato severe rugose
gb_v1:AF291705	-	291.00	656.76	2.6e-28	2622	AF291705 Tomato rugose mosaic
gb_v1:U92532	-	274.00	622.76	1.9e-26	1193	U92532 Leonurus mosaic virus
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gb_v1:MGARL	-	272.00	612.16	8.0e-26	2617	MGARL Bean golden mosaic virus
gb_v1:AF188708	-	270.00	613.23	7.0e-26	1365	AF188708 Cowpea golden mosaic
gb_v1:AF288227	-	270.00	613.12	7.1e-26	1383	AF288227 Sweet potato leaf curl
gb_v1:AF104036	-	270.00	608.77	1.6e-25	2828	AF104036 Sweet potato leaf curl
gb_v1:SC67926	-	267.00	614.19	6.2e-26	554	U97926 Sida golden mosaic virus
gb_v1:YE132548	-	266.00	597.58	5.2e-25	2763	U132548 Ipomoea yellow vein virus
gb_v1:MG7578	-	259.00	597.30	5.4e-25	447	U75278 Macropodium golden mosaic
gb_v1:AF098940	-	259.00	587.14	2.0e-24	1405	AF098940 Macropodium golden mosaic
gb_v1:AF026553	-	258.00	586.14	2.2e-24	1165	AF026553 Potato yellow mosaic
gb_v1:AB001315	-	252.00	578.70	5.9e-24	570	AB001315 Tobacco leaf curl virus
gb_v1:AB001318	-	252.00	578.70	5.9e-24	570	AB001318 Tobacco leaf curl virus
gb_v1:AB001303	-	249.00	571.66	1.4e-23	570	AB001303 Tobacco leaf curl virus
gb_v1:AB001294	-	249.00	570.84	1.6e-23	625	AB001294 Tobacco leaf curl virus
gb_v1:AF350330	-	249.00	557.64	8.7e-23	2767	AF350330 Tobacco leaf curl virus
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gb_v1:AB001298	-	245.00	561.45	3.4e-23	625	AB001298 Tobacco leaf curl virus
gb_v1:BCU56975	-	245.00	547.74	3.1e-22	2930	U56975 Beet curly top virus
gb_v1:CLCVA452	-	244.00	545.98	3.9e-22	2744	UJ002452 cotton leaf curl virus
gb_v1:CLCVA455	-	244.00	545.98	3.9e-22	2744	UJ002452 cotton leaf curl virus
gb_v1:PVVVA	-	242.00	541.78	6.7e-22	2593	U00940 Potato yellow mosaic virus
gb_v1:AF307861	-	239.00	534.26	1.8e-21	2734	AF307861 Ageratum yellow vein
gb_v1:AB001317	-	238.00	545.82	4.0e-22	570	AB001317 Tobacco leaf curl virus
gb_v1:CMVA3191	-	238.00	531.75	2.4e-21	287	AJ223191 Chayote mosaic virus
gb_v1:AB001308	-	237.00	538.31	6.0e-22	625	AB001308 Tobacco leaf curl virus
gb_v1:CVJA3853	-	237.00	529.51	1.0e-21	1020	AJ228563 cotton leaf curl virus
gb_v1:CVJA4447	-	237.00	529.51	1.0e-21	1020	AJ228563 cotton leaf curl virus
gb_v1:CLCVA445	-	237.00	529.51	1.0e-21	2751	AJ002447 cotton leaf curl virus
gb_v1:AF155064	-	237.00	529.47	3.2e-21	2751	AJ002447 cotton leaf curl virus
gb_v1:AB001293	-	236.00	524.31	3.1e-22	2764	AF155064 Okra enation virus
gb_v1:TCCTVCD	-	235.00	524.47	6.2e-21	2861	X84735 Tomato pseudo-curly top
gb_v1:AB014347	-	234.00	522.35	8.1e-21	2787	AB014347 Tomato yellow leaf curl

gb_v1:AB014346 - 234.00 522.34 8.1e-21 2791 i AB014346 Tomato yellow leaf
gb_v1:AF071228 - 234.00 522.34 8.1e-21 2791 i AF071228 Tomato yellow leaf
gb_v1:AF105975 - 234.00 522.33 8.1e-21 2793 i AF105975 Tomato yellow leaf
gb_v1:TYUCV12 - 233.00 519.99 1.1e-20 2790 i X76319 Tomato yellow leaf
gb_v1:AB001304 - 232.00 531.73 2.4e-21 570 i AB001304 Tobacco leaf curl v

seq_name: gb_v1:MTGA

seq_documentation_block:

LOCUS MTGA 2588 bp ss-DNA circular VRL 02-AUG-1993
DEFINITION Tomato golden mosaic virus, component A of complete genome.
ACCESSION K02029
VERSION K02029.1 GI:332213
KEYWORDS coat protein; complete genome; unidentified reading frame.
SOURCE TGMV cloned ds-DNA, clone PBH404.
ORGANISM Tomato golden mosaic virus
VIRUSES: ssDNA viruses; Geminiviridae; Begomovirus.
REFERENCES 1 (bases 1 to 2588)
Hamilton, W.D. O., Steyn, V.E., Coutts, R.H.A. and Buck, K.W.
Complete nucleotide sequence of the infectious cloned DNA
components of tomato golden mosaic virus: Potential coding regions
and regulatory sequences
EMBO J. 3, 2197-2205 (1984)

JOURNAL

COMMENT
Geminiviruses are characterised by twin isometric virions, major capsid polypeptides of about 28 kd, and ss-DNA genomes. The genomes of cassava latent virus (CLV) and tomato golden mosaic virus (TGMV) consist of two circular components, while that of maize streak virus (MSV) consists of a single circle.
[1] identifies the following additional open reading frames on the complementary strand that would code for proteins with >10 kd:
AL1 -- 13-1543 (passing through origin)
AL2 -- 1601-1212
AL3 -- 1465-1067

The sequence at 1-235 is highly homologous to an equivalent region on component B; it doesn't appear to code for protein and has the potential to form a stable hairpin [1]. An analogous region is found in CSV.
The virion-sense (+) strand is shown below.

FEATURES
Location/Qualifiers

source 1..2588
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327..1070
/note="coat protein (AR1)"
/codon_start=1
/protein_id="AA46582.1"
/db_xref="GI:332214"

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KSVYTLKIMDENIKLKNHNSVWMLVDRRPPVGTMDPGOVNMFEDNEPSTATVK
NDLRREPVYTRFRAKVTGGCOYASNEQALVRRFMKVNNNVYINQDEAKYENHTNAL
LTMACTASNVVATLKRIRFYDSTLN"
BASE COUNT 672 a 513 c 605 g 798 t
ORIGIN 140 bp upstream of HpaI site; beginning of A-B homology region.

alignment_scores:
Quality: 342.00 Length: 70
Ratio: 5.104 Gaps: 0
Percent Similarity: 95.714 Percent Identity: 95.714

alignment_block:

US-09-289-346a-7 x MTGA/rev ..

Align seg 1/1 to reverse of: MTGA from: 1 to: 2588

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17 TCGTCTTGTATGAGGAGATTCAGGTGACGTCGAGGTCCTTCAAGAGG 2222
|||||
2271 TCGTCTTGTATGAGGAGATTCAGGTGACGTCGAGGTCCTTCAAGAGG 2222
|||||
2221 TCGTCTTGTATGAGGAGATTCAGGTGACGTCGAGGTCCTTCAAGAGG 2172
|||||

```

34 ysglglualaleuGlnlleleargGluysIleProGluIuysTYrleu 50
|||||
2171 AAGAGAGAGCCCTCAGATANTTAGAGAGAAATCCAGAAAAATATTTTA 2122
|||||
51 PheGlnPheHIsAsnleuAsnSerAlaIeuaAlaIaIlePheAspIysTh 67
|||||
2121 TTTCAGTTCCACATCTAAATAGCAATTTAGATAGATATTTGATAGAC 2072
|||||
67 rProGluPro 70
|||||
2071 TCCGGAACCA 2062
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seq_name: gb_v1:AY029750

seq_documentation_block: 2588 bp DNA circular VRL 08-MAY-2001
LOCUS AY029750
DEFINITION Tomato severe rugose virus DNA-A, complete sequence.
ACCESSION AY029750
VERSION AY029750.1 GI:14009278
KEYWORDS
SOURCE Tomato severe rugose virus.
ORGANISM Tomato severe rugose virus.
REFERENCE 1 (bases 1 to 2588)
AUTHORS Rezende,W.L., Goulart,L.R., Parreira,K.S. and Figueiredo,J.E.F.
TITLE The full-length DNA-A nucleotide sequence of a novel
JOURNAL tomato-infecting begomovirus, Tomato severe rugose virus, in Brazil
REFERENCE 2 (bases 1 to 2588)
AUTHORS Rezende,W.L., Goulart,L.R., Parreira,K.S. and Figueiredo,J.E.F.
TITLE Direct Submission
JOURNAL Submitted (03-APR-2001) Instituto de Genetica e Biologumica,
Universidade Federal de Uberlandia, Av. Amazonas s/n, Bloco 2E,
Sala 24, Campus Umuarama, Uberlandia, Minas Gerais 38.400-000,
Brazil

FEATURES
source 1..2588
Location/Qualifiers
/organism="Tomato severe rugose virus"
/strain="Minas Gerais"
/db_xref="taxon:158463"
/country="Brazil"
/note="segment: DNA-A"
305..1060
/gene="AVI"
305..1060
/gene="AVI"
305..1060
/gene="AVI"
/codon_start=1
/product="coat protein"
/protein_id="AAK50360.1"
/db_xref="GI:14009282"
/translation="MPKRDAPWRLMAGTSKVSRSANSPRAGYGPYKKAEMVNRPM
YRKPRITLRGPDPVPRGCEGCKYOSIESRDYSHVGKVCISVYTGNGCTTHVKG
RVCVSLYTLGKVMDESIKLKNHNSVFWLVRDRPCTPMDGQVFNMDNEPST
RVCVSLYTLGKVMDESIKLKNHNSVFWLVRDRPCTPMDGQVFNMDNEPST
ENALLVMACIASNPYATLIRIFYFDSITN"
complement(1057..1455)
/gene="AC3"
complement(1057..1455)
/gene="AC3"
complement(1057..1455)
/gene="AC3"
/codon_start=1
/product="enhancer protein"
/protein_id="AAK50358.1"
/db_xref="GI:14009280"
/translation="MDSRTGGITARQAHNGYIWEISNPYFKINRVEDPMYTSRY
YHVQIRFNHNLRALHLHSFINTFOIWTSTLASGTYLNRPXYLVLLYLDRLGVISI
NNVIRAVRFATDKSYNAVLENNHLIKFXY"
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complement(1202..1591)
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/codon_start=1
/product="trpA"

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/protein_id="AAK50361.1"
/db_xref="GI:14009283"
/translation="MRNSSLTPPSIKYQHOAAKKRGTRRRRIDIECCSITYHICGR
GHGFTHRGTHNCTSGREMLYIGDKSLFQDKOSGGSVNHEDSLPRPNTVOPOPEZ
SIASPOLHQLPDMDFPDSFWMDIFK"
complement(1533..2588)
/gene="AC1"
complement(1533..2588)
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complement(1533..2588)
/gene="AC1"
/codon_start=1
/product="rep protein"
/protein_id="AAK50357.1"
/db_xref="GI:14009279"
/translation="MPSATKRROIKAKNYFLTPKCSLSKREALSOLKLTPTPKKF
IKVCEIHNENGEPHLHVLOPEGNCRONOREPFDLSPSTRSTHHPNIOAKSSDVK
SYVDKDDTTEKGEFOITGRSARGCOTANMAAEALAPSKDVALQITREKLEPFL
FOFPHNLSNLDRIFAPEPWAPTEPLSSFTNVPREMDADYFGRAARPERPISL
IEGDSRTGKTMMAAFGAHNYLSGHLDFNPRVSNHYEVNIDIAPHYLLKHWKE
LLGADKDMQSNCKYKGPVQIKGIIPCIEICNDPGEASVYKVPFRKENSLSNMWKHNA
KPVLPNPLXYGGTQSC"
complement(2171..2434)
/gene="AC4"
complement(2171..2434)
/gene="AC4"
/codon_start=1
/product="AC4 protein"
/protein_id="AAK50359.1"
/db_xref="GI:14009281"
/translation="MKWGLISTCFENSKAITAKINDSTWSPQOGHISIRPFREL
NHRPSSPMSTRETEILSNGANSSTAEVLEAVQITMLPOKP"
join(2583..2588,1..304)
/note="common region"

rep_origin
BASE COUNT 660 a 525 c 598 g 805 t
ORIGIN

alignment_scores:
Quality: 293.00 Length: 70
Ratio: 4.651 Gaps: 0
Percent Similarity: 90.000 Percent Identity: 78.571

alignment_block:
US-09-289-346a-7 x AY029750/rev ..
Align seg 1/1 to reverse of: AY029750 from: 1 to: 2588

1 ThleuValTrpGlyGluPheGlnValAspGlyArgSerAlaArgGlyG1 17
|||||
2258 ACTATCGAATGGGGCGCAATTCGCAAAATCGACGCGAGAAAGTCTAGAGCGCG 2209
|||||
17 YCYGlnThrSerAsnAspAlaIaIaGluAlaIeuaAsnAlaSerSerL 34
|||||
2208 TTGCGGAGACGACTAGCATCTCTCCGCGAGAAAGCTTGAAAGCACCTTCCA 2159
|||||
34 ysglglualaleuGlnlleleargGluysIleProGluIuysTYrleu 50
|||||
2158 AAGACGCGCGCTTGCAAGATATCCGGAGAGAACTACCGGAAAGTTTTA 2109
|||||
51 PheGlnPheHIsAsnleuAsnSerAlaIeuaAlaIaIlePheAspIysTh 67
|||||
2108 TTTCAGTTTCACATCTAAATAGCAATTTAGATAGATATTTGCAAGCGC 2059
|||||
67 rProGluPro 70
|||||
2058 TCCGGAACCA 2049
|||||
seq_name: gb_v1:AF291705

seq_documentation_block: 2622 bp DNA circular VRL 25-SEP-2000
LOCUS AF291705
DEFINITION Tomato mosaic virus DNA-A, complete sequence.
ACCESSION AF291705
VERSION AF291705.1 GI:10281644

```


JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1193)
 AUTHORS Faria, J.C. and Maxwell, D.P.
 TITLE Direct Submission
 JOURNAL Submitted (08-MAR-1997) Plant Pathology, University of Wisconsin,
 1630 Linden Dr., Madison, WI 53706-1598, USA
 FEATURES
 source 1. 1193
 /organism="Leonorius mosaic virus"
 /strain="LeMY- Brazil 1"
 /db_xref="taxon:58177"
 complement(1..678)
 /gene="rep"
 complement(<1..678)
 /gene="rep"
 /note="AC1; replication associated protein"
 /codon_start=1
 /product="Rep protein"
 /protein_id="AAB51157.1"
 /db_xref="GI:1916345"
 /translation="MPSKPRFRVOAKNIFLYPOCTLTKEFALSOLAIOLEPSKKKE
 IKICRELDHDDGPHLHVLIQLEKQVITNNRLPDLYSTRSHFHPNIOGAKSSDVK
 STYDKDGYEVEGEFOVDSRSGGQOTVNDAAALAPADKRTALQITKEKUPERYL
 FOYHNLSSNLDRIFAKAPPEWVPPPLSSFTVNPDEMOMADEYFGRSSAAARLPKMS
 LIVEGDSR"
 /length=797
 /note="origin of replication: common region"
 1039..1193
 /gene="cp"
 1039..>1193
 /note="cp"
 /note="AV1"
 /codon_start=1
 /product="coat protein"
 /protein_id="AAB51158.1"
 /db_xref="GI:1916346"
 /translation="MPKRDPSWRPMVGTSKISRTSNFSPRGIGPKFKASBMAVRPM
 YCSMKPMS"
 BASE COUNT 295 a 269 c 276 g 353 t
 ORIGIN

alignment_scores: Quality: 274.00 Length: 70
 Ratio: 4.492 Gaps: 0
 Percent Similarity: 87.143 Percent Identity: 77.143

alignment_block:
 US-09-289-346a-7 x LMU92532/rev ..

Align seg 1/1 to reverse of: LMU92532 from: 1 to: 1193

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1  ThrleuValTrpgIyglupheglValaspGlyarGserAlaargygl 17
   |||::: ||||| ||||| ||||| ||||| ||||| ||||| |||||
348 ACACTTGAATGGGTGAATTCACGTCACGCGAGAACTCTAAGAGAG 299
   |||::: ||||| ||||| ||||| ||||| ||||| ||||| |||||
17  ycySGlThrSerasnspAlaAlaAlaGluAlaAlaAsnAlaSer 34
   |||::: ||||| ||||| ||||| ||||| ||||| ||||| |||||
298 CCACACACACATTATGACGCTGACGCTGAAGCGCTTAATGCTCACATA 249
   |||::: ||||| ||||| ||||| ||||| ||||| ||||| |||||
34  yscgluaAlaLeuGlnIleleargGluLysIleProgluLysTyrleu 50
   |||::: ||||| ||||| ||||| ||||| ||||| ||||| |||||
248 AACGACGCGCTCTCAATATTAATTAAGAGAAATGCGGAGAAATATCTT 199
   |||::: ||||| ||||| ||||| ||||| ||||| ||||| |||||
51  PheglInhehtsasnlEaasnSerAlaLeuAlaAlaIlePheAspLys 67
   |||::: ||||| ||||| ||||| ||||| ||||| ||||| |||||
198 TTTCAATTTCATATTAAATTCATATTGATGATGATTTTCGCAAGGC 149
   |||::: ||||| ||||| ||||| ||||| ||||| ||||| |||||
67  rProgluPro 70
   |||::: ||||| ||||| ||||| ||||| ||||| ||||| |||||
148 TCCGGAGCCA 139
   |||::: ||||| ||||| ||||| ||||| ||||| ||||| |||||
seq_name: gb_v1:AF131071

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seq documentation block:
 LOCUS AF131071 1345 bp DNA VRU- 17-JUN-1999
 DEFINITION Tomato mild mottle geminivirus segment A replication-associated
 protein (rep) and coat protein (cp) genes, partial cds.
 ACCESSION AF131071
 VERSION AF131071.1 GI:4928223
 KEYWORDS
 SOURCE
 ORGANISM
 tomato mild mottle geminivirus.
 Virus; ssDNA viruses; Geminiviridae; Unclassified Geminiviridae.
 1 (bases 1 to 1345)
 /db_xref="taxon:92943"
 /chromosome="segment A"
 /country="Honduras: Comayagua Valley"
 /note="Obtained from a tomato plant collected in Dec. 1996
 by M.K. Nakha and D.P. Maxwell"
 complement(<1..678)
 /gene="rep"
 /note="rep"
 /note="ac1"
 complement(<1..678)
 /gene="rep"
 /note="rep protein"
 /codon_start=1
 /product="replication-associated protein"
 /protein_id="AAB33471.1"
 /db_xref="GI:4928224"
 /translation="MPLLPKFLINSKNYFLYPHQSLSKEETLQLRLNPTNKKY
 IKIARELDHDDGPHLHVLIQLEKQVITNNRLPDLYSTRSHFHPNIOGAKSSDVK
 SYVDKDGTYEVEGEFOVDSRSGGQOTVNDAAALAPADKRTALQITKEKUPERYL
 FOYHNLSSNLDRIFAKAPPEWVPPPLSSFTVNPDEMOMADEYFGRSSAAARLPKMS
 LIVEGDSR"
 /length=832
 /note="ori"
 1001..>1345
 /gene="cp"
 /note="cp"
 1001..>1345
 /note="cp"
 /note="capsid protein"
 /codon_start=1
 /product="coat protein"
 /protein_id="AAB33472.1"
 /db_xref="GI:4928225"
 /translation="MPKRDAPRLMSATPKVRSNNVPPDGLGKPKDKSSAMNRRPM
 YRKPRIVRSADVPRGCEGPKIOSFEORHDSHTGKVMCISDVTGNGITTHRYGK
 RFCEVSVYLCKV"
 BASE COUNT 329 a 289 c 313 g 414 t
 ORIGIN

alignment_scores: Quality: 274.00 Length: 70
 Ratio: 4.281 Gaps: 0
 Percent Similarity: 91.429 Percent Identity: 72.857

alignment_block:

US-09-289-346a-7 x AF131071/rev ..

Align seg 1/1 to reverse of: AF131071 from: 1 to: 1345

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1 ThrLeuValTTPGIYGIuPheGlnValAspGlyArgSerAlaArgIyl 17
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
348 ACAATCGATGATGGAGAAATTCAGATGACGACGAGATCTCTAGACAGC 299
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
17 ycyssGlnTrpSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSert 34
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
298 TCAGCAACAGCTACGACGCTCCGACAGCGCCCTAAATGCTCTCGA 249
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
34 ysgLuglualLeuGlnIleIleArgGluIuysIleProGluTyTyLeu 50
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
248 AGAGAGAACCGATCGCAATTATTAAAGAGAGCTCCCAAGAGTTCTT 199
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
51 PheGlnPheHisAsnLeuAsnSerAlaLeuAlaAlaIlePheAspIystrh 67
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
198 TTTCAATATTCACAACTGCTACTAGCTAGACAGATATTTCGTAAGCC 149
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
67 rProGluPro 70
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
148 TCCGGAACCG 139
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

seq_name: gb_v1:MBGARAL

seq_documentation_block:
LOCUS      MBGARAL                2617 bp ss-DNA      circular   VRL      02-AUG-1993
DEFINITION  Bean golden mosaic geminivirus viral coat protein (ARI) gene,
complete cds; putative replicative protein (ALI) gene, putative
cds; AL2 gene, complete cds; and AL3 gene, complete cds.
ACCESSION   M88686.1  GI:331462
VERSION     M88686
KEYWORDS    Bean golden mosaic protein,
            Bean golden mosaic virus (individual isolate Brazil, strain type I)
            Replicative form DNA.
SOURCE      bean golden mosaic virus
ORGANISM    Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
REFERENCE   1 (sites)
AUTHORS     Gilbertson,R.L., Farla,J.C., Hanson,S.F., Morales,F.J.,
            Ahlquist,P.G., Maxwell,D.P. and Russell,D.R.
TITLE       Cloning of the Complete DNA Genomes of Four Bean-Infecting
            Geminiviruses and Determining Their Infectivity by Electric
            Discharge Particle Acceleratio
            Phytopathology 81, 980-985 (1991)
JOURNAL     Phytopathology 81, 980-985 (1991)
AUTHORS     2 (sites)
            Gilbertson,R.L., Hidayat,S.H., Martinez,R.T., Leong,S.A., Farla,J.C.,
            Morales,F.J. and Maxwell,D.P.
TITLE       Differentiation of bean-infecting geminiviruses by nucleic acid
            hybridization probes and aspects of bean golden mosaic in Brazil
JOURNAL     Plant Dis. 75, 336-342 (1991)
AUTHORS     3 (bases 1 to 2617)
            Gilbertson,R.L., Farla,J.C., Ahlquist,P.G. and Maxwell,D.P.
TITLE       Genetic diversity in geminiviruses causing bean golden mosaic
            disease: The nucleotide sequence of the infectious cloned DNA
            components of a Brazilian isolate of bean golden mosaic geminivirus
            Unpublished (1992)
JOURNAL     Location/Qualifiers
FEATURES    1..2617
            /organism="bean golden mosaic virus"
            /proviral
            /isolate="Brazil"
            /strain="Type I"
            /db_xref="taxon:10839"
            /dev_stage="Replicative form"
            /gemline
            1..181
            /standard_name="Common Region"
            /note="putative"
            /function="putative origin of replication"
            /gene="ARI"
            358..1113
            CDS

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/note="putative"
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/product="coat protein"
/protein_id="AAA46313.1"
/db_xref="GI:331464"
/translation="MPKRDAGWRHMGCTSKTSRSANFSPRGNGPKYKAAEFWRPM
VRKPRVYILGKIMDENIKLKNHNSVAFMLYRRPRPGTMDGQFPMMDNERST
ATVKMDLDRQVRHKEFYGKVTGGOYASNECALVRFKVNNVYVNIODEAKYENHT
ENALLLYACTHASNVPYATLRIYFYDSITN"
complement(1110..1508)
/gene="AL3"
complement(1110..1508)
/gene="AL2"
complement(1255..1644)
/note="putative"
/codon_start=1
/protein_id="AAA46314.1"
/db_xref="GI:331465"
/translation="MDSRTGERITARQANGVYIEMISNPLYFKMYNVEDLOYTTRV
YHLOTRFNHNLKGLHKAFLNFQWNTSLDASGTTYLNKKYVLLYLDKIGVSL
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complement(1255..1644)
/note="putative"
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/protein_id="AAA46315.1"
/db_xref="GI:331466"
/translation="MRNSSSMPSPISIKVQHRAAKRAIRRRVYDECGCTIYVHNGS
GHGFTFRGTHRCTSGEMRYVYLDIKSPFDVQRGSTIHNDSIPPNYVQPOROE
QNGSTGEPPEPSLDDISSFWDDIK"
complement(1556..2617)
/gene="AL1"
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complement(1556..2617)
/note="putative"
/codon_start=1
/function="viral replication"
/product="replicative protein"
/protein_id="AAA46312.1"
/db_xref="GI:331463"
/translation="MPPKRFRKINKNIFLYTPQCSITRESATEQIOLQTPYNNKYI
RTEKREHENGEPHLALIQEGKFPQCTNCRVEDLKHPTTSSVSHANIOSAKSSDVS
VTEKEDYLEWGHFQVDGRSARQGTANDASSEALNASSKEPAMQIIIEKLEKFLF
QYHNLSSNLDRIETKAPDPMPSPYHLSSFTNVPREMEWADDFGGAARPERPTSI
ITEGDSRTGKTMMARALGTHNLYLSGHLSFNKVSFHAHEANVYDDIAPHYLKLHKKE
IMGACQDMQSNCKYKQPVOTKIGTIPSTICNPEGASVYKCFIDKENALAKNWTINNA
KTFIUSPFIYOSTOSCEETSNQTTSR"
complement(491..857)

BASE COUNT      677 a      491 c      592 g      857 t
ORIGIN
alignment_scores:
  Quality: 272.00      Length: 67
  Ratio: 4.387      Gaps: 0
  Percent Similarity: 92.537      Percent Identity: 76.119

alignment_block:
US-09-289-346a-7 x MBGARAL/rev ..

Align seg 1/1 to reverse of: MBGARAL from: 1 to: 2617

4 TTPGIYGIuPheGlnValAspGlyArgSerAlaArgIylcySglnTh 20
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
2305 TGGGGTCAFTTTCAAGTGGAGCAAGATCTGCTAGAGAGGTCAACAAC 2256
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
20 rSerAsnAspAlaAlaGluAlaLeuAsnAlaSerIySgluGluA 37
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
2255 AGCTAATGATGCGGACATCCGAACATGATGCTTCTCAAGGAAGAG 2206
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

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[illegible]

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/gene="AC4"
/feature="AC1"
/codon_start=1
/product="AC4"
/protein_id="AAB97865.1"
/db_xref="GI:1546802"
/translation="SISKREALSQLOTLPYNNKKFIRICRELHNGEPHLVLIQFE
KRYNCTNNRFPDLVSPTRSVHFPNIOGAKSSDYKSVYKDGDTLEMGVPOIDGRSA
RGGCOTANDAAAEALNSGTEKDALIKIREKLEPERLYFOYHNLSSNIDRIFSKPPEPMS
HPFLPSTFATVFGQHEADGTFGR"
BASE COUNT      741 a      606 c      675 g      806 t
ORIGIN

alignment_scores:
  Quality: 270.00      Length: 68
  Ratio: 4.500      Gaps: 0
Percent Similarity: 88.235      Percent Identity: 79.412

alignment_block:
US-09-289-346A-7 x AF104036/rev ..

Align seg 1/1 to reverse of: AF104036 from: 1 to: 2828

1  ThleuValTrrpGlyGluPheGlnValAspGlyArgSerAlaArgGlyG1 17
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
2354 ACCATCAGCTGGGGTGAATTCAGGTCGACGCGAGATCTGTAGAGAGG 2305
17  yCySGlnThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerL 34:
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
2304 CCAGCAGACTGCTACGACGCGCGAGGCTCTTAACGACGAGTTCTA 2255
34  ySGGluAlaLeuGlnIleLeArgGluLysIleProGluLysTyrLeu 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
2254 AAGAGCTGGGTGCAATATATCAGGAGAAACCTCGTGAATAATATTTA 2205
51  PheGlnPheHisAsnLeuAsnSerAlaLeuAlaAlaIlePheAspLysTh 67
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
2204 TTTCATATTCATATTAATTAGTGAATTTAGATGAGATTTTCTCTCC 2155
67  rPro 68
|||||
2154 ACCT 2151

seq_name: gb_v1:SGU67926

seq_documentation_block:
LOCUS      SGU67926      554 bp      DNA      VRL      28-JAN-1998
DEFINITION Side golden mosaic geminivirus Rep protein (AC1) gene, partial cds.
ACCESSION  U67926
VERSION    U67926.1 GI:1546801
KEYWORDS
SOURCE
ORGANISM   sida golden mosaic virus.
            sida golden mosaic virus.
            Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
REFERENCE
  1 (bases 1 to 554)
  Roye,M.E., McLaughlin,W.A., Nakhlia,N.K. and Maxwell,D.P.
  Genetic Diversity among geminiviruses associated with the weed
  species sida spp. Macroptilium lathyroides, and Missadula
  amplissima from Jamaica
  Plant Dis. 81, 1251-1258 (1997)
  2 (bases 1 to 554)
  Roye,M.E., McLaughlin,W.A. and Maxwell,D.P.
  Direct Submission
  Submitted (23-AUG-1996) Plant Pathology, University of Wisconsin,
  1630 Linden Drive, Madison, WI 53706-1598, USA
  Location/Qualifiers
    1..554
    /organism="sida golden mosaic virus"
    /strain="Jamaica"
    /isolate="Jamaica, May 1993"
    /db_xref="taxon:51034"
    /note="DNA A component"
    complement(1..554)
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CDs      complement(<1..>554)
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/feature="AC1"
/codon_start=1
/product="Rep protein"
/protein_id="AAB97865.1"
/db_xref="GI:1546802"
/translation="SISKREALSQLOTLPYNNKKFIRICRELHNGEPHLVLIQFE
KRYNCTNNRFPDLVSPTRSVHFPNIOGAKSSDYKSVYKDGDTLEMGVPOIDGRSA
RGGCOTANDAAAEALNSGTEKDALIKIREKLEPERLYFOYHNLSSNIDRIFSKPPEPMS
HPFLPSTFATVFGQHEADGTFGR"
BASE COUNT      121 a      127 c      139 g      167 t
ORIGIN

alignment_scores:
  Quality: 267.00      Length: 70
  Ratio: 4.238      Gaps: 0
Percent Similarity: 90.000      Percent Identity: 70.000

alignment_block:
US-09-289-346A-7 x SGU67926/rev ..

Align seg 1/1 to reverse of: SGU67926 from: 1 to: 554

1  ThleuValTrrpGlyGluPheGlnValAspGlyArgSerAlaArgGlyG1 17
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
290 ACCATCAGATGGGGGTGTTTCACATGACGAGAAAGTCTGCTGAGG 241
17  yCySGlnThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerL 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
240 TCAGCAACAGCTAACGACGCGCGCGAGGCTTGAATTCGACAA 191
34  ySGGluAlaLeuGlnIleLeArgGluLysIleProGluLysTyrLeu 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
190 AGGAGCATGCGCAATCAATCAAGAGAAATCAAGAAAGTAAATCTC 141
51  PheGlnPheHisAsnLeuAsnSerAlaLeuAlaAlaIlePheAspLysTh 67
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
140 TTTCATATTCACACACTATTCAGTAAATATCGATAGGATTTTCAGTAAGCC 91
67  rProGluPro 70
|||||
90 TCCAGAACCG 81

seq_name: gb_v1:IYEL32548

seq_documentation_block:
LOCUS      IYEL32548      2763 bp      DNA      circular      VRL      01-FEB-1999
DEFINITION Ipomoea yellow vein virus V2, V1, C3 and C2 genes.
ACCESSION  AJ132548
VERSION    AJ132548.1 GI:4210720
KEYWORDS   C2 gene; C2 protein; C3 gene; C3 protein; coat protein; V1 gene; V2
            gene; V2 protein.
SOURCE
ORGANISM   Ipomoea yellow vein virus.
            Ipomoea yellow vein virus.
            Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
REFERENCE
  1 (bases 1 to 2763)
  Banks,G.K.
  Direct Submission
  Submitted (26-JAN-1999) Banks G.K., Virus Research, John Innes
  Centre, Norwich Research Park, Colney lane, Norwich, NR4 6JU, UK
  2 (bases 1 to 2763)
  Banks,G.K., Bedford,I.D., Beitia,F.J., Cerezo,E.R. and Markham,P.G.
  A novel geminivirus of Ipomoea indica (Convolvulaceae) from southern
  Spain
  Location/Qualifiers
    1..2763
    /organism="Ipomoea yellow vein virus"
    /viral_host="Ipomoea indica"
    /specific_host="Ipomoea indica"
    /db_xref="taxon:87832"

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          /gene="V2"
CDS       995..1390
          /gene="V2"
          /codon_start=1
          /product="V2 protein"
          /protein_id="CA10695.1"
          /db_xref="GI:4210721"
          /translation="MTLLTKKQSDRCRANCFSTAEWMDPLQNPDLPTLXGFCQMLSVK
LQGLTKVEPTGFEUCSELIILFVROIVRANSRAEISSLMGETGTETSELDSTY
RALHWCCPNCCPLCPGFKRRPDEKEG"
1215..1979
          /gene="V1"
          /gene="V1"
          /db_xref="GI:4210722"
          /codon_start=1
          /product="coat protein"
          /protein_id="CA10696.1"
          /db_xref="GI:4210722"
          /translation="MTGRIYSPRPHPGHROVRSILNLETAIVPYTCNAVPIAARSY
VPKRVKRMKRRRDRIPKGCVGPKIODYEPKADVPRTGTGFCVSDTIRGTGLTHRL
GKRVCIKSMSTIDGKVMMDNVAKKDHTNITITWLIIDRRPNKDPLNFQGITMYDNEP
TTAKIRMDLRDMQVLKFSVTVSGPYSHKEQALIRKFEKCLYNHVTYNKKEAKE
NOLENALMLYSASSHASNPVQTLRCRAYFYDSHK"
complement(1976..2413)
          /gene="C3"
          /complement(1976..2413)
          /gene="C3"
          /codon_start=1
          /product="C3 protein"
          /protein_id="CA10697.1"
          /db_xref="GI:4210723"
          /translation="MDSRTGESLSIAOTTRAEPFNPNMVCQTAPFHLRLMYTFNN
LDSITMKVQLQVNHNRNRETGFQKIFLQFRIIPRLGALPNWGISNRLKWLICNS
IASIGVPSLNFNLVVIIRHLPOQCLWEEVDVIDCKDILKILLY"
complement(2127..2576)
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          /complement(2127..2576)
          /gene="C2"
          /codon_start=1
          /product="C2 protein"
          /protein_id="CA10698.1"
          /db_xref="GI:4210724"
          /translation="MSTAPSGYKRCPCAPDEPIHAARKRORKEPPTRIWVKGCGCS
AFITNDCKFOGFTHRGYTKSCDTDESSRIIQGSIVCSDCITPTTIVCPKQPRLK
DDHESASQSPDEGNWIPEDUPITPDHTNASDWCYSQLDWTFQSP"

BASE COUNT      734 a      570 c      671 g      788 t
ORIGIN

alignment_scores:
  Quality: 266.00      Length: 68
  Ratio: 4.508      Gaps: 0
  Percent Similarity: 86.765      Percent Identity: 76.471

Percent Similarity: 86.765      Percent Identity: 76.471

alignment_block:
US-09-289-346A-7 x IYE132548/rev ..

Align seg 1/1 to reverse of: IYE132548 from: 1 to: 2763

1 ThrlEualtrpglyglupheglInValaspGlyArGserAlaAyslyG1 17
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469 ACCCTCATATGGGGTCAATTCCAGATCGACGGCAGATCTGCTGAGGAGG 420

17 yCysGlnThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerL 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
419 TCAGCAGTGTCTACAGCAGCGCAGCGCGCTAACGCGATGTTCTA 370

34 yslgluAlaLeuGlnIleleargGluYslleprGluYslYleu 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
369 AAGAACCTGCGTTCGCAATAATCAGGAGAAACCTCGAAAATAATATTTA 320

51 PhcGlnPheHisAsnLeuAsnSerAlaLeuAlaIlePheAspLysTh 67

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|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
319 TTTCATATCATATTAATTAGTGAATTTAGATAGATTTTTCCTCC 270

67 rPro 68
|||||
269 TCCCT 266

seq_name: gb_v1:MGU75278

seq_documentation_block:
LOCUS      MGU75278      447 bp      DNA
DEFINITION Macropitllium golden mosaic geminivirus replication-associated
protein (Ac1) gene, partial cds.
ACCESSION  U75278
VERSION     U75278.1 GI:1688188
KEYWORDS
SOURCE
ORGANISM
REFERENCE
  1 (bases 1 to 447)
  Macropitllium golden mosaic geminivirus.
  Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
  2 (bases 1 to 447)
  Thesis (1996)
  Diversily and phylogeny of whitefly-transmitted geminiviruses from
  Jamaica
  3 (bases 1 to 447)
  Roye, M.E., McLaughlin, W.A. and Maxwell, D.P.
  Three distinct geminiviruses infecting M. lathyroides from Jamaica
  but not BGWY
  Unpublished (1996)
  Roye, M.E., McLaughlin, W.A. and Maxwell, D.P.
  Three distinct geminiviruses infecting M. lathyroides from Jamaica
  but not BGWY
  Unpublished (1996)
  Roye, M.E., McLaughlin, W.A. and Maxwell, D.P.
  Direct Submission
  Submitted (17-OCT-1996) Biochemistry, University of the West
  Indies, Mona, Kingston 7, Jamaica
  Location/Qualifiers
    1..447
    /organism="Macropitllium golden mosaic geminivirus"
    /strain="Jamaican"
    /isolate="2"
    /db_xref="taxon:51676"
    /clone="PMGJA2"
    /complement(1..447)
    /gene="Ac1"
    /complement(<1..>447)
    /gene="Ac1"
    /codon_start=1
    /product="replication-associated protein"
    /protein_id="AAB36919.1"
    /db_xref="GI:1688189"
    /translation="HYLIQFOGKFNCTNNRLFDIYSPSRSAHPHPYIOGAKSSDYKS
YVEKDSPTIEKGVFOIDGRSARCGOOTSDAALNSGTREKAMRIYAEKLPKILF
QYHNLSNNDRIFMKDPEWPAPPPLSFTNPVDEKQEWATNIFGCG"

BASE COUNT      97 a      112 c      110 g      128 t
ORIGIN

alignment_scores:
  Quality: 259.00      Length: 70
  Ratio: 4.246      Gaps: 0
  Percent Similarity: 87.143      Percent Identity: 68.571

Percent Similarity: 87.143      Percent Identity: 68.571

alignment_block:
US-09-289-346A-7 x MGU75278/rev ..

Align seg 1/1 to reverse of: MGU75278 from: 1 to: 447

1 ThrlEualtrpglyglupheglInValaspGlyArGserAlaArGlyG1 17
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
294 ACCATCCAGATGGGAGCTTCCAGATCGACGGAAGAATGCTCGAGGCGG 245

17 yCysGlnThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerL 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
244 TCAGCAAAACATCTAACGATCGACGCGCGGAAGCATTAATTCTGGAACAA 195

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34  YSGIUGUALALEUGNILEILEARGIULYSILEPROGILIYSTYRLEU 50
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194 AGGAGCGCGCATGATGATGACAGGAGATGCGCGAAGATTCTC 145
51  PheGlnPheHisAsnLeuAsnSerAlaLeuAlaAlaIlePheAspLysTh 67
|||||:|||||:|||||:|||||:|||||:|||||:|||||
144 TTTCATATATCAACACCTATCCAGTAACCTGATAGATTTTCATGAAGA 95
67  rProGluPro 70
|||||
94  TCCGGAACCA 85

seq_name: gb_vl:AF098940

seq_documentation_block:
LOCUS AF098940 1405 bp DNA VRL 04-MAR-1999
DEFINITION Macroptilium golden mosaic geminivirus strain Jamaica 1
replication associated protein (rep) and coat protein (cp) genes,
partial cds.
ACCESSION AF098940 GI:4336584
KEYWORDS Macroptilium golden mosaic geminivirus.
SOURCE Viruses: ssDNA viruses; Geminiviridae; Begomovirus.
REFERENCE 1 (bases 1 to 1405)
AUTHORS Roye,M.E.
TITLE Genetic diversity and phylogeny of whitefly-transmitted
geminiviruses from Jamaica
JOURNAL 2 (bases 1 to 1405)
AUTHORS Roye,M.E., McLaughlin,W.A. and Maxwell,D.P.
TITLE Molecular characterization of two distinct geminiviruses infecting
M. lathyroides from Jamaica
JOURNAL 3 (bases 1 to 1405)
REFERENCE Roye,M.E., McLaughlin,W.A. and Maxwell,D.P.
AUTHORS Direct Submission
JOURNAL Submitted (14-OCT-1998) Biotechnology Centre, University of the
West Indies, Mona, Kingston 7, Jamaica
FEATURES
source 1. 1405
/organism="Macroptilium golden mosaic geminivirus"
/strain="Jamaica strain 1"
/specific_host="Macroptilium lathyroides"
/db_xref="taxon:51676"
/country="Jamaica"
/clone="PMGJAZ; PMGJA3"
/complement(<1..701)
/gene="rep"
/complement(<1..701)
/gene="rep"
/codon_start=1
/product="replication associated protein"
/protein_id="AAD17850.1"
/db_xref="GI:4336586"
/translation="MPKRSFSIKAKNYFLIYPOCSLTKKEPALSQTINLPVKKFI
KICRFHEDGQHLHVLIOFGKFNCTNNRLFDIVSPRSATFHFNIGCASSSVKS
YVERDGTIEWGVFOIDGRSARGGQOTSDAAEALNSGTAEAAIRVKEKLPKFLF
QYHNLSSNLDRIFKMDPEPMAPPPPLSFTNPDEMOMADDYFGGSAARPERMSI
IVEGDSRTGKTMAC"
misc_feature 702..1030
/note="intergenic region"
gene 1031..>1405
/gene="cp"
1031..>1405
/gene="cp"
/codon_start=1
/product="coat protein"
/protein_id="AAD17849.1"
/db_xref="GI:4336585"
/translation="MPKRDGSMRTTPGVAKYSRLNISPFGYGRSKAQDEWVRPM

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RVCVFEVYILGKIMDENINCSG"
BASE COUNT 328 a 333 c 357 g 386 t 1 others
ORIGIN

alignment_scores:
Quality: 259.00 Length: 70
Ratio: 4.246 Gaps: 0
Percent Similarity: 87.143 Percent Identity: 68.571

alignment_block:
US-09-289-346A-7 x AF098940/rev

Align seq 1/1 to reverse of: AF098940 from: 1 to: 1405

1 ThrLeuValTrpGlyGluPheGlnValAspGlyArgSerAlaArgLyl 17
||||| |||:||||| |||:|||||:|||||:|||||:|||||:|||||
374 ACCATCGAATGGGGAGTGTTCAGATCGACGAGGAAGATGCTCGAGCGG 325
17  YCysGlnThrSerAsnAspAlaAlaAlaGluAlaLeuAsnAlaSerSerL 34
| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
324 TCACCAACATCTACATACGATGACGCCGGAAGCATTAATTCGGAACAA 275
34  YSGIUGUALALEUGNILEILEARGIULYSILEPROGILIYSTYRLEU 50
||||| |||:|||||:|||||:|||||:|||||:|||||:|||||
274 AGGAGCGCGCATGATGATGACAGGAGATGCGCGAAGATTCTCTC 225
51  PheGlnPheHisAsnLeuAsnSerAlaLeuAlaAlaIlePheAspLysTh 67
|||||:|||||:|||||:|||||:|||||:|||||:|||||
224 TTTCATATATCAACACCTATCCAGTAACCTGATAGATTTTCATGAAGA 175
67  rProGluPro 70
|||||
174 TCCGGAACCA 165

seq_name: gb_vl:AF026553

seq_documentation_block:
LOCUS AF026553 1165 bp DNA VRL 03-NOV-1997
DEFINITION Potato yellow mosaic virus Tomato strain AV1 and AC1 genes, partial
cds.
ACCESSION AF026553 GI:2583073
KEYWORDS Geminiviridae.
SOURCE Viruses: ssDNA viruses.
ORGANISM Viruses: ssDNA viruses.
REFERENCE 1 (bases 1 to 1165)
AUTHORS Guzman,P., Arredondo,C.R., Esmaty,D., Portillo,R.J. and
Gibbertson,R.L.
TITLE Partial Characterization of Two Whitefly-Transmitted Geminiviruses
Infecting Tomatoes in Venezuela
JOURNAL Plant Dis. 81, 312-312 (1997)
AUTHORS 2 (bases 1 to 1165)
JOURNAL Guzman,P., Arredondo,C.R., Esmaty,D., Portillo,R.J. and
Gibbertson,R.L.
TITLE Direct Submission
JOURNAL Submitted (24-SEP-1997) Plant Pathology, University of
California-Davis, Department of Plant Pathology, Davis, CA 95616,
USA
FEATURES
source 1. 1165
/organism="Geminiviridae"
/strain="Tomato strain"
/db_xref="taxon:10811"
/note="Bipartite genome; whitefly-transmitted; DNA-A
fragment obtained by PCR from tomato sample from State of
Monagas (Venezuela)"
/complement(<1..153)
/note="capsid protein"
/codon_start=1
/product="AV1"

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CDS
    /protein_id="AAB82606.1"
    /db_xref="GI:2583075"
    /translation="MPKRDAPWMSMAGTSKVSNRNANSPRSGIGPINKAAEMVNRPM
464..>1165
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    /product="AC1"
    /protein_id="AAB82605.1"
    /db_xref="GI:2583074"
    /translation="MPKGSFSIKAKNYFLITYPOCSISKEDALSQIONLTPVKKRT
KICREIHEGEPHILVLIQEGKFNCTNNRIFDIYSEPTSTHPIHQAKSSSDVKS
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OYHNLSSDLDRIFMKAPNPMWAPPPLSSFTNVHEMOEMSHDYGRSAARGETISII
IEBDSRTGKTMNARC"

BASE COUNT      350 a      264 c      256 g      295 t

ORIGIN
alignment_scores:
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    Ratio: 4.095      Gaps: 0
    Percent Similarity: 90.000      Percent Identity: 68.571

alignment_block:
US-09-289-346a-7 x AF026553 ..
Align seg 1/1 to: AF026553 from: 1. to: 1165

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791 ACCATCGATGGGATGTTTCCAGATTGACGAGAGAGTGCCTCGAGATCG 840
17 ycgsglnThrSerAsnAspAlaIaIaGluAlaLeuAsnAlaSerSerL 34
| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
841 CCACAGACAGCCGACGACGACGACGACGACGACGACGACGACGACGAC 890
34 ysglGluAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeu 50
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
891 AGGAGAGAGCCATGAAATCATTAAGAGAGAGTGCCTGGAAGAGTTCTT 940
51 PheGlnPheHisAsnLeuAsnSerAlaLeuAlaIaIePheAspLysThr 67
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
941 TTTCAGTATCATACCTATTCAGTGCCTGACCTCATGATTTTTCATGAAGC 990
67 rProGluPro 70
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
991 TCCAAATCCG 1000

seq_name: gb_v1:AB001315
seq_documentation_block:
LOCUS      AB001315      570 bp      DNA      VRL      13-FEB-1999
DEFINITION Tobacco leaf curl virus C1 and C4 genes, clone YOKOHAMA3-1, partial
and complete cds.
ACCESSION  AB001315
VERSION     AB001315.1
KEYWORDS    GI:3798714
SOURCE      tobacco leaf curl virus (isolate:YOKOHAMA3,
            specific host:Eupatorium makinoi) DNA, clone:YOKOHAMA3-1.
            tobacco leaf curl virus
            Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
ORGANISM    Ooi.K.
REFERENCE   1 (bases 1 to 570)
AUTHORS    Direct Submission
TITLE      Submitted (19-FEB-1997) to the DDBJ/EMBL/GenBank databases.
JOURNAL    Kazuyuki Ooi, Kyushu University, Department of Biology; 6-10-1
            Hakozaki Higashi-ku, Fukuoka, Fukuoka 812, Japan
            (E-mail:kooi@chembox.nc.kyushu-u.ac.jp, Tel:+81-92-642-2624,
            Fax:+81-92-642-2645)
            2 (bases 1 to 570)
REFERENCE   Ooi,K., Ohshita,S., Ishii,I. and Yahara,T.
AUTHORS    Molecular phylogeny of geminivirus infecting wild plants in Japan
TITLE

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JOURNAL      J. Plant Res. 110, 247-257 (1997)
FEATURES
    source
        location/Qualifiers
            1..570
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            /isolate="YOKOHAMA3"
            /specific_host="Eupatorium makinoi"
            /db_xref="taxon:67762"
            /clone="YOKOHAMA3-1"
            /complement(1..570)
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            /complement(<1..570)
            /gene="C1"
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            /protein_id="BAA34034.1"
            /db_xref="GI:4426541"
            /translation="EELASQIONINTPNKIXIKICREIHEGSPHILVLIQFRRKY
CONNRFDLVSPTRSAHPHNPINIQKSSSDVKSITDKDGTLEKGTFOIDRSARGG
QMANDACAEALNASSKAELAIIRKLPKDFIFYHNLNLSNLDRTFAPLLEVFVCPPT
ASSFDQVPEELEWASERNVMSAARWPRM"
            /complement(231..488)
            /gene="C4"
            /complement(231..488)
            /gene="C4"
            /codon_start=1
            /protein_id="BAA34034.1"
            /db_xref="GI:3798715"
            /translation="HEALSMCFCSKANTNAKITDSSWTYRPPDQHSIRFREINP
APTSPSTIRKIRNSGHSRSTEELEEARMLTTHVQR"

BASE COUNT      141 a      121 c      126 g      182 t

ORIGIN
alignment_scores:
    Quality: 252.00      Length: 85
    Ratio: 4.065      Gaps: 1
    Percent Similarity: 72.941      Percent Identity: 58.824

alignment_block:
US-09-289-346a-7 x AB001315/rev ..
Align seg 1/1 to reverse of: AB001315 from: 1 to: 570

1 ThrleuValTrpGlyGluPheGlnValaIAspGlyArgSerAlaArgGlyL 17
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
318 ACCGTCGATGGGAGACATTCCAGATCGACGAGAGAGTGCCTAGAGAGG 269
17 ycgsglnThrSerAsnAspAlaIaIaGluAlaLeuAsnAlaSerSerL 34
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
268 CTGCAGAAATGCTAACGACGATGTCAGAGCGCTTAATGCAAGTTCTA 219
34 ysglGluAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeu 50
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
218 AGCGAGAGCATTAAGCAATATTAGGAAAGCCCTTAAGATTATATA 169
51 PheGlnPheHisAsnLeuAsnSerAlaLeu..... 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
168 TTTCATATATCATTAATTAAATAGTAATTATAGATGATTTTGTCTCTCC 119
61 .....AlaAlaIlePheAspLysThr 68
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
118 GTTGACGCTTTTGTGTCCTTTCACAGCGCTCATCTTTGATCAAGATTC 69
68 rGlu 69
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
68 CAGAA 64

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OM of: US-09-289-346a-7 to: N.Geneseq_1101:* out_format : pfs
Date: Jan 3, 2002 3:50 PM
About: Results were produced by the GenCore software, version 4.5.
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

-MODEL=frame+ p2n.model -DRV=xip
-O=/cgn1.1/USPTO.spool/US09289346/runat_03012002_153304_16393/app_query.fasta.1.1163
-DB=N.Geneseq_1101 -Qfmt=firstap -SUFFIX=p2n.rng -GAPOP=12.000
-GAPEXT=4.000 -MTNMAFCH=0.100 -LOOPEL=0.000 -LOOPEXT=0.000
-FGAPOP=4.500 -OGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELPOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blomsun62
-TRANS=human40.cdi -LIST=45 -DOCAIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
-NORM=ext -MINLEN=0 -MAXLEN=200000000
-USFR=US09289346_@cgn1_1_396 -NCPU=6 -ICPU=3 -LONGLOG -NO_XLPHY
-WAIT -THREADS=1

Search information block:

Query: US-09-289-346a-7
Query length: 70
Database: N.Geneseq_1101:*
Database sequences: 930621
Database length: 428662619
Search time (sec): 715.120000

score_list:

Sequence	Strd Orig	zscore	EScore	len	Documentation
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/cgn1_8/gcgdata/geneseq/geneseq/NA1995.DAT:AAQ84371			222.00	558.42	5.0e-23
/cgn1_8/gcgdata/geneseq/geneseq/NA1995.DAT:AAQ84372			222.00	557.37	5.7e-23
/cgn1_8/gcgdata/geneseq/geneseq/NA1995.DAT:AAQ84375			221.50	554.59	8.2e-23
/cgn1_8/gcgdata/geneseq/geneseq/NA1997.DAT:AAAT93291			213.00	525.53	3.4e-21
/cgn1_8/gcgdata/geneseq/geneseq/NA1997.DAT:AAAT93292			213.00	525.53	3.4e-21
/cgn1_8/gcgdata/geneseq/geneseq/NA1997.DAT:AAAT93293			213.00	525.53	3.4e-21
/cgn1_8/gcgdata/geneseq/geneseq/NA1997.DAT:AAAT93314			213.00	524.37	3.9e-21
/cgn1_8/gcgdata/geneseq/geneseq/NA1997.DAT:AAAT93290			213.00	520.81	6.2e-21
/cgn1_8/gcgdata/geneseq/geneseq/NA2000.DAT:AAA94700			213.00	520.81	6.2e-21
/cgn1_8/gcgdata/geneseq/geneseq/NA2000.DAT:AAA94701			213.00	520.81	6.2e-21
/cgn1_8/gcgdata/geneseq/geneseq/NA2000.DAT:AAA94703			213.00	519.34	7.5e-21
/cgn1_8/gcgdata/geneseq/geneseq/NA2000.DAT:AAA94702			213.00	518.37	8.5e-21
/cgn1_8/gcgdata/geneseq/geneseq/NA1998.DAT:AAV29761			212.00	512.69	1.8e-20
/cgn1_8/gcgdata/geneseq/geneseq/NA1996.DAT:AAAT12904			211.00	520.17	6.7e-21
/cgn1_8/gcgdata/geneseq/geneseq/NA1996.DAT:AAAT12905			211.00	520.17	6.7e-21
/cgn1_8/gcgdata/geneseq/geneseq/NA1996.DAT:AAAT12906			211.00	520.17	6.7e-21
/cgn1_8/gcgdata/geneseq/geneseq/NA1997.DAT:AAAT93294			211.00	519.32	7.5e-21
/cgn1_8/gcgdata/geneseq/geneseq/NA1997.DAT:AAAT93282			211.00	519.32	7.5e-21
/cgn1_8/gcgdata/geneseq/geneseq/NA1997.DAT:AAAT93283			211.00	519.32	7.5e-21
/cgn1_8/gcgdata/geneseq/geneseq/NA1997.DAT:AAAT93284			211.00	519.32	7.5e-21
/cgn1_8/gcgdata/geneseq/geneseq/NA1995.DAT:AAO84378			211.00	515.34	1.3e-20
/cgn1_8/gcgdata/geneseq/geneseq/NA1997.DAT:AAAT93309			211.00	510.76	2.3e-20
/cgn1_8/gcgdata/geneseq/geneseq/NA1996.DAT:AAAN60611			211.00	510.57	2.3e-20
/cgn1_8/gcgdata/geneseq/geneseq/NA1987.DAT:AAAT70630			205.50	513.66	1.6e-20
/cgn1_8/gcgdata/geneseq/geneseq/NA1987.DAT:AAAT70897			205.50	498.61	1.1e-19
/cgn1_8/gcgdata/geneseq/geneseq/NA1995.DAT:AAAN70853			205.00	511.85	2.0e-20
/cgn1_8/gcgdata/geneseq/geneseq/NA1995.DAT:AAO84377			203.00	489.48	3.5e-19
/cgn1_8/gcgdata/geneseq/geneseq/NA1997.DAT:AAAT11646			193.00	472.91	2.9e-18
/cgn1_8/gcgdata/geneseq/geneseq/NA1997.DAT:AAAT93287			193.00	472.91	2.9e-18
/cgn1_8/gcgdata/geneseq/geneseq/NA1997.DAT:AAAT93288			193.00	472.91	2.9e-18
/cgn1_8/gcgdata/geneseq/geneseq/NA1997.DAT:AAAT93289			193.00	472.91	2.9e-18
/cgn1_8/gcgdata/geneseq/geneseq/NA1995.DAT:AAO84376			191.00	475.58	2.1e-18
/cgn1_8/gcgdata/geneseq/geneseq/NA1997.DAT:AAAT93311			185.00	450.18	4.1e-17
/cgn1_8/gcgdata/geneseq/geneseq/NA1997.DAT:AAAT93285			184.50	452.69	5.0e-17
/cgn1_8/gcgdata/geneseq/geneseq/NA1997.DAT:AAAT93286			161.00	389.10	1.3e-13
/cgn1_8/gcgdata/geneseq/geneseq/NA1987.DAT:AAAT70900			125.00	311.18	0.0147
/cgn1_8/gcgdata/geneseq/geneseq/NA1997.DAT:AAAT93318			86.00	190.93	0.0147
/cgn1_8/gcgdata/geneseq/geneseq/NA2001.DAT:AAZ96042			68.00	141.91	7.91
/cgn1_8/gcgdata/geneseq/geneseq/NA2001.DAT:AAAD11655			68.00	141.91	7.91

/cgn1_8/gcgdata/geneseq/geneseq/NA2000.DAT:AAZ43808	66.00	141.87	7.95	224
/cgn1_8/gcgdata/geneseq/geneseq/NA2001.DAT:AAF97925	66.00	141.82	8.01	225
/cgn1_8/gcgdata/geneseq/geneseq/NA2000.DAT:AAZ65090	66.00	141.69	8.14	226
/cgn1_8/gcgdata/geneseq/geneseq/NA2001.DAT:AAAF4236	68.00	141.69	8.14	228
/cgn1_8/gcgdata/geneseq/geneseq/NA2000.DAT:AAAF43180	66.00	141.51	8.33	232

seq_name: /cgn1_8/gcgdata/geneseq/geneseq/NA1997.DAT:AAAT93317

seq_documentation block:

ID	AAAT93317 standard: DNA; 2744 BP.
XX	
AC	AAAT93317:
XX	
DT	27-APR-1998 (first entry)
DE	Tomato leaf curl virus from Southern India (stem-loop begin).
XX	
KW	Geminivirus; TLGV-IND; AC1 gene; transdominant mutation;
KW	transgenic plant; disease resistance; ss; cyclic; circular.
XX	
OS	Tomato leaf curl virus from Southern India.
XX	
PN	W09739110-A1.
XX	
PD	23-OCT-1997.
XX	
PF	15-APR-1997; 97WO-US06300.
XX	
PR	16-APR-1996; 96US-0015517.
XX	
PA	(SEMI-) SEMINIS VEGETABLE SEEDS INC.
PA	(MISC) WISCONSIN ALUMNI RES FOUND.
XX	
PI	Ahlquist PC, Hanson SF, Luu HT, Maxwell DP, Stout JT;
XX	
DR	WPI, 1997-526447/48.
XX	
PT	Transgenic plants expressing geminivirus AC1 and CI wild-type and
PT	mutant genes - have increased resistance to geminivirus infection
PT	e.g. tomato mottle virus, tomato yellow leaf curl virus or bean
XX	golden mosaic geminivirus
XX	
PS	Disclosure: Page 119-121; 132pp; English.
XX	
CC	This genomic DNA sequence comprises a full-length sequence
CC	(stem-loop begin) from a tomato leaf curl virus from Southern
CC	India. The invention involves production of transgenic plants
CC	containing DNA comprising geminivirus AC1 or CI wild-type or mutant
CC	sequences (see AAAT93282-93) that negatively interfere in trans with
CC	geminiviral replication during infection. Such transgenic plants
CC	are resistant to viral infection. The AC1/CI genes are especially
CC	from tomato mottle virus, tomato yellow leaf curl virus or bean
CC	golden mosaic virus.
XX	
SQ	Sequence 2744 BP; 742 A; 539 C; 637 G; 826 T; 0 other;
XX	
alignment_scores:	
Quality:	225.00
Ratio:	4.167
Percent Similarity:	83.077
Percent Identity:	69.231
alignment_block:	
US-09-289-346a-7 x AAAT93317/rev	
Align seg 1/1 to reverse of: AAAT93317 from: 1 to: 2744	
4 TrpGtGtAupheGInvaSpGtYArGSeRAlArGtGtYcYgSnTh 20	
2266 TGGGGTACGTTTCAGATCGATGCAAGATCTCCACGAGAGGCTAACACGAC 2217	
20 TSeRAsnAspAlaAlaAlaGtAlaLeuAsnAlaSerSerLyScIuGtA 37	

```

2216 AGCTAATGATGCTGCCAGAGCCCTTAATGCAGTTACGTGACAGCAG 2167
37  lalenglnlleleargglulysileproglulyslyrlaunphcglphe 53
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2166 CTTTAGCAATTAATTAATGAGAAACCTCCCTAAGATTTTATTTTCAATAT 2117
54  HisAsnLeuAsnSerAlaLeuAlaAlaIlePheAspIysThrPro 68
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2116 CATTAATTTAAATCTAATTAATGATGATTTT.....ACACCT 2078
seq_name: /cgnl_8/gcgdata/geneseq/geneseqn/NA1995.DAT:AAQ84371
seq_documentation_block:
ID  AAQ84371 standard; DNA; 434 BP.
XX
AC  AAQ84371;
XX
DT  19-AUG-1995 (first entry)
XX
DE  Gemini virus-specific polyribozyme-E target sequence.
XX
XX  ribozyme target sequence; polyribozyme-E;
KM  tomato leaf curl virus; RNA cleavage; tomato transgenic plant;
XX  virus disease-resistance; ss.
OS  Tomato leaf curl virus.
XX
FH  Key Location/Qualifiers
FT  misc_feature 13..43
    /tag= a
    /note= "ribozyme R1 target sequence"
FT  misc_feature 26..28
    /tag= b
    /note= "ribozyme R1 cleavage site"
FT  misc_feature 312..342
    /tag= c
    /note= "ribozyme R2 target sequence"
FT  misc_feature 325..327
    /tag= d
    /note= "ribozyme R2 cleavage site"
FT  misc_feature 384..414
    /tag= e
    /note= "ribozyme R3 target sequence"
FT  misc_feature 397..399
    /tag= c
    /note= "ribozyme R3 cleavage site"
FT
XX
PN  WO9503404-A.
XX
PD  02-FEB-1995.
XX
PF  22-JUL-1993; 93WO-EP01946.
XX
PR  22-JUL-1993; 93AU-0047014.
PR  22-JUL-1993; 93WO-EP01946.
XX
PA  (BIOC-) BIOCEM SA.
PA  (CSTR) COMMONWEALTH SCT & IND RES ORG.
XX
PI  Baudino S, Comeau D, Dry IB, Gruber V, Lenee P;
PI  Mason J, Rezaian MA, Rigden JE, Rezaian MA;
XX
DR  WPI: 1995-075232/10.
XX
XX  Synthetic DNA virus ribozyme(s) - reduce replication, infection
XX  and/or assembly of viruses by cleaving target virus sequence,
XX  useful for preparing resistant plants, esp tomatoes.
PS  Example 10; Fig 11b; 90pp; English.
XX
XX  The sequence is a tomato leaf curl virus target sequence for
XX  polyribozyme-E, which hybridizes to and cleaves the sequence and
XX  thereby reduces replication, infection and/or assembly of the virus

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CC  substantially. The ribozyme may be expressed in a transgenic plant,
CC  e.g. tomato, to confer virus disease-resistance.
XX
SQ  Sequence 434 BP; 126 A; 86 C; 91 G; 131 T; 0 other;

alignment_scores:
    Quality: 222.00 Length: 85
    Ratio: 3.700 Gaps: 1
    Percent Similarity: 70.588 Percent Identity: 52.941

alignment_block:
US-09-289-346A-7 x AAQ84371 ..
Align seg 1/1 to: AAQ84371 from: 1 to: 434

1  ThrLeuValTrpGlyIlePheGlnValAspGlyArgSerAlaArgIle 17
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
95  ACCCTCGAATGCGGAGAGATTTCAGATCGATGACGATCTCGAAGAGCGG 144
17  yCysGlnThrSerAsnAspAlaAlaIleArgGluLysIleProGluLysThr 34
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
145  ACAACAATTCAGCCAAATGATGATGATGATGATGATGATGATGATGATG 194
34  ysgGluAlaLeuGlnlleleargglulysileproglulyslyrlaunph 50
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
195  AGTCAGAGGCTCTTAACGCTCTTAGGCAATTAAGCCCTTAAGGATTATGTT 244
51  PheGlnPheHisAsnLeuAsnSerAlaLeuAlaAlaIle..... 63
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
245  TTACAAATTCATATTAATTAATTAATTAATTAATTAATTAATTAATTA 294
64  .....PheAspIysThrP 68
295  GTTGAGAGTTTATGCTTCCTTTTATCTCTTCTTTGATCGAGGTTTC 344
68  roglu 69
   |||||
345  CAGCA 349

seq_name: /cgnl_8/gcgdata/geneseq/geneseqn/NA1995.DAT:AAQ84372
seq_documentation_block:
ID  AAQ84372 standard; DNA; 479 BP.
XX
AC  AAQ84372;
XX
DT  19-AUG-1995 (first entry)
XX
DE  Gemini virus-specific polyribozyme-F target sequence.
XX
XX  ribozyme target sequence; polyribozyme-F;
KM  tomato leaf curl virus; RNA cleavage; tomato transgenic plant;
XX  virus disease-resistance; ss.
OS  Tomato leaf curl virus.
XX
FH  Key Location/Qualifiers
FT  misc_feature 46..96
    /tag= a
    /note= "ribozyme R4-R5 target sequence"
FT  misc_feature 58..60
    /tag= b
    /note= "ribozyme R4 cleavage site"
FT  misc_feature 81..83
    /tag= c
    /note= "ribozyme R5 cleavage site"
FT  misc_feature 356..386
    /tag= d
    /note= "ribozyme R2 target sequence"
FT  misc_feature 370..372
    /tag= c
    /note= "ribozyme R2 cleavage site"
FT

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FT misc_feature 429..459
FT /*tag= e
FT /note= "ribozyme R3 target sequence"
FT 442..444
FT /*tag= d
FT /note= "ribozyme R3 cleavage site"
XX
XX WO9503404-A.
XX
XX 02-FEB-1995.
XX
XX 22-JUL-1993; 93WO-EP01946.
XX
XX 22-JUL-1993; 93AU-0047014.
XX
XX 22-JUL-1993; 93WO-EP01946.
XX
XX (BIOC-) BIOCEM SA.
XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX
XX Baudino S, Comeau D, Dry IB, Gruber V, Lenée P;
XX Mason J, Rezaian MA, Rigiden JE, Rezaian MA;
XX
XX WPI: 1995-075232/10.
XX
XX Synthetic DNA virus ribozyme(s) - reduce replication, infection
XX PT and/or assembly of viruses by cleaving target virus sequence,
XX useful for preparing resistant plants, esp tomatoes.
XX
XX Example 10; Fig 11c; 90pp; English.
XX
XX The sequence is a tomato leaf curl virus target sequence for
XX CC polyribzyme-F, which hybridizes to and cleaves the sequence and
XX thereby reduces replication, infection and/or assembly of the virus
XX CC substantially. The ribozyme may be expressed in a transgenic plant,
XX e.g. tomato, to confer virus disease-resistance.
XX
XX Sequence 479 BP; 145 A; 95 C; 97 G; 142 T; 0 other:

```

```

alignment_scores:
  Quality: 222.00      Length: 85
  Ratio: 3.700        Gaps: 1
  Percent Similarity: 70.588      Percent Identity: 52.941

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alignment_block:
US-09-289-346a-7 x AA084372 ..

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Align seg 1/1 to: AA084372 from: 1 to: 479

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```

1 ThrleuValTrpGluupheGlnValAspGlyArgSerAlaArgGlyG 17
||||| ||||||||| ||||||||| ||||||||| |||||||||
140 ACCCTCGAATGGGAGAGCTTCAGATCGATGAGATCTGCCAAGAGGG 189
17 ycySGlnThrSerAsnAspAlaAlaIaGluAlaLeuAsnAlaSer 34
| ||||| ||||| ||||| ||||| ||||| ||||| |||||
190 ACAACAGATGAGCCATGAGCTTACGCCAGCGCTTACACAGGA 239
34 ysglGluAlaLeuGlnIleIleArgIuLysIleProGluLysTyr 50
||:||||| ||||| ||||| ||||| ||||| ||||| |||||
240 AGTCAGAGGCTCTTACGCTCTTACGGAATTAGCCCTAAGATTA 289
51 pheGlnPheHisAsnLeuAsnSerAlaLeuAlaIle..... 63
||||| ||||| ||||| ||||| ||||| ||||| |||||
290 TTACAAATTCATTAATTAATTAATTAATTAATTAATTAATTA 339
64 .....PheAspLysIle 68
||||| ||||| ||||| ||||| ||||| ||||| |||||
340 GTTGCAGGTTATGTTCTCTTTTATATCTCTCTTTTATGATGAG 389
68 roGlu 69
|||||
390 CAGAA 394

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seq_name: /cgnl_8/gcgcdata/geneseq/geneseqn/NA1995.DAT:AA084375
seq_documentation_block:
ID AA084375 standard; DNA; 550 BP.
XX
XX
XX AA084375;
XX
XX 19-AUG-1995 (first entry)
XX
XX Tomato leaf curl virus Australian strain DNA sequence.
XX
XX Tomato leaf curl virus; Australia strain; plant disease; ds.
XX
XX Tomato leaf curl virus (Australia).
XX
XX WO9503404-A.
XX
XX 02-FEB-1995.
XX
XX 22-JUL-1993; 93WO-EP01946.
XX
XX 22-JUL-1993; 93AU-0047014.
XX
XX 22-JUL-1993; 93WO-EP01946.
XX
XX (BIOC-) BIOCEM SA.
XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX
XX Baudino S, Comeau D, Dry IB, Gruber V, Lenée P;
XX PI Mason J, Rezaian MA, Rigiden JE, Rezaian MA;
XX
XX WPI: 1995-075232/10.
XX
XX Synthetic DNA virus ribozyme(s) - reduce replication, infection
XX PT and/or assembly of viruses by cleaving target virus sequence,
XX useful for preparing resistant plants, esp tomatoes.
XX
XX Disclosure: Fig 1; 90pp; English.
XX
XX The sequence represents the complementary sense DNA strand of an
XX CC Australian strain of tomato leaf curl virus. Ribozymes specific
XX CC for this sequence may be used in generation of transgenic plants
XX with disease-resistance.
XX
XX Sequence 550 BP; 148 A; 120 C; 134 G; 142 T; 6 other:

```

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alignment_scores:
  Quality: 221.50      Length: 86
  Ratio: 3.692        Gaps: 1
  Percent Similarity: 69.767      Percent Identity: 52.326

```

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alignment_block:
US-09-289-346a-7 x AA084375 ..

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Align seg 1/1 to: AA084375 from: 1 to: 550

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```

1 ThrleuValTrpGluupheGlnValAspGlyArgSerAlaArgGlyG 17
||||| ||||||||| ||||||||| ||||||||| |||||||||
201 ACCCTCGAATGGGAGAGCTTCAGATCGATGAGATCTGCCAAGAGGG 250
17 ycySGlnThrSerAsnAspAlaAlaIaGluAlaLeuAsnAlaSer 34
| ||||| ||||| ||||| ||||| ||||| ||||| |||||
251 ACAACAGATGAGCCATGAGCTTACGCCAGCGCTTACACAGGA 300
34 ysglGluAlaLeuGlnIleIleArgIuLysIleProGluLysTyr 50
||:||||| ||||| ||||| ||||| ||||| ||||| |||||
301 AGTCAGAGGCTCTTACGCTCTTACGGAATTAGCCCTAAGATTA 350
51 pheGlnPheHisAsnLeuAsnSerAlaLeuAlaIle..... 63
||||| ||||| ||||| ||||| ||||| ||||| |||||
351 TTACAAATTCATTAATTAATTAATTAATTAATTAATTAATTA 400
64 .....PheAspLysIle 67

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401 TCCGTTGAGGTTTATGTTCTCCTTTTATCTTCTTTGATGAG 450
67 hrProglu 69
:::|||||
451 TTCAGAA 458

```

seq_name: /cgnl_8/gcgdata/geneseq/geneseqn/NA1997.DAT:AA193291

seq_documentation_block:

ID AA193291 standard; DNA; 1062 BP.

AC AA193291;

DF 27-APR-1998 (first entry)

DE Bean golden mosaic geminivirus CI mutant ORF BGAC221.

KW Geminivirus; BGW; CI gene; transdominant mutation;

KW transgenic plant; disease resistance; ss; cyclic; circular.

OS Bean golden mosaic virus type II isolate Guatemala.

PN WO9739110-A1.

PD 23-OCT-1997.

PF 15-APR-1997; 97WO-US06300.

PR 16-APR-1996; 96US-0015517.

PA (SEMI-) SEMINIS VEGETABLE SEEDS INC.

PA (MISC) WISCONSIN ALUMNI RES FOUND.

PI Ahlquist PG, Hanson SF, Lau HT, Maxwell DP, Stout JT;

DR WPI; 1997-526447/48.

DR P-PSDB; AAW34333.

PT Transgenic plants expressing geminivirus AC1 and CI wild-type and
PT mutant genes - have increased resistance to geminivirus infection
e.g. tomato mottle virus, tomato yellow leaf curl virus or bean
PT golden mosaic geminivirus

PS Claim 13; Page 107-109; 132pp; English.

CC This DNA sequence comprises construct BGAC221 that codes for a
CC transdominant lethal mutant (see AAW34333) of the CI protein (see
CC AAW34338) of bean golden mosaic virus (BGW). It was obtained by
CC Kunzel mutagenesis of the wild-type CI gene (see AA193314). CI is
CC required for replication. The invention involves production of CI
CC transgenic plants containing DNA comprising geminivirus CI or AC1
CC wild-type or mutant sequences that negatively interfere in trans
CC with geminiviral replication during infection. Such transgenic
CC plants are resistant to viral infection. The AC1/CI genes are
CC especially from BGW, tomato mottle virus or tomato yellow leaf
CC curl virus (see AA193282-93) and encode polypeptides (see AAW34324-35)
CC that have mutations in the highly conserved DNA-nicking and/or the
CC NTP-binding domains.

XX Sequence 1062 BP; 339 A; 245 C; 219 G; 259 T; 0 other;

XX alignment_scores:

Quality:	213.00	Length:	70
Ratio:	3.672	Gaps:	0
Percent Similarity:	82.857	Percent Identity:	58.571

XX alignment_block:

XX US-09-289-346A-7 x AA193291 ..

XX Align seg 1/1 to: AA193291 from: 1 to: 1062

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1 ThrLeuValTrpGlyIupheGlnValAspGlyArgSerAlaArgGly 17
|||||
328 ACATTCGAAATGGGACAAATTCAGTCACGCGAGATTCGACAGAGCAG 377
17 yCysGlnThrsAsnAspAlaAlaGluAlaLeuAsnAspSerL 34
|||||
378 TCACGAGCTGCGCCACGACATCATATGCAAAAGCATTAACCCAGATTC 427
34 ysgGluAlaLeuGlnIleArgGlyIupheGlnValAspGlyArgSer 50
|||||
428 TTGAAATCTGCTTCACAAATATTCAGAGACACCAAGCAAGATTCAG 477
51 PheGlnPheHisAsnLeuAsnSerAlaLeuAlaAlaIlePheAspLys 67
|||||
478 CTTCACATCATCAGACATCCGTTCTAATCTGCAACGATCTTCGCAAG 527
67 rProgluPro 70
528 GCCCGAACA 537

```

seq_name: /cgnl_8/gcgdata/geneseq/geneseqn/NA1997.DAT:AA193292

seq_documentation_block:

ID AA193292 standard; DNA; 1062 BP.

AC AA193292;

DF 27-APR-1998 (first entry)

DE Bean golden mosaic geminivirus CI mutant ORF BGAC228.

KW Geminivirus; BGW; CI gene; transdominant mutation;

KW transgenic plant; disease resistance; ss; cyclic; circular.

OS Bean golden mosaic virus type II isolate Guatemala.

PN WO9739110-A1.

PD 23-OCT-1997.

PF 15-APR-1997; 97WO-US06300.

PR 16-APR-1996; 96US-0015517.

PA (SEMI-) SEMINIS VEGETABLE SEEDS INC.

PA (MISC) WISCONSIN ALUMNI RES FOUND.

PI Ahlquist PG, Hanson SF, Lau HT, Maxwell DP, Stout JT;

DR WPI; 1997-526447/48.

DR P-PSDB; AAW34334.

PT Transgenic plants expressing geminivirus AC1 and CI wild-type and
PT mutant genes - have increased resistance to geminivirus infection
e.g. tomato mottle virus, tomato yellow leaf curl virus or bean
PT golden mosaic geminivirus

PS Claim 13; Page 111-112; 132pp; English.

CC This DNA sequence comprises construct BGAC228 that codes for a
CC transdominant lethal mutant (see AAW34334) of the CI protein (see
CC AAW34338) of bean golden mosaic virus (BGW). It was obtained by
CC Kunzel mutagenesis of the wild-type CI gene (see AA193314). CI is
CC required for replication. The invention involves production of CI
CC transgenic plants containing DNA comprising geminivirus CI or AC1
CC wild-type or mutant sequences that negatively interfere in trans
CC with geminiviral replication during infection. Such transgenic
CC plants are resistant to viral infection. The AC1/CI genes are
CC especially from BGW, tomato mottle virus or tomato yellow leaf
CC curl virus (see AA193282-93) and encode polypeptides (see AAW34324-35)
CC that have mutations in the highly conserved DNA-nicking and/or the
CC NTP-binding domains.

```

SQ      Sequence 1062 BP; 338 A; 247 C; 218 G; 259 T; 0 other:
Alignment_scores:
    Quality: 213.00      Length: 70
    Ratio: 3.672         Gaps: 0
    Percent Similarity: 82.857   Percent Identity: 58.571

Alignment_block:
US-09-289-346a-7 x AAT93292 ..
Align seg 1/1 to: AAT93292 from: 1 to: 1062

1 ThleuValTrpglyGluPheGlnValAspGlyArgSerAlaArgGlyG1 17
|||||: |||||:|||||:|||||:|||||:|||||:|||||:|||||:
328 ACAATGCAATGGGACATTCACAAAGTCGACGACATCTGCAGAGG 377
17 yCysGlnThrSerAsnAspAlaAlaAlaGluAlaLeuAsnAlaSerSerL 34
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
378 TCAGCAGTCTGCCACGACCTCATATGCAAGGCAATTAACGCAATTCAA 427
428 TTGAATCTGCTTGACAAATATGACAGGAAGAACACCGAAAGATTACGTC 477
34 ysgIugIAlaLeuGlnIleIleArgGluysIleProGluLysTyrLeu 50
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
428 TTGAATCTGCTTGACAAATATGACAGGAAGAACACCGAAAGATTACGTC 477
51 PheGlnPheHisAsnLeuAsnSerAlaLeuAlaAlaIlePheAspLysTh 67
: | | | | : | | | | | : | | | | | : | | | | | : | | | | |
478 CTTCAACATCTGCACAAATCTGCAAGCGATCTTCGTCAAAGT 527
67 rProGluPro 70
: | | | | |
528 GCCGGAACCA 537

seq_name: /cgnl_8/gcgdata/geneseq/geneseqn/NA1997.DAT: AAT93293
seq_documentation_block:
ID      AAT93293 standard; DNA; 1062 BP.
XX
AC      AAT93293:
XX
DT      27-APR-1998 (first entry)
XX
DE      Bean golden mosaic geminivirus C1 mutant ORF BGAC262.
XX
KM      Geminivirus; BGWV; C1 gene; transdominant mutation;
XX      transgenic plant; disease resistance; ss: cyclic; circular.
XX
OS      Bean golden mosaic virus type II isolate Guatemala.
XX
PN      WO9739110-A1.
XX
PD      23-OCT-1997.
XX
PF      15-APR-1997; 97WO-US06300.
XX
PR      16-APR-1996; 96US-0015517.
XX
PA      (SEMI-) SEMINIS VEGETABLE SEEDS INC.
XX      (WISC) WISCONSIN ALUMNI RES FOUNDD.
XX
PI      Ahlquist PG, Hanson SF, Luu HT, Maxwell DP, Stout JT;
XX      WPI; 1997-526447/48.
XX      P-PSDB: AAW34335.
XX
DR      Transgenic plants expressing geminivirus AC1 and C1 wild-type and
XX      mutant genes - have increased resistance to geminivirus infection
XX      e.g. tomato mottle virus, tomato yellow leaf curl virus or bean
XX      golden mosaic geminivirus
XX
PS      Claim 13; Page 115-116; 132pp; English.
XX
CC      This DNA sequence comprises construct BGAC262 that codes for a
```

```

CC      transdominant lethal mutant (see AAW34335) of the C1 protein (see
CC      AAW34338) of bean golden mosaic virus (BGWV). It was obtained by
CC      kunekel mutagenesis of the wild-type C1 gene (see AAT93314). C1 is
CC      required for replication. The invention involves production of
CC      transgenic plants containing DNA comprising geminivirus C1 or AC1
CC      wild-type or mutant sequences that negatively interfere in trans
CC      with geminiviral replication during infection. Such transgenic
CC      plants are resistant to viral infection. The AC1/C1 genes are
CC      especially from BGWV, tomato mottle virus or tomato yellow leaf
CC      curl virus (see AAT93282-93) and encode polypeptides (see AAW34324-35)
CC      that have mutations in the highly conserved DNA-nicking and/or the
CC      NTP-binding domains.
XX
SQ      Sequence 1062 BP; 340 A; 245 C; 219 G; 258 T; 0 other:
Alignment_scores:
    Quality: 213.00      Length: 70
    Ratio: 3.672         Gaps: 0
    Percent Similarity: 82.857   Percent Identity: 58.571

Alignment_block:
US-09-289-346a-7 x AAT93293 ..
Align seg 1/1 to: AAT93293 from: 1 to: 1062

1 ThleuValTrpglyGluPheGlnValAspGlyArgSerAlaArgGlyG1 17
|||||: |||||:|||||:|||||:|||||:|||||:|||||:|||||
328 ACAATGCAATGGGACATTCACAAAGTCGACGACGACATCTGCAGAGG 377
17 yCysGlnThrSerAsnAspAlaAlaAlaGluAlaLeuAsnAlaSerSerL 34
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
378 TCAGCAGTCTGCCACGACCTCATATGCAAGGCAATTAACGCAATTCAA 427
428 TTGAATCTGCTTGACAAATATGCAAGGCAAGAACCGAAAGATTACGTC 477
34 ysgIugIAlaLeuGlnIleIleArgGluysIleProGluLysTyrLeu 50
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
428 TTGAATCTGCTTGACAAATATGCAAGGCAAGAACCGAAAGATTACGTC 477
51 PheGlnPheHisAsnLeuAsnSerAlaLeuAlaAlaIlePheAspLysTh 67
: | | | | : | | | | | : | | | | | : | | | | | : | | | | |
478 CTTCAACATCTGCACAAATCTGCAAGCGATCTTCGTCAAAGT 527
67 rProGluPro 70
: | | | | |
528 GCCGGAACCA 537

seq_name: /cgnl_8/gcgdata/geneseq/geneseqn/NA1997.DAT: AAT93314
seq_documentation_block:
ID      AAT93314 standard; DNA; 1183 BP.
XX
AC      AAT93314:
XX
DT      27-APR-1998 (first entry)
XX
DE      Bean golden mosaic geminivirus C1 open reading frame.
XX
KM      Geminivirus; BGWV; C1 gene; transdominant mutation;
XX      transgenic plant; disease resistance; ss: cyclic; circular.
XX
OS      Bean golden mosaic virus type II isolate Guatemala.
XX
PN      WO9739110-A1.
XX
PD      23-OCT-1997.
XX
PF      15-APR-1997; 97WO-US06300.
XX
PR      16-APR-1996; 96US-0015517.
XX
XX      Key      Location/Qualifiers
XX      FT      CDS      1..1062
XX      FT      /*tag= a
```

XX (SEMI-) SEMINIS VEGETABLE SEEDS, INC.
 PA (WISC.) WISCONSIN ALUMNI RES. FOUND.
 XI
 XII
 XIII
 XIV
 XV Abtquist PG, Hanson SF, Lau HT, Maxwell DP, Stout JT;
 XVI
 XVII WPI: 1997-526447/48.
 XVIII P-PSDB; AAW34338.
 XIX
 XX Transgenic plants expressing geminivirus AC1 and CI wild-type and
 XX mutant genes - have increased resistance to geminivirus infection
 XX e.g. tomato mottle virus, tomato yellow leaf curl virus or bean
 XX golden mosaic geminivirus
 XX
 XX
 XX
 XX Example 5; Page 100-102; 132pp; English.
 XX
 XX This genomic DNA sequence includes the open reading frame (ORF) of
 XX the wild-type CI gene of bean golden mosaic virus (BGWV), a
 XX geminivirus that has a monopartite genome. The CI protein (see
 XX AAW34338) is required for replication. The wild-type CI ORF was
 XX subjected to Kunkel mutagenesis (see AAT93290-93). The invention
 XX involves production of transgenic plants containing DNA comprising
 XX CI or AC1 wild-type or mutant sequences that negatively interfere
 XX in trans with geminiviral replication during infection. Such
 XX transgenic plants are resistant to viral infection. The AC1/CI
 XX genes are especially from BGWV, tomato mottle virus or tomato
 XX yellow leaf curl virus (see AAT93282-93) and encode polypeptides
 XX (see AAW34324-35) that have mutations in the highly conserved
 XX DNA-nicking domain and/or the NTP-binding domains.
 XX
 XX Sequence 1183 BP; 372 A; 276 C; 248 G; 287 T; 0 other;

XX	Geminivirus; BGMV; C1 gene; transdominant mutation;
KM	transgenic plant; disease resistance; ss; cyclic; circular.
OS	Bean golden mosaic virus type II isolate Guatemala.
XX	
FH	Key
FT	CDS
FT	Location/Qualifiers
XX	1..1062
XX	/+tag- a
PN	WO9739110-A1.
XX	
PD	23-OCT-1997.
XX	
PE	15-APR-1997; 97MO-US06300.
XX	
PR	16-APR-1996; 96US-0015517.
XX	
PA	(SEMI-) SEMINIS VEGETABLE SEEDS INC.
PA	(MISC) WISCONSIN ALUMNI RES FOUND.
XX	
PI	Ahlquist PG, Hanson SF, Luu HT, Maxwell DP, Stout JT;
DR	WPI; 1997-526447/48.
DR	P-PsDB; AAM34332.
PT	Transgenic plants expressing geminivirus AC1 and C1 wild-type and
PT	mutant genes - have increased resistance to geminivirus infection
PT	e.g. tomato mottle virus, tomato yellow leaf curl virus or bean
XX	golden mosaic geminivirus
XX	

alignment_scores:	quality: 213.00	length: 700
	ratio: 3.672	gaps: 0
	percent similarity: 82.857	percent identity: 58.571
alignment_block:		
US-09-289-346A-7 x AAT93314		..

Align seg 1/1 to: AAT93314 from: 1 to: 1183

[illegible]

```
seq_name: /cynl_8/gcgdata/geneseq/geneseqn/NA1997.DAT:AAT93290
```

```
seq_documentation_block:
ID    AAT93290 standard; DNA; 1183 BP.
```

AC	AAT933290;
XX	
DT	27-APR-1998 (first entry)
XX	
DE	Bean golden mosaic geminivirus C1 mutant gene

```
alignment_scores:      Length: 70
      Quality:      213.00
      Ratio:      3.672
      Gaps:      0
Percent Similarity: 82.857
Percent Identity: 58.571
```

```
alignment_block:
US-09-289-346A-7 x AAT93290
```

Align seg 1/1 to: AAT93290 from: 1 to: 1183

1 ThrLeuValTPGlyYGIuPhcGlnValAspLysArgSerAlaArgLysL 17
 |||||
 328 ACAATTCGAATGGGCAATTCCAATGCCAGCGGCAATCTCGCAAGAGGAGG 377
 |||||
 17 yCystGlnThrSerAsnAspAlaAlaIaGluAlaLeuAsnAlaSerSerL 34
 | |||||
 378 TCAGCAGCTTGGCAACGACCTATTCGCAAGGCCATTAAACCGAATTCAA 427
 |||||
 34 ySGLGluAlaLeuLuuLleIleArgGluLysIleProGluLysTyrLeu 50
 |||||
 428 TTGAATCTGCCCTTGGACATATTGGAAGGAGAACACCCGAAAGATTACGTC 477
 |||||
 51 PhcGlnPhcHisAsnLeuAsnSerAlaLeuAlaIaIlePhcAspLysTh 67


```

      ::::: |||||::: |||
478 CTTCAACATCACACATCCGTTCTATCTCGAACGATCTCGTCAAGT 527
      67 rProGUpro 70
      528 GCCGGAACCA 537
seq_name: /cgnl_8/gcgdata/geneseg/geneseg/NA2000.DAT:AAA94700
seq_documentation_block:
ID   AAA94700 standard; DNA; 1651 BP.
XX
XX   AAA94700;
AC   15-JAN-2001 (first entry)
DT
XX   15-JAN-2001 (first entry)
DE   pWRG 2288 35S-rep gene cassette.
XX
XX   Geminivirus; DNA-A; geminivirus replication inhibition; ac3 gene;
KW   transgenic plant; antiviral; gene therapy; bean golden mosaic virus;
KW   BGWV; alfalfa mosaic virus; AMV; cauliflower mosaic virus; CaMV; ds.
XX
XX   Bean golden mosaic virus.
OS   Cauliflower mosaic virus.
OS   Alfalfa mosaic virus.
OS   Synthetic.
XX
XX   US6118048-A.
PD   12-SEP-2000.
XX
XX   24-APR-1998; 98US-0065999.
XX
XX   25-APR-1997; 97US-0044925.
XX
XX   (WISC ) WISCONSIN ALUMNI RES FOUND.
PA
XX   WPI; 2000-610861/58.
DR
XX   Genetic construct comprising a mutant geminiviral rep gene, useful for
PT   producing a plant resistant to geminiviral infection -
XX
XX   Example: Column 15-16; 14pp; English.
PS
XX   The present sequence is a 35S-rep gene cassette comprising the rep gene
CC   of bean golden mosaic virus (BGWV)-GA cloned downstream of the CaMV
CC   35S promoter and an alfalfa mosaic virus (AMV) leader sequence. The
CC   sequence was integrated into pBSII-KS+ to produce a rep gene expression
CC   vector. DNA-nicking domain mutations may be incorporated into rep gene
CC   of geminiviral replication. When expressed in a plant cell, this
CC   inhibitor is able to dramatically reduce replication of geminivirus.
CC   Genetic constructs that include sequences containing a portion of the
CC   ac3 gene in addition to the trans-dominant inhibitor exhibit increased
CC   efficiency and broadened specificity of inhibition of geminiviral
CC   replication. Geminiviruses are one of the greatest constraints on
CC   production of important crops, including cassava, beans, cowpeas,
CC   peppers, tomatoes and cotton. The effects of the virus can be overcome
CC   by using the genetic construct.
XX
XX   Sequence 1651 BP; 517 A; 393 C; 342 G; 399 T; 0 other:
SO

```

```

1 ThrLeuValTrpGlyLupheGlnValAspGlyArgSerAlaArgGlyc1 17
::: |||||::: |||
796 ACAATGCAATGGGACAAATTCGAAGTCGACGACATCTCGCAAGAGAG 845
17 yCysGlnThrSerAsnAspAlaAlaAagUaLalaLeuAsnAlaSerSert 34
::: |||||::: |||
846 TCAGCAGCTCGCCACACGACATCATATGCAAAAGCATTAACGACGATCAA 895
34 ysgLugLualaleuGlnIlelleArgGlnLysIleProGluLysTyrLeu 50
::: |||||::: |||
896 TTGAATCTGCTTGACAAATATGTGAAGAACACACCAAGGATTTACGTC 945
51 PheGlnPheHisAsnLeuAsnSerAlaLeuAlaAlaIlePheAspLysTyr 67
::: |||||::: |||
946 CTTCAACATCACACATCCGTTCTATCTCGAACGATCTCGTCAAGT 995
67 rProGUpro 70
::: |||||::: |||
996 GCCGGAACCA 1005
seq_name: /cgnl_8/gcgdata/geneseg/geneseg/NA2000.DAT:AAA94701
seq_documentation_block:
ID   AAA94701 standard; DNA; 1651 BP.
XX
XX   AAA94701;
AC   15-JAN-2001 (first entry)
DT
XX   15-JAN-2001 (first entry)
DE   pTrepn nucleotide sequence.
XX
XX   Geminivirus; DNA-A; geminivirus replication inhibition; ac3 gene;
KW   transgenic plant; antiviral; gene therapy; bean golden mosaic virus;
KW   BGWV; alfalfa mosaic virus; AMV; cauliflower mosaic virus; CaMV; ds.
XX
XX   Bean golden mosaic virus.
OS   Cauliflower mosaic virus.
OS   Alfalfa mosaic virus.
OS   Synthetic.
XX
XX   US6118048-A.
PD   12-SEP-2000.
XX
XX   24-APR-1998; 98US-0065999.
XX
XX   25-APR-1997; 97US-0044925.
XX
XX   (WISC ) WISCONSIN ALUMNI RES FOUND.
PA
XX   WPI; 2000-610861/58.
DR
XX   Genetic construct comprising a mutant geminiviral rep gene, useful for
PT   producing a plant resistant to geminiviral infection -
XX
XX   Example: Column 17-18; 14pp; English.
PS
XX   The present sequence is pTrepn, a vector containing a CaMV-35S
CC   promoter-driven rep gene derived from bean golden mosaic virus (BGWV)-GA.
CC   Site-directed mutagenesis was used to engineer an NcoI site in the start
CC   codon of the rep gene to facilitate cloning of DNA-nicking domain
CC   mutants. The resulting genetic constructs act as trans-dominant
CC   inhibitors of geminiviral replication. When expressed in a plant cell,
CC   these inhibitors are able to dramatically reduce replication of
CC   geminivirus. Genetic constructs that include sequences containing a
CC   portion of the ac3 gene in addition to the trans-dominant inhibitor
CC   exhibit increased efficiency and broadened specificity of inhibition of
CC   geminiviral replication. Geminiviruses are one of the greatest
CC   constraints on production of important crops, including cassava, beans,
CC   cowpeas, peppers, tomatoes and cotton. The effects of the virus can be
CC   overcome by using the genetic construct.
XX
XX   Sequence 1651 BP; 517 A; 392 C; 343 G; 399 T; 0 other:
SO

```


mutants in the rep gene may be used as trans-dominant inhibitors of geminiviral replication. When expressed in a plant cell, these inhibitors are able to dramatically reduce replication of geminiviruses. Genetic constructs that include sequences containing a portion of the ac3 gene in addition to the trans-dominant inhibitor exhibit increased efficiency and broadened specificity of inhibition of geminiviral replication. Geminiviruses are one of the greatest constraints on production of important crops, including cassava, beans, cowpeas, peppers, tomatoes and cotton. The effects of the virus can be overcome by using the genetic construct.

SQ Sequence 2072 BP; 661 A; 467 C; 421 G; 523 T; 0 other;

[illegible]

alignment_block:
US-09-289-346A-7 x AAA94702 . .

Align seg 1/1 to: AAA94702 from: 1 to: 2072

1 TheLeuValTrpGlyIuPheGlnValAspGlyArgSerAlaArgIgi 17
 11:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
 796 ACATATGCAATGGGACAAATTCACAGTCCAGCGCAGATTCGAAGAAGNC 84.5
 17 yCysGlnThrSerAsnAspAlaAlaIaGluAlaLeuAsnAAserSerL 34
 11:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
 846 TCAGCGAGTCTGCCCAACGACATCTATATGCAAGACATTAAACCGATTACAA 89.5
 34 yGluIuAlaIuLeuGlnIleIleArgGlyLysIleProGluLysTyrLeu 50
 11:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
 896 TTGAATCTCTGCTTGACAAATATTGAAGAAGAACCAACGAAAGATTACGTC 94.5
 51 PheGlnPheHisAsnIuLeuAsnSerAlaLeuAlaAlaIlePheAspLysTh 67
 11:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
 946 CTTCACACATCACACACATCGCTTCATATTCGAAGCAGATCTTCGTCANAGT 99.5
 67 rProGluPro 70
 11:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
 996 GCCGGAACCA 100.5

seq_name: /cgn1_8/gcgdata/geneseq/geneseqn/NA1998.DAT:AAV29761

seq_documentation_block:

ID AAV29761 standard; DNA; 2766 BP.

AC AAV29761;

DT 11-AUG-1998 (first entry)

DE Tobacco leaf curling virus gene.

KW Tobacco leaf curling virus gene; TLCV; promoter; ds.

OS Tobacco leaf curling virus.

PN JP10070982-A.

PD 17-MAR-1998.

PF 30-AUG-1996; 96JP-0230394.

PR 30-AUG-1996; 96JP-0230394.

PA (NORQ) NORINSUISANSHO KYUSHU NOGYO SHIKENJYO

DR WPI; 1998-233630/21.

PT Tobacco leaf curling virus gene - useful for inserting into vectors
PT for expression in, e.g. tomato plants

XX	
PS	Claim 1; Figs 1-3; 9pp; Japanese.

CC This sequence represents the tobacco leaf curling virus (TLCV) gene ob
CC the Invention. TLCV gene or its promoter can be inserted into a vector
CC for expression in plants, e.g. tobacco and tomato. This sequence is
CC believed to encode the TLCV proteins shown in AAM56493-W56498.

SQ Sequence 2766 BP; 722 A; 576 C; 609 G; 859 T; 0 other;

[illegible]

```
alignment_block:
US-09-289-346A-7 x AAV29761/rev ..
```

Align seg 1/1 to reverse of: AAV29761 from: 1 to: 2766

[illegible]

seq_name: /cgn1_8/gcgdata/geneseq/geneseqn/NA1996.DAT:AAT12904

```
seq_documentation_block:
```

XX

XX

XX

XX

KW modification; viral replication; deficient; inhibition; mutation;

KW Sardinian isolate; STYLCV; transgenic plant; P-loop; C1 gene;

XX

XX

FT	CDS	1.1080
----	-----	--------

FT /product= Rep_(K227A)

at position 227, i.e. within the NTP-

XX WO9608573-A1.
PN

```

XX 21-MAR-1996.
PD
XX 15-SEP-1995; 95WO-FR01192.
XX PF
XX 15-SEP-1994; 94FR-0011040.
XX PR
XX (CNRS ) CENT NAT RECH SCI.
XX PA
XX Gronenborn B;
XX PI
XX WPI: 1996-179947/18.
XX DR P-PSDB; AAR88870.
XX
XX Prodn. of virus-resistant transgenic plants - using mutated genomic
XX sequence from phytopathogenic DNA virus
XX
XX PS Disclosure: Fig 13; 93p; French.
XX
XX Mutation of consensus amino acids in the NTP-binding site of
XX geminivirus Rep protein is used to produce replication deficient
XX viruses. The mutated viral nucleic acid is used for producing
XX transgenic plants that are resistant to, or tolerant of, the native
XX virus. The present sequence encodes a mutant form of the Rep (or C1)
XX protein from the Sardinian isolate of tomato yellow leaf curl virus
XX (STYLVCV) in which the wild-type lys227 residue has been changed to an
XX Ala residue; transgenic Nicotiana benthamiana plants generated by
XX transformation with the mutated virus were found to be resistant to
XX STYLVCV, i.e the mutation results in a dominant negative phenotype.
XX
XX SQ Sequence 1080 BP; 355 A; 248 C; 210 G; 267 T; 0 other;

```

```

alignment_scores:
  Quality: 211.00      Length: 69
  Ratio: 3.768        Gaps: 0
  Percent Similarity: 81.159   Percent Identity: 56.522

```

```

alignment_block:
US-09-289-346A-7 x AAT12904 ..

```

```

Align seg 1/1 to: AAT12904 from: 1 to: 1080

```

```

2 LeuValTrpGlyGluPheGlnValAspGlyArgSerAlaArgGlyGly 18
   ||| ||||| |||||:||||||| ||||| ||||| |||||
331 CTGGAATGGGGTACTTCCAGATCGACGAGCATCTGCTAGGGAGGACA 380
   |||||ThSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerlySG 35
   |||||:||||||| |||||:||||||| |||||:|||||||
381 ACAACACGACGACGACGCTTACGCAAGCAATTAACGACGAGTAAGT 430
   35 IugIuAlaLeuGlnIleIleArgGluIleProGluIleTyrLeuPhe 51
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||
431 CGCAGGCTCTGTGATTAATTAAGATTAGCGCTAGAGATTACGTTCTA 480
   52 GlnPheHisAsnLeuAsnSerAlaLeuAlaAlaIlePheAspLysThrPr 68
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||
481 CATTCATATATAAATAGTAATTAGTAAGTTTCCAGGTGCCTCC 530
   68 OGluPro 70
   | |||
531 GGCACCT 537

```

OM of: US-09-289-346a-7 to: EST:* out_format : pfs

Date: Jan 3, 2002 6:15 PM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

-MODEL=framer-p2n.model -DEV=xlp
-O=/cgl1_1/USPRO.spool/US09289346/runat_03012002_153303_16354/app_query.fasta.1.1163
-DB=EST -QMT=fastap -SUFFIX=p2n.rst -GAPOP=12.000 -GAPEXT=4.500
-MINMATCH=0.050 -LOOPEXT=0.000 -LOOPEXT=0.000 -GAPOP=4.500
-GAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
-FGAEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELDP=6.000
-DEEXT=7.000 -START=1 -MATRIX=blomsum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIG=200 -THR_SCORE=pcr -THR_MAX=100 -THR_MIN=0
-ALIGN=15 -MODE=LOCAL -OUTEXT=pfs -NORM=ext -MINLEN=0
-MAXLEN=200000000 -USER=US09289346 -ECGN1_1_6788 -NCPU=6
-ICPU=3 -LONGLOG -NO_XLPHY -WAIT -THREADS=1

Search information block:

Query: US-09-289-346a-7

Query length: 70

Database: EST*

Database sequences: 11351937

Database length: 1077921985

Search time (sec): 8697.120000

Score list:

Sequence	Strd Orig	ZScore	Escore	Len	Documentation
gb_gss: A0906722	+	71.00	159.48	412	A0906722 GSSTC03166 Trypanosoma
gb_gss: A0950848	+	69.00	151.79	572	A0950848 Sheared DNA-51M3.TF SH
gb_gss: A0947513	+	69.00	151.76	587	A0947513 Sheared DNA-51M3.TF SH
gb_est1: BE472200	-	69.00	151.78	31.03	BE472200 PSR6111 ITC PSR Wheat
gb_est1: A0707625	-	68.00	151.87	496	A0707625 ah4611.s1 Scores test
gb_est1: BG165174	+	68.00	148.56	629	BG165174 602344034F1 NIH.MGC.89
gb_est1: BF342302	+	68.00	148.32	646	BF342302 602013083F1 NCI.CGAP.10
gb_est1: B1251979	+	68.00	147.90	677	B1251979 602952610F1 NIH.MGC.10
gb_est1: BG720738	+	68.00	147.86	680	BG720738 602691947F1 NIH.MGC.97
gb_est1: BG722387	+	68.00	146.97	751	BG722387 602693588F1 NIH.MGC.97
gb_est1: BG711946	+	68.00	146.75	770	BG711946 602721629F1 NIH.MGC.97
gb_est1: BG723348	+	68.00	146.69	775	BG723348 602694030F1 NIH.MGC.97
gb_est1: BE798529	+	68.00	146.62	781	BE798529 601583248F1 NIH.MGC.7
gb_est1: BE792438	+	68.00	146.47	800	BE792438 601467534F1 NIH.MGC.67
gb_est1: BE304728	+	68.00	146.37	803	BE304728 601106020F1 NIH.MGC.15
gb_est1: BG711437	+	68.00	146.08	829	BG711437 602682658F1 NIH.MGC.95
em_esthum: BG7117534	+	68.00	145.79	857	BG7117534 602698310F1 NIH.MGC.97
gb_est1: B1256931	+	68.00	144.20	1023	B1256931 602975537F1 NIH.MGC.1
gb_hic: B0006308	+	68.00	137.25	2224	B0006308 Homo sapiens, Stimulat
gb_est1: A0883354	+	67.50	152.80	343	A0883354 OH04E07.s1 NCI.CGAP.K1
gb_est1: H37423	+	67.50	149.19	513	H37423 15552 Lambda-PRU2 Arabid
gb_gss: C05042JD	+	67.00	142.48	90.04	AL314338 Tetraodon nigroviridis
gb_gss: A0926150	+	66.50	147.64	468	A0926150 476.d1041h11.s1 Saccha
gb_est1: A0003868	-	66.50	146.39	538	A0003868 m079a08.r1 Soares mous
gb_est1: BF506184	+	66.50	143.24	765	BF506184 AT08588.5prime AT Dros
gb_gss: C0504P82	+	66.50	140.99	983	AL300971 Tetraodon nigroviridis
gb_est1: A1945584	+	66.00	148.50	41.57	A1945584 bs14604.y1 Drosophila
gb_gss: A0003580	+	66.00	147.65	46.36	A0003580 RPCI-23-344P10.TJ RPCI
gb_gss: A0003584	+	66.00	147.33	424	A0003584 RPCI-23-344P11.TJ RPCI
gb_gss: A0003584	+	66.00	145.80	503	BG75828 NXS1_148.D05.F NXS1 (N
gb_gss: C05055M	-	66.00	138.79	1101	AL322277 Tetraodon nigroviridis
gb_est1: AV304772	+	65.50	149.00	308	AV304772 AV304772 RIKEN full.16
gb_est1: BF293368	-	65.50	137.34	580	BF293368 WHE2157.B02.D0325 Trif
gb_gss: C0502M27	-	65.50	137.60	1100	AL216520 Tetraodon nigroviridis
gb_gss: C05036J6	+	65.50	137.46	1118	AL230091 Tetraodon nigroviridis
gb_est1: AA729475	+	65.00	147.25	328	AA729475 nx66009.s1 NCI.CGAP.AL
gb_est1: BF488298	+	65.00	145.08	418	BF488298 AT22536.5prime AT Dros
gb_est1: BE583340	+	65.00	140.91	666	BE583340 8-12C-WY Psojaemy Phyt
gb_gss: C0502K02	+	64.50	138.44	877	AL178643 Tetraodon nigroviridis
gb_est1: AW774381	+	64.50	140.24	628	AW774381 EST333532 KV3 Medicag
gb_est1: BE892066	+	64.50	139.85	656	BE892066 601434960F1 NIH.MGC.72

gb_est1: BF502238	-	64.50	138.54	149.25	760	BF502238 AT17906.5prime AT D
gb_gss: A0908538	+	64.00	146.35	54.78	278	A0908538 GSSTC05496 Trypanos
gb_est1: R24811	-	64.00	142.24	92.81	440	R24811 y943f12.r1 Soares inf
gb_gss: A2967502	+	64.00	141.73	99.14	466	A2967502 2M0238403R Mouse 10

seq_name: gb_gss: A0906722

seq_documentation block:

LOCUS A0906722 412 bp DNA 09-JAN-2001
DEFINITION GSSTC03166 Trypanosoma cruzi random genomic library trypanosoma
cruzi genomic clone G40C19, DNA sequence.

ACCESSION A0906722
VERSION A0906722.3 GI:10136203

KEYWORDS GSS
SOURCE Trypanosoma cruzi.
ORGANISM Trypanosoma cruzi
Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma; Schizotrypanum.

REFERENCE 1 (bases 1 to 412)
Aguero, F., Verdun, R., Frasch, A.C.C. and Sanchez, D.O.
A random sequencing approach for the analysis of the trypanosoma
cruzi genome: general structure, large gene and repetitive DNA
families, and gene discovery
Genome Res. 10 (12), 1996-2005 (2000)

JOURNAL MEDLINE
On Sep 14, 2000 this sequence version replaced gi:9377231.
Contact: Sanchez D.O.
Instituto de Investigaciones Biotecnologicas (Univ. Nac. de Gral
San Martin)
Av. Gral Paz entre Albarillos y Constituyentes, INTI edificio 24
CP(1650) San Martin, Prov. de BS AS. Argentina
Tel: 54-11-4580-7255 ext 309
Fax: 54-11-4752-9639

FEATURES
Class: Shotgun.
Seq primer: T7
Location/Qualifiers
1..412
/organism="Trypanosoma cruzi"
/strain="Cl-Brener"
/db_xref="taxon:5693"
/clone_lib="Trypanosoma cruzi random genomic library"
/note="Vector: pBS(-) (Stratagene); T. cruzi DNA was
randomly sheared using a nebulizer and the 1 to 2 Kb range
was gel purified and cloned into the dephosphorylated
HincII site of the vector"

BASE COUNT 113 a 110 c 99 g 90 t

ORIGIN
113 a 110 c 99 g 90 t

alignment_scores:
Quality: 71.00 Length: 52
Ratio: 2.029 Gaps: 1
Percent Similarity: 67.308 Percent Identity: 36.538

alignment_block:
US-09-289-346a-7 x A0906722 ..

Align seg 1/1 to: A0906722 from: 1 to: 412

8 GlnValAspGlyArgSerAlaArgGlyGlyCysGlnPrsAsnAspAl 24
: ::::::::::::::::::::

218 AGAGCGAGTGCGTACCGACAGAGCGCGCTATCTACGATTCAGCGC 267
: ::::::::::::::::::::

24 AlaAlaGlnAlaLeuAsnAlaSerLeuGlnGlnAlaLeuGln 40
: ::::::::::::::::::::

268 CCGACCGTGGAGGAGAAATCCACGACGACGACGATTCCTCTCTTA 317
: ::::::::::::::::::::

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41  ILAARGLUYSILPEProGluLysTYrLeuPheGlnPheHisAsnLeuAS 57
   :::::::::::::: :::: ::::: :::::
318  CTTCGAGAGCGCTTCCGCAACAGCTATCTACGTCGCTAGCAATTAA 367
57  nSer 58
   ||||
368  TTCA 371

seq_name: gb_gss:A0950848

seq_documentation_block:
LOCUS      A0950848          572 bp          DNA          27-JAN-2000
DEFINITION Sheared DNA-51M3.TF Sheared DNA Trypanosoma brucei genomic clone
ACCESSION  A0950848.1 GI:6774113
VERSION    A0950848.1 GI:6774113
KEYWORDS   GSS.
SOURCE     Trypanosoma brucei.
ORGANISM   Trypanosoma brucei
            Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE  1 (bases 1 to 572)
AUTHORS   El-Sayed,N., Zhao,S., Zhao,H., Gill,S., Suh,E., Malek,J., Fujii,C.,
            Gerrard,C., Leech,V., de Jong,P., Ullu,E., Melville,S., Donelson,J.,
            Fraser,C. and Adams,M.
            Determination of clone end sequences from Trypanosoma brucei GUTat
            10.1 sheared DNA library
            Unpublished (1999)
JOURNAL    Other_GSSs: Sheared DNA-51M3.TF
COMMENT    Contact: Najib M. El-Sayed
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: nelsayed@tigr.org
            Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared
            DNA library constructed at TIGR. Clones will be available for
            distribution through ATCC. Sheared DNA end sequences search page:
            http://www.tigr.org/cdb/mdb/tbdb/.
            Seq primer: M13-Forward
            Class: Shotgun.

FEATURES
    source             1..572
                        Location/Qualifiers
                        /organism="Trypanosoma brucei"
                        /strain="TREU927/4 GUTat 10.1"
                        /db_xref="taxon:5691"
                        /clone="Sheared DNA-51M3"
                        /note="Vector: pUC18; Site.1: SmaI; Constructed at The
                        Institute for Genomic Research (TIGR), Rockville, MD.
                        Genomic DNA isolated from a cloned population of
                        Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically
                        sheared to give a tight size distribution (approx 2 kb).
                        The v + i method used for the library construction is
                        described in detail in Smith, H.O. and Venter, J.C.
                        (Making small insert libraries for whole genome shotgun
                        sequencing projects. In Genome Sequencing: A Practical
                        Approach, eds. M. Vaudin and B. Barrell, Oxford University
                        Press, 1999)."

BASE COUNT      115 a      118 c      180 g      159 t
ORIGIN
alignment_scores:
    Quality:      69.00      Length:      84
    Ratio:        1.500      Gaps:        4
    Percent Similarity: 54.762      Percent Identity: 27.381

alignment_block:
US-09-289-346A-7 x A0950848

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Align seg 1/1 to: A0950848 from: 1 to: 572

11  GLYASerAlaIarGlyGlyGlnThrSerAsnAspAlaIaIaG1 27
   |||
   |||
291  GGTCCTCCGGCATGGCGGTGCGCAACGACAGATGAGGTGATTTGA 340
27  uAlaLeuAsnAlaSerSerLysGlnGlnAlaLeuGlnIlele..... 41
   |||
   |||
341  AGTGTCTCTCGCGGAGACTCTCCGCAACGAGATTACAGTATGTGGGAT 390
42  ....ArgGluLysIlePro.....
   |||
   |||
391  GTGATGGGTGAAGATCCCTTCGCGGATTCATCCGGTGGGTTAAGAC 440
47  .....GluLysTyrLeuPheGlnP 53
   |||
   |||
441  GTGCCGATGCTCTTGGCGGATTTGGAGCTGAGAGAAATTTTCGCCCTA 490
53  eHisAsnLeuAsnSerAlaLeuAlaIaIeAspLysThrProGluP 70
   |||
   |||
491  TTTC...CTTGCAGTCTCTCCGCGAGG...TTTGATCAACCACTTAAC 534
70  ro 70
   ||
535  CG 536

seq_name: gb_gss:A0947513

seq_documentation_block:
LOCUS      A0947513          587 bp          DNA          27-JAN-2000
DEFINITION Sheared DNA-49M17.TF Sheared DNA Trypanosoma brucei genomic clone
ACCESSION  A0947513
VERSION    A0947513.1 GI:6770778
KEYWORDS   GSS.
SOURCE     Trypanosoma brucei.
ORGANISM   Trypanosoma brucei
            Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE  1 (bases 1 to 587)
AUTHORS   El-Sayed,N., Zhao,S., Zhao,H., Gill,S., Suh,E., Malek,J., Fujii,C.,
            Gerrard,C., Leech,V., de Jong,P., Ullu,E., Melville,S., Donelson,J.,
            Fraser,C. and Adams,M.
            Determination of clone end sequences from Trypanosoma brucei GUTat
            10.1 sheared DNA library
            Unpublished (1999)
JOURNAL    Other_GSSs: Sheared DNA-49M17.TF
COMMENT    Contact: Najib M. El-Sayed
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: nelsayed@tigr.org
            Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared
            DNA library constructed at TIGR. Clones will be available for
            distribution through ATCC. Sheared DNA end sequences search page:
            http://www.tigr.org/cdb/mdb/tbdb/.
            Seq primer: M13-Forward
            Class: Shotgun.

FEATURES
    source             1..587
                        Location/Qualifiers
                        /organism="Trypanosoma brucei"
                        /strain="TREU927/4 GUTat 10.1"
                        /db_xref="taxon:5691"
                        /clone="Sheared DNA-49M17"
                        /note="Vector: pUC18; Site.1: SmaI; Constructed at The
                        Institute for Genomic Research (TIGR), Rockville, MD.
                        Genomic DNA isolated from a cloned population of
                        Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically
                        sheared to give a tight size distribution (approx 2 kb).
                        The v + i method used for the library construction is

```



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source
1.496
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_11b="Soares_testis_NHT"
/sex="male"
/lab_host="DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker. Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clonech Laboratories
, Inc., and primed with a Not I - oligo(dT) primer [5'
TGTTCACATCTGAGTGGAGCGCCGCCAATTTTATTTTATTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization to Cots5, and was
constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT      131 a      115 c      139 g      111 t
ORIGIN

alignment_scores:
Quality: 68.50      Length: 68
Ratio: 1.712      Gaps: 1
Percent Similarity: 58.824      Percent Identity: 30.882

alignment_block:
US-09-289-346A-7 x AA707625/rev ..

Align seg 1/1 to reverse of: AA707625 from: 1 to: 496

1 ThrLeuValTrrpGlyIupheGlnValAspQlyArgSerAlaArgGly 17
:::||||| :::::||||| :::::||||| :::::|||||
295 TCTTTAGTGGCTACATTCACAGTGTGCTGTGATGCACACTGGGCGC 246
17 YCysGlnThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerL 34
: ||||||| :::::||||| :::::||||| :::::|||||
245 TTCACAACTGTGAACTCCTGCACTGTGAAAGTGCCACATGCCCTCCC 196
34 YsgIuGluAlaLeuGlnIleLeuArgGlyLysIleProGluLysTyrLeu 50
||||| :::::||||| :::::||||| :::::|||||
195 CAGATCCACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 152
51 PheGlnPheHisAsnLeuAsnSerAlaLeuAlaIlePheAspLysTrh 67
||| ||| ||| :::::||||| :::::||||| :::::|||||
151 ...CAGACCAACCCCTTGAAACCCCAATCTTACTGAGCCTGTGCTGAC 105
67 rPro 68
|||||
104 GCCT 101

seq_name: gb_est2:Bg165174

seq_documentation_block:
LOCUS      Bg165174      629 bp      mRNA      EST      06-FEB-2001
DEFINITION 602344034F1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:4453977 5',
MRNA sequence.
ACCESSION  Bg165174
VERSION    Bg165174.1 GI:12671877
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 629)
AUTHORS   NIH-MGC http://mgi.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
           Email: cgaabs-remail.nih.gov
           Tissue Procurement: ATCC
           cDNA Library Preparation: Life Technologies, Inc.
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

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FEATURES
source
1.629
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_11b="NIH_MGC_89"
/clone_11b="NIH_MGC_89"
/tissue_type="hypertrophoma, cell line"
/note="Organ: kidney; Vector: pCMV-Sport6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH-MGC Library."

BASE COUNT      150 a      186 c      184 g      109 t
ORIGIN

alignment_scores:
Quality: 68.00      Length: 49
Ratio: 2.125      Gaps: 0
Percent Similarity: 65.306      Percent Identity: 32.653

alignment_block:
US-09-289-346A-7 x Bg165174 ..

Align seg 1/1 to: Bg165174 from: 1 to: 629

12 ArgSerAlaArgGlyGlyCysGlnThrSerAsnAspAlaAlaGluAl 28
||||| :::::||||| :::::||||| :::::|||||
123 AGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 172
28 AlaAsnAlaSerSerLysGluGluAlaLeuGlnIleLeuArgGlyLys 45
:::::||||| :::::||||| :::::||||| :::::|||||
173 ATCTCGCGGATCCAGAGACGAGAAACAATATTCAGCGGATTCGAGAGA 222
45 leProGluLysTyrLeuPheGlnPheHisAsnLeuAsnSerAlaLeu 60
||||| :::::||||| :::::||||| :::::|||||
223 AGCTCAACAACAACACTTACCCACCGCCTCTGCTGCTGCTGCTGCTG 269

seq_name: gb_est2:BF342302

seq_documentation_block:
LOCUS      BF342302      646 bp      mRNA      EST      22-NOV-2000
DEFINITION 602013083F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4148757
5', mRNA sequence.
ACCESSION  BF342302
VERSION    BF342302.1 GI:11289259
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 646)
AUTHORS   NIH-MGC http://mgi.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
           Email: cgaabs-remail.nih.gov
           Tissue Procurement: David N. Louis, M.D.
           cDNA Library Preparation: Life Technologies, Inc.
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Incyte Genomics, Inc.
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: ILAM9409 row: f column: 22
           High quality sequence stop: 613.

```



```

FEATURES
SOURCE                                Location/Qualifiers
                                     1..646
      /organism="Homo sapiens"
      /db_xref="taxon:9606"
      /clone="IMAGE:4148757"
      /tissue_type="NCI_CGAP_Brn64"
      /tissue_type="gliblastoma with EGFR amplification"
      /lab_host="DH10B (m1 phage-resistant)"
      /note="Organ: brain; Vector: PCMV-SpOrf6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT
Average insert size 1.57 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT          150 a       158 c       197 g       141 t
ORIGIN

alignment_scores:
    quality:      68.00           Length:      42
    Ratio:        2.345           Gaps:         2
Percent Similarity: 69.048     Percent Identity: 42.857

alignment_block:
US-09-289-346A-7 x BF342302 ..

Align seg 1/1   to: BF342302   from: 1   to: 646

3 valTTpGly...GlupheGlnValaspGlyargSerAlaArgGlyGlyCy 18
||||||| || :||| | |||||:|||||:|||||
202 GTGTGGGGCGTAGAGGACGCTGCTGCTGAGGGAGGCCGCGGGGGATG 251

18 scInthrserAsnApAlaAlaAlaGluAlaLeuAsnAlasrserLySG 35
|::: ::::: ||| ::::: ||| ::::: ||| ::::: |||
252 TGAACTCGGGGAGCGGGGCACCACCAAGGCGTCAAGGGCCCAAAACCTTG 301

35 lucGuaLaLeuglntleileArgGlu 43
|| |||||
302 AA.....ATCGGTGA 312

seq_name: gb_est2:B1251979

seq_documentation_block:
LOCUS             B1251979              mRNA               677 bp            17-JUL-2001
DEFINITION        602952610F1 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:5086779 5' ,
ACCESSION         B1251979
VERSION           B1251979.1 GI:14801989
KEYWORDS          EST .
SOURCE            human.
ORGANISM          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE         1 (bases 1 to 677)
AUTHORS           NIH-MGC http://mgc.ncl.nih.gov/.
TITLE             National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL           Unpublished (1999)
COMMENT           Contact: Robert Strausberg, Ph.D.
                  Email: cgabs@email.nih.gov
                  Tissue Procurement: CGAP (Stanford)
                  CDNA Library Preparation: Ling Hong/Rubin Laboratory
                  DNA Sequencing by: Incyte Genomics, Inc.
                  Clone distribution: MGC clone distribution information can be
                  found through the I.M.A.G.E. Consortium/LNL at:
                  http://image.jnl.gov
                  Plate: LECM1843 row: c column: 04
                  High quality sequence stop: 676.
                  Location/Qualifiers
                    1..677
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:5086779"
                      /clone_ltb="NIH_MGC_100"
                      /tissue_type="hepatocellular carcinoma, cell line"

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/!db_host="Dhl0B (phage-resistant)"
/note="Organ: Liver; Vector: pORF7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACAGCAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: This is a NIH-MGC library."
BASE COUNT      162 a       197 c       198 g       120 t
ORIGIN
Alignment_scores:
    Quality:     68.00      Length:      49
    Ratio:        2.125      Gaps:         0
Percent Similarity: 65.306   Percent Identity: 32.653
alignment_block:
US-09-289-346A-7 x BI251979 ..
Align seg 1/1 to: BI251979 from: 1 to: 677
12 ATGSEATAAATgGlyGlyCysGlnThrSerAsnApAlaAlaGluAl 28
|||||:::|||| ::|||:::||||| ::::
127 AGCAACGCCCGCCGCCCTGTCCAAAACAATGATTCACACTGACGA 176
28 ALeuASnAlaSerSerLysGLuGLuAlaLeuGlnlIleLeArgGluYSI 45
|||||:::|||||:::|||||::: ||| |||||:::
177 ATCTTCGGGATCCAAGAAGACAGAACAAATATCATGAGGGATTGGGAAGGAGA 226
45 lEprOgiULySfTyRLeuPhenIleGlnPheHisASnLeuASnERAlaLeu 60
|||||:::||||| ::||| ::||| ::|||:::
227 AGCGTCACACACACAACTTCACCACCGCCGCTCGTGCGACGCTGTG 273
seq_name: gb_est2:BG720738
seq_documentation_block:
LOCUS          BG720738           680 bp      mRNA                      EST              08-MAY-2001
DEFINITION     BG2691947FL NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4824371 5', mRNA sequence.
ACCESSION      BG720738
VERSION        BG720738.1 GI:13999925
KEYWORDS       EST.
SOURCE         human.
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE      1 (bases 1 to 680)
AUTHORS       NIH-MGC http://mgc.ncl.nih.gov/.
JOURNAL       National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT       Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: rgapds@remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiroaki Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM10735 row: m column: 12
High quality sequence stop: 675.
Location/Qualifiers
1 . 680
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4824371"
/cbone.lib="NIH_MGC_97"
/lab_host="DHL0B"
/note="Organ: testis; Vector: pBluescriptR (modified

```


for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIH/NHGRI, National
Institutes of Health). Note: this is a NIH-MGC Library."

BASE COUNT 184 a 227 c 223 g 135 t 1 others
ORIGIN

alignment_scores:
Quality: 68.00 Length: 49
Ratio: 2.125 Gaps: 0
Percent Similarity: 65.306 Percent Identity: 32.653

alignment_block:
US-09-289-346a-7 x BG771946 ..

Align seg 1/1 to: BG771946 from: 1 to: 770

12 ArgSerAlaArgGlyGlyCysGlnThrSerAsnAspAlaAlaGluAl 28
|||||:||||| :|||:||||| :|||:
168 AGGAGCGGGCGGGCCGCTGCCAAAAGCAATGATTTCCACCTGACAA 217
28 aleuAsnAlaSerSerLySGluGluAlaLeuGlnIleIleArgGluLysI 45
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
218 ATCTTCGGATCCAGACAGACAGAAATATCAGCGGATTCGAGAGAGA 267
45 leProGluLysTyrlLeuPheGlnPheHisAsnLeuAsnSerAlaLeu 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
268 AGCCTCAGACACACTTCACCCACCGCTCCTGGCTGAGCTCTG 314

seq_name: gb_est2:BG723348

seq_documentation_block: 775 bp mRNA EST 08-MAY-2001
LOCUS BG723348
DEFINITION 602694003F1 NIH-MGC_97 Homo sapiens cDNA clone IMAGE:4826113 5',
mRNA sequence.
ACCESSION BG723348
VERSION BG723348.1 GI:14002535
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 775)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: Miklos Palokovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

Plate: LHAM10740 row: f column: 02
High quality sequence stop: 762.
Location/Qualifiers

FEATURES

source 1..775
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/db_xref="taxon:9606"
/clone="IMAGE:4826113"
/clone_id="NIH-MGC_97"
/lab_host="DH10B"
/note="Organ: testis; Vector: pBluescriptR (modified
pBluescript KS+); Site1: BamHI; Site2: SalI-XhoI (gtgag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTTVN-3',
size-selected for average insert size 2.2 kb and
normalized to R0T 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library

constructed by M. Brownstein (NIH/NHGRI, National
Institutes of Health). Note: this is a NIH-MGC Library."

BASE COUNT 180 a 231 c 230 g 134 t
ORIGIN

alignment_scores:
Quality: 68.00 Length: 49
Ratio: 2.125 Gaps: 0
Percent Similarity: 65.306 Percent Identity: 32.653

alignment_block:
US-09-289-346a-7 x BG723348 ..

Align seg 1/1 to: BG723348 from: 1 to: 775

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|||||:||||| :|||:||||| :|||:
191 AGGAGCGGGCGGGCCGCTGCCAAAAGCAATGATTTCCACCTGACAA 240
28 aleuAsnAlaSerSerLySGluGluAlaLeuGlnIleIleArgGluLysI 45
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
241 ATCTTCGGATCCAGACAGACAGAAATATCAGCGGATTCGAGAGAGA 290
45 leProGluLysTyrlLeuPheGlnPheHisAsnLeuAsnSerAlaLeu 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
291 AGCCTCAGACACACTTCACCCACCGCTCCTGGCTGAGCTCTG 337

seq_name: gb_est2:BE798529

seq_documentation_block: 781 bp mRNA EST 20-SEP-2000
LOCUS BE798529
DEFINITION 601583248F1 NIH-MGC_7 Homo sapiens cDNA clone IMAGE:3937787 5',
mRNA sequence.
ACCESSION BE798529
VERSION BE798529.1 GI:10219727
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 781)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: DCTD/DRP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LHCN783 row: p column: 12
High quality sequence stop: 768.
Location/Qualifiers

FEATURES

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/clone_id="NIH-MGC_7"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pOTB7; Site1: XhoI; Site2:
EcoRI; CDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

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BASE COUNT      117 a      263 c      282 g      119 t
ORIGIN

alignment_scores:
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    Ratio:     2.125         Gaps:     0
Percent Similarity: 57.143    Percent Identity: 35.714

alignment_block:
US-09-289-346A-7 x BE798529 ..
Align seg 1/1 to: BE798529 from: 1 to: 781

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31 aserSerLysGLuGLuAlaLeuGLnIleIleArgGIuLySLeProGLu 48
: :::::||::: :: || | |
418 GAGGGGGGTCTGCAGACTGCCCTTCACATTTCCAGAGCTGGAGACC CGGACA 467
48 ysTryrLeuPheGLInPheHisAsnLeuAsnSerAsnLeuAlaAlaIlePhe 64
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468 GTTGCGTCTCCCTTCAGCTCTCACTGCTCAACACAGCGCGCGCGGGCGGCA 517
65 AsplyStThrProGLuPro 70
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518 CATCCAGACGCCGCGCGCG 535

seq_name: qb_est1:BE782438

seq documentation block:
LOCUS       BE782438             800 bp            mRNA           EST           20-OCT-2000
DEFINITION  60146755471 NIH_MGC_67 Homo sapiens CDNA clone IMAGE:3870853 5',
            mRNA sequence.
ACCESSION   BE782438
VERSION     BE782438.1 GI:10203636
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE   1 (bases 1 to 800)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: rs9apbs@email.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Life Technologies, Inc.
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LNL at:
            http://image.llnl.gov
            Plate: LMA9632 row: k column: 14
            High quality sequence stop: 687.
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                /clone="IMAGE:3870853"
                /clone_lib="NIH_MGC_67"
                /tissue_type="retinoblastoma"
                /lab_host="DH10B (phage-resistant)"
                /note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
                Site_2: SalI; Cloned unidirectionally. Primer: oligo dr.
                Average insert size 1.75 kb. Library constructed by Life
                Technologies."
BASE COUNT      193 a      224 c      233 g      150 t
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alignment_scores:
  Quality: 68.00      Length: 49
  Ratio: 2.125      Gaps: 0
  Percent Similarity: 65.306      Percent Identity: 32.653

alignment_block:
  US-09-289-346A-7 x BE782438 ..

Align seg 1/1 to: BE782438 from: 1 to: 800

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107 AGAGAGGGGGGGCCCGCCCTGCCAAAAACCAATGATTTCACCTGCACAA 156
28 aleuAsnAlaSerIysrIysGlnGluAlaLeuGlnIleIleArgGluLysI 45
157 ATCTTCGGGATCTCAAGACGAAACAATATCATCGAGGATTCGGGAAGAGA 206
45 leProGluLysrIysrLeuPheGlnPheHisAsnLeuAsnSerAlaLeu 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
207 ACCCTCAACACACACACTTCACCCACCCGCCCTCGGCTGACGACTCTG 253

seq_name: gb_est1:BE304728

seq_documentation_block:
LOCUS BE304728 803 bp mRNA EST 13-JUL-2000
DEFINITION 601106020F1 NIH_MGC_15 Homo sapiens CDNA clone IMAGE:3349227 5',
mRNA sequence.
ACCESSION BE304728
VERSION BE304728.1 GI:9176165
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 803)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapds@mail.nih.gov
Tissue Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMNL at: Image.lnl.gov
Plate: ILGM43 row: 9 column: 06
High quality sequence start: 31
High quality sequence stop: 690.
Location/Qualifiers
1..803
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/db_xref="taxon:9606"
/clone="IMAGE:3349277"
/clone_lib="NIH_MGC_15"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: colon; Vector: pOTB7; Site_1: XhoI; Site_2
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"
BASE COUNT 190 a 227 c 241 g 145 t
ORIGIN

alignment_scores:
  Quality: 68.00      Length: 49
  Ratio: 2.125      Gaps: 0
  Percent Similarity: 65.306      Percent Identity: 32.653

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Ratio: 2.125 Gaps: 0
Percent Similarity: 65.306 Percent Identity: 32.653

alignment_block:
US-09-289-346a-7 x BE304728 ..

Align seg 1/1 to: BE304728 from: 1 to: 803

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144 AGGAGCGCGCGCCGCTGCCAAAAAGCAAAATGATTTCCACCTGACAA 193
   :::::||||:::||||:::|||||:::
28 aLeuAsnAlaSerSerLysGluGluAlaLeuGlnIleIleArgGluLysI 45
   :::::||||:::||||:::|||||:::
194 ATCTTCGGGATCCAGAGAGCAACAATATTCAGCGGATTTCGAGAGGAGA 243
   :::::||||:::||||:::|||||:::
45 leProGluLysTyrLeuPheGlnPheHisAsnLeuAsnSerAlaLeu 60
   ||:::||||:::||||:::|||||:::
244 AGCCTCAACACACAACTTCACCCACCGCCTCTGGGCTGCAGGCTCTG 290

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2216 AGCTAATGATCTGCCCCAGAGCCCTTAATGACGTTTCACCTGACAG 2167
37 1aleugl1le1learglulys1leproglulys1tyrleuphag1phe 53
||||| ||||||||| ||||||| ||||||| ||||||| |||||||
2166 CTTAGCAATTAATTAGGAAGAACTCCCTAAGATTATTTATTTCAATAT 2117
54 H1sAnleuAsnSerAlaLeuAla1le1lephAsp1ys1ThrPro 68
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2116 CATAAATTAATAATGTAATTTAGATGATTTT.....ACACCT 2078

seq_name: /cgul_7/ptodata/1/ina/6B_COMB.seq:US-08-838-151A-48

seq_documentation_block:
; Sequence 48, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Gemlinivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1062 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bean Golden Mosaic Gemlinivirus
; STRAIN: Type II
; INDIVIDUAL ISOLATE: Guatemala
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1059
; US-08-838-151A-48

alignment_scores:
Quality: 213.00 Length: 70
Ratio: 3.672 Gaps: 0
Percent Similarity: 82.857 Percent Identity: 58.571

alignment_block:
US-09-289-346a-7 x US-08-838-151A-48

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Align seg 1/1 to: US-08-838-151A-48 from: 1 to: 1062

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328 ACAATCGAATGGGCAATTCGACGCGAGATCTGCAAGAGAGG 377
17 YCysGln1ThrSer1Asn1Ser1Ala1Leu1Ala1Glu1Ala1Leu1Asn1Asp1Ser1 34
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
378 TCACAGCTCTGCCACAGCATCATGCAAGGCAATTAAAGCGACATTCAA 427
428 TTCAATCTGCCCTTGCATATTGCAAGCAAGCAACCGAAAGATTACGTC 477
34 YsGlu1Glu1Ala1Leu1Gln1le1learglulys1leproglulys1tyrleu 50
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
478 CTTCAACATGCACACATCCGTTCTAATCTGCACGATCTTCGTCAAAGT 527
67 rProGluPro 70
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528 GCCGGAACCA 537

seq_name: /cgul_7/ptodata/1/ina/6B_COMB.seq:US-08-838-151A-51

seq_documentation_block:
; Sequence 51, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Gemlinivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1062 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bean Golden Mosaic Gemlinivirus
; STRAIN: Type II
; INDIVIDUAL ISOLATE: Guatemala

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?     TYPE: nucleic acid
?     STRANDEDNESS: single
?     TOPOLOGY: circular
?     MOLECULE TYPE: DNA (genomic)
?     HYPOTHEetical: NO
?     ANTI-SENSE: NO
?     ORIGINAL SOURCE:
? ORGANISM: Bean Golden Mosaic Geminiivirus
? STRAIN: Type II
? INDIVIDUAL ISOLATE: Guatemala
? FEATURE:
?     NAME/KEY: CDS
?     LOCATION: 1..1059
? US-08-838-151A-54

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?     Ratio: 3.672        Gaps: 0
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? 328 ACATGTCGATGGGGACATTCCTCAAGTCGACGGCGCATTCGACAGGAGG 377
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?   | |||:::|||||::: |||:::|||||:::|||||:::|||||:::
? 378 TCAGCAGCTGCGCACGACGTCATATGCAAGCATTTAAACGACGATCCA 427
? 34 yScGlutAlaLeuGlnIleIleArgGlnLysIleProGluLysTrleu 50
?   |||:::||||| |||:::|||||::: |||::: |||::: |||:::
? 428 TGCAAATCGCTTCACATATATTGGAAGGAAGAACCAACGAAAGATTACGTC 477
? 51 PheGlnPheHisnLeuAsnSerAlaLeuAlaAlaIlePheAspLysTh 67
?   ::||| |||||:::||||| ||| ||| ||||| |||:::
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?   ::||| |||||
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?   Patent No. 6291743
?   GENERAL INFORMATION:
?     APPLICANT: Stout, John T
?     APPLICANT: Luu, Hang T
?     APPLICANT: Maxwell, Douglas
?     APPLICANT: Ahlquist, Paul
?     APPLICANT: Hanson, Steve
?     TITLE OF INVENTION: Transgenic Plants Expressing Geminiiviruses
?     NUMBER OF SEQUENCES: 63
?     CORRESPONDENCE ADDRESS:
?     ADDRESSEE: Dressler, Rocky, Milnamow & Katz
?     STREET: Two Prudential Plaza, Suite 4700
?     CITY: Chicago
?     STATE: Illinois
?     COUNTRY: U.S.A.
?     ZIP: 60601
? COMPUTER READABLE FORM:
?     MEDIUM TYPE: Floppy disk
?     COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 1183 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bean Golden Mosaic Geminivirus
STRAIN: Type II Isolates
INDIVIDUAL ISOLATE: Guatemala
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1059
PUBLICATION INFORMATION:
AUTHORS: Faria, JC
AUTHORS: Gilbertson, RL
AUTHORS: Hanson, SP
AUTHORS: Morales, FJ
AUTHORS: Ahlquist, P
AUTHORS: Lomello, AO
AUTHORS: Maxwell, D
TITLE: Bean Golden Mosaic Geminivirus Type II
TITLE: Isolates from the Dominican Republic and
TITLE: Guatemala: Nucleotide Sequences, Infectious
TITLE: Pseudorecombinants, and Phylogenetic Relationships
JOURNAL: Phytopathology
VOLUME: 84
ISSUE: 3
PAGES: 321-329
DATE: 1994
US-08-838-151A-43

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alignment_scores:

Quality	213.00	Length	70
Ratio	3.672	Gaps	0
Percent Similarity	82.857	Percent Identity	58.571

alignment_block:

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US-09-289-346a-7 x US-08-838-151A-43
Align seg 1/1 to: US-08-838-151A-43 from: 1 to: 1183

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34 yscGluAlaLeuGlnIleLeuArgGluLysIleProGluLysTyLeu 50
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428 TTGAATCTGCTTGCACATATTGAAGAGACACACCAAGATTACGTC 477
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; Sequence 45, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Dressler, Rockey, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1183 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bean Golden Mosaic Geminivirus
; STRAIN: Type II
; INDIVIDUAL ISOLATE: Guatemala
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1059
; US-08-838-151A-45

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alignment_scores:

Quality	213.00	Length	70
Ratio	3.672	Gaps	0
Percent Similarity	82.857	Percent Identity	58.571

alignment_block:

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US-09-289-346a-7 x US-08-838-151A-45
Align seg 1/1 to: US-08-838-151A-45 from: 1 to: 1183

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Align seg 1/1 to: US-09-065-999-7 from: 1 to: 2072

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1  ThleuValTrpGlyGluPheGlnValAspGlyArgSerIleArgGly 17
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796 ACATGCAATGGGACATTCGACGAGCGAGATCTCCAGAGAGG 845
17  yCysGlnThrSerAsnAspAlaIleAlaGluAlaLeuAsnAlaSerSer 34
   | |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
846 TCAGCGATCTGCCACGACTCATATGCAAGGCAATTAACCGCATTTCA 895
34  ySclGluAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeu 50
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
896 TTGATGCTGCTTGACATATTTGAGAGAACACCGCAAGATTACGTC 945
51  PheGlnPheHisAsnLeuAsnSerAlaLeuAlaIlePheAspLysThr 67
   :||| |||:|||||:|||||:|||||:|||||:|||||:|||||
946 CTTCACATCTCAACATCCCTCTTAATCTCGAACGATCTTCGTCAAAGT 995
67  rProGluPro 70
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seq_name: /cgn1_7/ptodata/1/ina/6A.COMB.seq:US-08-809-103B-7

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; seq_documentation_block:
; Sequence 7, Application US/08809103B
; Patent No. 6133505
;
; GENERAL INFORMATION:
; APPLICANT: GROENENBORN, Bruno
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809.103B
; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 800
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94.11040
; FILING DATE: 15-SEP-1994
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR95/01192
; FILING DATE: 15-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 685-0573
; TELEX: 248425 EMBON
;
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1145 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1077

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US-08-809-103B-7

alignment_scores:	Quality:	211.00	Length:	69
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Percent Similarity:	81.159		Percent Identity:	56.522

alignment_block:

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331 CTGGAATGGGGTACTTCCAGATCGACGAGCATCTGCTTAGGGGAGACA 380
18  sGlnThrSerAsnAspAlaIleAlaGluAlaLeuAsnAlaSerLysG 35
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
381 ACAGACAGCCACGACGCTTAGCGAAGGCAATTAAACCGCAAGTAAGT 430
35  lGluAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeuPhe 51
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
431 CGCAGCGCTTGATGATTAATTAAGAAATTAGCCGCTAGAGATTAAGTCTA 480
52  GlnPheHisAsnLeuAsnSerAlaLeuAlaIlePheAspLysThr 68
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
481 CATTTCATATATTAATTAAGTAATTAAGTAAGGATTTCCAGGTGCTC 530
68  oGluPro 70
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531 GGCACCT 537

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seq_name: /cgn1_7/ptodata/1/ina/6A.COMB.seq:US-08-809-103B-1

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; seq_documentation_block:
; Sequence 1, Application US/08809103B
; Patent No. 6133505
;
; GENERAL INFORMATION:
; APPLICANT: GROENENBORN, Bruno
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809.103B
; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 800
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94.11040
; FILING DATE: 15-SEP-1994
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR95/01192
; FILING DATE: 15-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 685-0573
; TELEX: 248425 EMBON

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; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1148 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1077
; US-08-809-103B-1

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alignment_scores:
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alignment_block:
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Align seg 1/1 to: US-08-809-103B-1 from: 1 to: 1148

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18 sGlnThSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerIysG 35
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
381 ACAGACGACGACGACGCTTACGCAAGGCAATTACGCAAGGATGACT 430
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
35 LuGuaLaLeuGlnIleIleArgGluIleProGluIleTyrLeuPhe 51
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
431 CGCAGGCTCTTGATGATTAATAAGATTACGCTAGAGATTACGTTCTA 480
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
52 GlnPheHisAsnLeuAsnSerAlaLeuAlaIlePheAspIleThrPr 68
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
481 CATTTTCATATATATAATAGTAATTGATTAAGCTTTTCCAGGTGCTCC 530
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68 oGluPro 70
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531 GGCACCT 537

seq_name: /cgn1_7/plodata/1/lna/6A_COMB.seq:US-08-809-103B-3

seq_documentation_block:
; Sequence 3, Application US/08809103B
; Patent No. 6133505
; GENERAL INFORMATION:
; APPLICANT: GROENBORN, Bruno
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809/103B
; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94.11040
; FILING DATE: 15-SEP-1994
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: WO PCT/FR95/01192
; FILING DATE: 15-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 685-0573
; TELEX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1150 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1077
; US-08-809-103B-3

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alignment_scores:
    Quality: 211.00      Length: 69
    Ratio: 3.768         Gaps: 0
    Percent Similarity: 81.159   Percent Identity: 56.522

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alignment_block:
US-09-289-346A-7 x US-08-809-103B-3 ..

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Align seg 1/1 to: US-08-809-103B-3 from: 1 to: 1150

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331 CTTGAATGGCGTACTTCCAGATCGACGACGATCTGCTAGGAGAGACA 380
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
18 sGlnThSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerIysG 35
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
381 ACAGACGACGACGACGCTTACGCAAGGCAATTACGCAAGGATGACT 430
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
35 LuGuaLaLeuGlnIleIleArgGluIleProGluIleTyrLeuPhe 51
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
431 CGCAGGCTCTTGATGATTAATAAGATTACGCTAGAGATTACGTTCTA 480
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
52 GlnPheHisAsnLeuAsnSerAlaLeuAlaIlePheAspIleThrPr 68
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
481 CATTTTCATATATATAATAGTAATTGATTAAGCTTTTCCAGGTGCTCC 530
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
68 oGluPro 70
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531 GGCACCT 537

seq_name: /cgn1_7/plodata/1/lna/6A_COMB.seq:US-08-809-103B-5

seq_documentation_block:
; Sequence 5, Application US/08809103B
; Patent No. 6133505
; GENERAL INFORMATION:
; APPLICANT: GROENBORN, Bruno
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809/103B
; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94.11040
; FILING DATE: 15-SEP-1994
; PRIOR APPLICATION DATA:

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,103B
FILING DATE: 17-MAR-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94.11040
FILING DATE: 15-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR95/01192
FILING DATE: 15-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: PATCH, Andrew J.
REGISTRATION NUMBER: 32,925
REFERENCE/DOCKET NUMBER: US894AL CNR TOM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 521-2297
TELEFAX: (703) 685-0573
TELEX: 248425 EMBON
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1150 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1077
US-08-809-103B-5
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Quality: 211.00      Length: 69
Ratio: 3.768         Gaps: 0
Percent Similarity: 81.159   Percent Identity: 56.522
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Align seg 1/1 to: US-08-809-103B-5 from: 1 to: 1150

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331 CTTGAAATGGGGTACTTCCAGATCGAGCGAGCATCTGCTAGGGGAGGACA 380
18 sglnttrserasnaspalaalalaglualaleuasnalaserserlysg 35
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
381 ACAGACAGCGACGACGCTTACGCAAGCAATTACGCCAGAGTAAGT 430
35 lucualaleuglnlelleatrgglllslleproclulystytleuphe 51
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
431 CGCAGCGCTCTTGATCTAATTAAAGAAATTAGCGCCTAGCATTTACGTTCTA 480
52 GluPheHisAsnLeuAsnSerAlaLeuAlaAlaIlePheAspLysThr 68
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
481 CATTTCATTAATATAATAGTAATTAGATTAAGCTTTTCCAGGTGCTCC 530
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68 ogluPro 70
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531 GGCACCT 537
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; Sequence 1, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Scout, John T
; APPLICANT: Lau, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
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APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Gemlinivirus
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rockey, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1162 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Tomato Mottle Gemlini Virus
INDIVIDUAL ISOLATE: Florida
FEATURE:
NAME/KEY: CDS
LOCATION: 44..1127
PUBLICATION INFORMATION:
AUTHORS: Gilbertson, RL
AUTHORS: Hidayat, SH
AUTHORS: Paplomatas, EJ
AUTHORS: Rojas, MR
AUTHORS: Hou, YM
AUTHORS: Maxwell, DP
TITLE: pseudorecombination between the infectious
TITLE: cloned DNA components of tomato mottle and bean
TITLE: dwarf mosaic gemliniviruses.
JOURNAL: Jour. General Virol.
VOLUME: 74
PAGES: 23-31
DATE: 1993
US-08-838-151A-1
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Ratio: 3.638         Gaps: 0
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Align seg 1/1 to: US-08-838-151A-1 from: 1 to: 1162

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```

17 yCysGlnThrSerAsnAspAlaAlaAlaGluAlaLeuAsnAlaSerSerL 34
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421 CCAGCAGTCTGCTAATCATTCATATCGAAGCGCTAATGCAAGTTCGG 470
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34 ySGLuGluAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeu 50
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471 TTCAAATCTGCTTAGCAGTTCTAAGGAGAGAACCAACCAAGATTGTGA 520
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51 PheGlnPheHisAsnLeuAsnSerAlaLeuAlaAlaIlePheAspLysTh 67
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521 TTACAAATCATTAACATCCGCTTAACCTAGACGAATATTCCGAAGGC 570
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67 rProGluPro 70
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571 TCCGGAACCG 580

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34 ysglguiaaleuaglnlellearglulyslleproglulystytleu 50
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51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArg11IlePheAspLysThr 67
|||||
2121 TTTCAGTTCACCAATCTAATAGCAATTGATAGATATTGATTAAGAC 2072
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67 rProGluPro 70
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seq_name: gb_v1:AY029750
seq_documentation_block:
LOCUS AY029750 2588 bp DNA circular VRL 08-MAY-2001
DEFINITION Tomato severe rugose virus DNA-A, complete sequence.
ACCESSION AY029750
VERSION AY029750.1 GI:14009278
KEYWORDS
SOURCE Tomato severe rugose virus.
ORGANISM Tomato severe rugose virus.
REFERENCE 1 (bases 1 to 2588)
AUTHORS Rezende,W.L., Goulart,L.R., Parreira,K.S. and Figueiredo,J.E.F.
TITLE The full-length DNA-A nucleotide sequence of a novel
JOURNAL tomato-infecting begomovirus, Tomato severe rugose virus, in Brazil
Unpublished
2 (bases 1 to 2588)
AUTHORS Rezende,W.L., Goulart,L.R., Parreira,K.S. and Figueiredo,J.E.F.
TITLE Direct Submission
JOURNAL Submitted (03-APR-2001) Instituto de Genetica e Biolumica,
Universidade Federal de Uberlandia, Av. Amazonas s/n, Bloco 2E,
Sala 24, Campus Umuarama, Uberlandia, Minas Gerais 38.400-000,
Brazil
FEATURES
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/note="segment: DNA-A"
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Ratio: 4.703 Gaps: 0
Percent Similarity: 91.429 Percent Identity: 80.000
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1 ThLeuValTrpGlyAlaIalaIalaSPGlyArgSerAlaArgIyl 17
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2258 ACTATCGAATGGGCGCAATCCAAATCGACGGCAGAAATGCTAGAGCGG 2209
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17 YcysGlnThrSerAsnAspAlaIalaIalaIalaAsnAlaSerSert 34
|||||
2208 TTCCGACAGAGCTACGATGCTCCGACAGAGCTTGAGACGACCTTCA 2159
|||||
34 ysglguiaaleuaglnlellearglulyslleproglulystytleu 50
|||||
2158 AAGAGCGCGCTTGCAAGATATCCGGAGAGCTACCGGAAAAGTTTAA 2109
|||||
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArg11IlePheAspLysThr 67
|||||
2108 TTTCAGTTCACCAATCTAATAGCAATTGATAGATATTGCAAGGCG 2059
|||||
67 rProGluPro 70
|||||
2058 TCCTGAACCA 2049
|||||
seq_name: gb_v1:AF291705
seq_documentation_block:
LOCUS AF291705 2622 bp DNA circular VRL 25-SEP-2000
DEFINITION Tomato rugose mosaic virus DNA-A, complete sequence.
ACCESSION AF291705
VERSION AF291705.1 GI:10281644

```


JOURNAL. Unpublished
REFERENCE 2 (bases 1 to 1193)
AUTHORS Faria,J.C. and Maxwell,D.P.
TITLE Direct Submission
JOURNAL Submitted (08-MAR-1997) Plant Pathology, University of Wisconsin,
1630 Linden Dr, Madison, WI 53706-1598, USA

FEATURES
source
1..1193
/organism="Leonurus mosaic virus"
/strain="Lemv- Brazil 1"
/db_xref="taxon:58177"
complement(1..678)
/gene="rep"
complement(<1..678)
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/note="AC1: replication associated protein"
/codon_start=1
/product="Rep protein"
/protein_id="AAB51157.1"
/db_xref="GI:1916345"
/translation="MPSKPKFRVQAKNIFLTITVQCTLTKEEALSQLOAIOLPSNKKF
IKICRELHDGQPLHLVLDLEGVQITNNKLFVLSTSRSAHPHPNIQAKSSDVAK
SYIDKDDTIVMGFEQVGRSSRGQCTVNDAAEALNAPDKFTALQIIEKILPEKYL
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LIVGGSR"
676..797
/note="origin of replication; common region"
1039..1193
/gene="cp"
/gene="cp"
1039..>1193
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/note="AV1"
/codon_start=1
/product="coat protein"
/protein_id="AAB51158.1"
/db_xref="GI:1916346"
/translation="MPKRDESWRMVWGNSKISRNSNPSRGIGIPKFNKASDWKRPDM
YCSMKRPS"

BASE COUNT 295 a 269 c 276 g 353 t
ORIGIN

alignment_scores:
Quality: 282.00 Length: 70
Ratio: 4.548 Gaps: 0
Percent Similarity: 88.571 Percent Identity: 78.571

alignment_block:
US-09-289-346a-x LMU92532/rev ..

Align seg 1/1 to reverse of: LMU92532 from: 1 to: 1193

1 ThTleuValTtRpCluAlaIaValaIaSPGlyArgSerAlaArgLysCl 17
||||: ||||||| |||||||:|||||||
348 ACAGTGTGATGGGGTGATTCACAGTCGACGGGAGAAAGTTCTAGAGAGAG 299
17 yCysgIntHrSerAsnAspAlaIaIaGluAlaLeuAsnAlaSerSerL 34
1 ||||| ||||||| ||||||| ||||||| |||||
298 CCAACAGACAGTTAATGACGCTGCACGCTGAGCGCTTAATGCTCCAGATA 249
34 yGgLuGlulAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeu 50
||::: ||||||| |||||||:|||||||
248 AACGAACGGCTCTTCAATTAATTAAGGAATAATTCGCCGAGAAATTCYT 199
51 PhGclnPhHtAsnLeuAsnSerAsnLeuAspArgIlePhAspLysTh 67
||||| ||||||| ||||||| ||||||| |||||
198 TTTCATTTCAATTAATTAATTCZATTTTGATAGAAATTCGCANAAGC 149
67 rProGluPro 70
:|||||||
148 TCCGAGACCA 139

seq_name: gb_v1:AF131071

seq documentation block:					
LOCUS	AF131071	1345 bp	DNA	VRL	17-JUN-1999
DEFINITION	Tomato mild mottle geminivirus segment A replication-associated protein (rep) and coat protein (cp) genes, partial cds.				
ACCESSION	AF131071				
VERSION	AF131071.1				
KEYWORDS	GI:4928223				
SOURCE	tomato mild mottle geminivirus.				
ORGANISM	Viruses; ssDNA viruses; Geminiviridae; Unclassified Geminiviridae.				
REFERENCE	1 (bases 1 to 1345)				
AUTHORS	Nakhla,M.K., Mejia,L., Ramirez,P., Karkashian,J.P., Doyle,M.M. and Maxwell,D.P.				
TITLE	Molecular characterization and DNA-based detection methods for vegetable-infecting geminiviruses in Central America				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 1345)				
AUTHORS	Nakhla,M.K., Welland,G., Kamal,S. and Maxwell,D.P.				
TITLE	Direct Submission				
JOURNAL	Submitted (25-FEB-1999) Plant Pathology, University of Wisconsin-Madison, 1610 Linden Dr., Madison, WI 53706-1598, USA				
FEATURES	Location/Qualifiers				
SOURCE	1..1345				
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	/isolate="HN96-H5Kv"				
	/specimen_voucher="H5"				
	/db_xref="taxon:92943"				
	/chromosome="segment A"				
	/clone="PHNH5Kv"				
	/country="Honduras: Comayagua Valley"				
	/note="Obtained from a tomato plant collected in Dec. 1996 by M.K. Nakhla and D.P. Maxwell"				
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	/gene="rep"				
	/note="ac1"				
CDS	complement<1..678)				
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	/note="rep protein"				
	/codon_start=1				
	/product="replication-associated protein"				
	/protein_id="AAD33471.1"				
	/db_xref="GI:4928224"				
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rep_origin	676..832				
	/note="ori"				
gene	1001..>1345				
	/gene="cp"				
	/note="av1"				
CDS	1001..>1345				
	/gene="cp"				
	/note="capsid protein"				
	/gene="cp"				
	/codon_start=1				
	/product="coat protein"				
	/protein_id="AAD33472.1"				
	/db_xref="GI:4928225"				
	/translation="MPKRDAIPWRIMASTPVVSNSSNVPPDGLGRKFEDKSAAANPRMYRKRIIRTVASADVPRGCGPCIKIOSFEQRHDISHTGKVMCISDYTRNGITRHRRGKRFVCVSVIILGVK"				
BASE COUNT	329 a	289 c	313 g	414 t	
ORIGIN					
alignment_scores:	Quality:	282.00	Length:	70	
	Ratio:	4.338	Gaps:	0	
Percent Similarity:	92.857	Percent Identity:	74.286		
Alignment block:					

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US-09-289-346A-8 x AFL131071/rev ..
Align seg 1/1 to reverse of: AFL131071 from: 1 to: 1345

1   ThrLeuValTTPG1yGUaLaLaValaaspG1yArGserAlaArG1yG1 17
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348 ACAATCGAATGGGAGAAATTCACATCCAGCGCAGATCTGCTAGAGGAG 299

17  yCysGlnThrSerAsnAspAlaAlaAG1uLaLeuAsnAlaSerSerL 34
    1 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
298 TCAGAAACAGCTTAACGACGCTGCCGACAGGAGCCCTAAATGCTCCTGCA 249

34  yGcUGcUaLaLeuGlnTlelleArG1uLuLyLleProG1uLyStyLeu 50
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
248 AGAAGAAACCCATGCCAATTAAGAAACACCTCCCAAGAGTTTCTT 199

51  PheGlnPheHisnLeuAsnSerAsnLeuAsParG1lePheAspLySth 67
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
198 TTTCATATACACAACTGTCTAGTAACCTAGACAGATATTGCTTAGGC 149

67  rProG1uPro 70
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
148 TCCGGAACCG 139

seq_name: gb_v1:MEGARAL

seq_documentation_block:
LOCUS      MEGARAL      2617 bp ss-DNA      circular VRL      02-AUG-1993
DEFINITION  Bean golden mosaic geminivirus viral coat protein (ARI) gene,
            complete cds; putative replicative protein (AL1) gene, putative
            cds; AL2 gene, complete cds; and AL3 gene, complete cds.
ACCESSION   M86686
VERSION     M86686.1 GI:331462
KEYWORDS    coat protein; replicative protein.
SOURCE      Bean golden mosaic virus (individual isolate Brazil, strain Type I)
            Replicative form DNA.
ORGANISM    Bean golden mosaic virus
            Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
REFERENCE   1 (sites)
AUTHORS     Gilbertson,R.L., Faria,J.C., Hanson,S.F., Morales,F.J.,
            Ahlquist,P.G., Maxwell,D.P. and Russell,D.R.
TITLE       Cloning of the Complete DNA Genomes of Four Bean-Infecting
            Geminiviruses and Determining Their Infectivity by Electric
            Discharge Particle Acceleratio
            Phytopathology 81, 980-985 (1991)
JOURNAL     2 (sites)
REFERENCE   Gilbertson,R.L., Hidayat,S.H., Martinez,R.T., Leong,S.A., Faria,J.C.,
AUTHORS     Morales,F.J. and Maxwell,D.P.
TITLE       Differential infection of bean-infecting geminiviruses by nucleic acid
            hybridization probes and aspects of bean golden mosaic in Brazil
            Plant Dis. 75, 336-342 (1991)
JOURNAL     3 (bases 1 to 2617)
REFERENCE   Gilbertson,R.L., Faria,J.C., Ahlquist,P.G. and Maxwell,D.P.
AUTHORS     Genetic diversity in geminiviruses causing bean golden mosaic
            disease: The nucleotide sequence of the infectious cloned DNA
            components of a Brazilian isolate of bean golden mosaic geminivirus
            Unpublished (1992)
FEATURES
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        location/Qualifiers
            1..2617
                /organism="bean golden mosaic virus"
                /proviral
                /isolate="Brazil"
                /strain="Type I"
                /db_xref="taxon:10839"
                /dev_strage="Replicative form"
                /gemline
            1..181
                /standard_name="Common Region"
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                /function="putative origin of replication"
            358..1113
                /gene="ARI"
            358..1113

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/gene="A1"
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 /product="coat protein"
 /protein_id="AAA6313.1"
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 /translation="MRRDQQRHMGSTKISISANFSPRGNGPKYKNAAEVYNRM
 YRPRYRILRGDPVPRGCGPCVQSYEDRHVSHVGVKVCVSDVTRNGTIRHVGK
 RFPVCSYILGKIMDENIKLKNHTSVFMVLVDRPRGTGPDGQVFMFPNEPST
 ATRKNDLRDFQVHMKFYGVGTGGVYASNEQALVYKRPWKVNNYVYVNHQBAKYENHT
 ENLLIYMACTHASNPYATLRIIFYEDISTN"
 complement(1110..1508)
 /gene="A13"
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 /note="putative"
 /codon_start=1
 /protein_id="AAA6314.1"
 /db_xref="GI:331465"
 /translation="MDSRTGERTTARQANGVYIWEISNPLYEKMYNVEDLQYTTTRV
 YHLDIRFNHILRNKLGHKAFKALFQVWTLISLQSGTAYLNRPFKYLVLVLDRIQVLSL
 NNVRAVFAFDKSYVYVLEHETKRYF"
 complement(1255..1644)
 /gene="A12"
 complement(1255..1644)
 /gene="A12"
 /note="putative"
 /codon_start=1
 /protein_id="AAA6315.1"
 /db_xref="GI:331466"
 /translation="MRNSSSTPPSIKIVQHRANKRAIRRRVDECGTIVYHINCS
 GHGTHRGTHCTSSGEMRYLGIKSPLEODVORSGSTIHNDOSIPPPTVGPQPD
 QTSYQGFPEPESLDDISSFWDDIFK"
 complement(join(1556..2617,1..24))
 /gene="A11"
 complement(join(1556..2617,1..24))
 /gene="A11"
 /note="putative"
 /codon_start=1
 /function="viral replication"
 /product="replicative protein"
 /protein_id="AAA6312.1"
 /db_xref="GI:331463"
 /translation="MPPPKRPRKINAKNYFLTYPOCSITTKESAIPEOLONLQTPVKKYYI
 RICEIHENGEPHLLIOFEGCFQCTNGRVEFDLKHPTTSVSHANIOSAKSSSDVKS
 YIEDQSYIEGHWGROVGRSARGGOOTANDAASLMAKSEEMOILKEKLPKPLF
 OYHLSNLDRTFTKAPDPWSPRPHLSSFTTVPREMOEMADDTYGRGAANRPERPIS
 IIEEDSRGTQMAARALGTHNYLSGHLDFNSKVSNAEYVNDIDIAHYIKLHMBE
 LMGQKDWOSNCKYKGPVOIKGIPSYLCLNPGGASYSKFLDKREENAALKNMTIHNA
 KFIPLNSPLVOSTSCSEETSNQYTSR"
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 BASE COUNT 677 a 491 c 592 g 857 t
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 alignment_scores:
 Quality: 280.00 Length: 67
 Ratio: 4.44 Gaps: 0
 Percent Similarity: 94.030 Percent Identity: 77.612
 alignment_block:
 US-09-289-346a-8 x MBGARAL/rev ..
 Align seg 1/1 to reverse of: MBGARAL from: 1 to: 2617
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 |||||::: |||||::: |||||::: |||||::: |||||
 2305 TGGGTCATTTTCACGTGACGACGAACATGTGCTAAGGAGGATCACGAC 2256
 20 rSerAsnaSPaIaIaIaGluaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 37
 ||:::|||||:::|||||:::|||||:::|||||:::|||||
 2255 AGCTAAATGATGCGGATCCGACACATTGAATGCTTCTTCAAGGAAGAGAG 2206

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37 laLeuGlnIleIleAArgGluLysIleProGluLysTyrLeuPheGlnPhe 53
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2205 CCATGCAAAATTAATCAAGAACTACCGGAAAGTTCTCTCCATAT 2156
54 HisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysThrProGluP 70
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2155 CACAATTATTCAGTACCTGATAGATATATTCACAAAGACTCCGATCC 2106
70 o 70
2105 G 2105

seq_name: gb_v1:AF188708
seq_documentation_block: 1365 bp DNA VRL 07-NOV-1999
LOCUS AF188708
DEFINITION Cowpea golden mosaic geminivirus replication associated protein
(rep) and coat protein (cp) genes, partial cds.
ACCESSION AF188708
VERSION AF188708.1 GI:6273115
KEYWORDS
SOURCE cowpea golden mosaic geminivirus.
ORGANISM cowpea golden mosaic geminivirus.
REFERENCE 1 (bases 1 to 1365)
VIRUSES: ssDNA viruses; Geminiviridae; Begomovirus.
AUTHORS Faria,J.C.
TITLE Partial nucleotide sequence of cowpea golden mosaic geminivirus
from Brazil
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1365)
AUTHORS Faria,J.C.
TITLE Direct Submision
JOURNAL Submitted (21-SEP-1999) Biotechnology Laboratory, EMBRAPA, Caixa
Postal 179, Goiania, GO 75375, Brazil
FEATURES
source
1..1365
/organism="Cowpea golden mosaic geminivirus"
/strain="CGMV-BR"
/specific_host="cowpea"
/db_xref="taxon:69263"
/complement(<1..676)
/gene="rep"
/complement(<1..676)
/gene="rep"
/note="AC1"
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/product="replication associated protein"
/protein_id="AAF06318.1"
/db_xref="GI:6273117"
/translation="MPPPRFKINAKNYFLTYPOCSIGKESAIETOLQTLQTPVNNKYL
RVCREIHENGEPHLALIOFEKGFQCTNCRLLDLKHPHSSVSHNIOASKSSSDVKS
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IIEGDSR"
rep_origin
674..820
1021..>1365
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1021..>1365
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/codon_start=1
/product="coat protein"
/protein_id="AAF06317.1"
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/translation="WKRDAPEWRHNSGTSKYSRTNNSPDSGGCFKYKAAEMNRPM
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BASE COUNT 339 a 259 c 332 g 435 t
ORIGIN
alignment_scores:
Quality: 278.00 Length: 67

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Ratio: 4.557 Gaps: 0
Percent Similarity: 91.045 Percent Identity: 77.612
alignment_block:
US-09-289-346a-8 x AF188708/rev ..
Align seg 1/1 to reverse of: AF188708 from: 1 to: 1365

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340 TGGGGTCAITTTCAATCGACGAGAGATCTGTAGAGAGAGTCAAGAC 291
20 rSerAsnAspAlaAlaIaGluAlaLeuAsnAlaSerSerLysGluGlnA 37
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
290 AATTAAATGATGCAGCATCGGAGCGTTAATGCTTCTTCAAGAGAGAG 241
37 laLeuGlnIleIleAArgGluLysIleProGluLysTyrLeuPheGlnPhe 53
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
240 CCATGCAAAATTAATCAAGAACTACCGGAGAAAGTTCTCTCCAGTAT 191
54 HisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysThrProGluP 70
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
190 CACAACTTATTCAGTACCTGATAGATATTCACAAAGCTCCGATACC 141
70 o 70
140 A 140

seq_name: gb_v1:AF288227
seq_documentation_block: 1383 bp DNA VRL 20-AUG-2000
LOCUS AF288227
DEFINITION Sweet potato leaf curl virus replication association protein (AC1)
and AC4 (AC4) genes, complete cds.
ACCESSION AF288227
VERSION AF288227.1 GI:9858125
KEYWORDS
SOURCE sweet potato leaf curl virus.
ORGANISM sweet potato leaf curl virus.
REFERENCE 1 (bases 1 to 1383)
VIRUSES: ssDNA viruses; Geminiviridae; Begomovirus.
AUTHORS Lotrakul,P., Valverde,R.A., Clark,C.A., Sim,J. and De la Torre,R.
TITLE Detection of a geminivirus infecting sweet potato in the United
States
JOURNAL Plant Dis. 82, 1253-1257 (1998)
REFERENCE 2 (bases 1 to 1383)
AUTHORS Lotrakul,P. and Valverde,R.A.
TITLE Direct Submision
JOURNAL Submitted (18-JUL-2000) Plant Pathology and Crop Physiology,
Louisiana State University, 302 Life Sciences Bldg., Baton Rouge,
LA 70803, USA
FEATURES
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1..1383
/organism="sweet potato leaf curl virus"
/db_xref="taxon:100755"
/note="subgenomic DNA"
/complement(285..1229)
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/protein_id="AAG01006.1"
/db_xref="GI:9858126"
/translation="MAPPKRPKIOAKNYFLTYPPCSISKEDCLAQLANIQTSPNNKKYI
HVARELHEDGEPHLVLVQFEKGFVCTNSRFDLYSPKSNHFPNIOGAKSSSDVKS
YVDKGDITWGEFOVDGRSARGGOQITINDASSELNMSKREANQIIKEKLPETLF
QYHNLVSNIDRLTFSPPSVSSPSSSSSSFNAPDITSDMAENWDSARDRPSTIV
IEGFSRIGKTYWASRLGPHANTLCGLHLSDFPVYSSANYNITDDVNPQYLAKHKEFMG
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complement(815..1072)
/gene="AC4"
gene

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/gene="AC4"
/note="AL4"
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/translation="MGNTSMCWSSKANSASQIADSSIMSHRTDITFTPTSHLNP
APMSPSIRGIPSPGVNSRSTADLLEASRLITTOPL"
BASE COUNT      741 a      606 c      675 g      806 t
ORIGIN

alignment_scores:
  Quality: 278.00      Length: 68
  Ratio: 4.557      Gaps: 0
  Percent Similarity: 89.706      Percent Identity: 80.882

alignment_block:
US-09-289-346a-8 x AF104036/rev ..

Align seg 1/1 to reverse of: AF104036 from: 1 to: 2828

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2354 ACCATCAGCTGGGGGTAAATCCAGCTCGACGCGCATCTCTAGAGAGG 2305
17 yCysGlnThrSerAsnAspAlaAlaIaGluAlaLeuAsnAlaSerSertL 34
|||||:|||||
2304 CCAGCAGACTGCTACGACGACGCGAGGCTTAACGACAGTTCTA 2255
34 ySGLuAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeu 50
|||||:|||||
2254 AAGAGCTGCGTGCATATATCAGGAGAACCTCCGTGAATAATTTA 2205
51 PhcGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
|||||:|||||
2204 TTTCATTTTCATTAATTTAGTTAGTAATTTAGATGATTTTCTCTCC 2155
67 rPro 68
|||||
2154 ACCT 2151

seq_name: gb_v1:SGU67926

seq_documentation_block:
LOCUS      SGU67926      554 bp      DNA      VRL      28-JAN-1998
DEFINITION Sida golden mosaic geminivirus Rep protein (AC1) gene, partial cds.
ACCESSION  U67926
VERSION    U67926.1 GI:1546801
KEYWORDS
SOURCE
ORGANISM   sida golden mosaic virus.
            ssDNA viruses; Geminiviridae; Begomovirus.
REFERENCE  1 (bases 1 to 554)
            Roye,M.E., McLaughlin,W.A., Nakhla,N.K. and Maxwell,D.P.
            Genetic Diversity among geminiviruses associated with the weed
            species sida spp. Macroptilium lathyroides, and Wissadula
            amplissima from Jamaica
            Plant Dis. 81, 1251-1258 (1997)
JOURNAL
AUTHORS    Roye,M.E., McLaughlin,W.A. and Maxwell,D.P.
TITLE      Direct Submission
SUBMITTED  (23-AUG-1996) Plant Pathology, University of Wisconsin,
JOURNAL    1630 Linden Drive, Madison, WI 53706-1598, USA
FEATURES
SOURCE
1. 554
   /organism="sida golden mosaic virus"
   /strain="Jamaica"
   /isolate="Jamaica, May 1993"
   /db_xref="taxon:51034"
   /note="DNA A component"
   /complement(1..554)
   /gene="AC1"
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CDS
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GKYNTNNRPFDLVSPTRSYHFHNIGAKSSDVKSVKEDGPTIEMGVQIDGRSA
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HPPPLPSRTAVPGQMEKADQYRGR"
BASE COUNT      121 a      127 c      139 g      167 t
ORIGIN

alignment_scores:
  Quality: 275.00      Length: 70
  Ratio: 4.297      Gaps: 0
  Percent Similarity: 91.429      Percent Identity: 71.429

alignment_block:
US-09-289-346a-8 x SGU67926/rev ..

Align seg 1/1 to reverse of: SGU67926 from: 1 to: 554

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|||||:|||||
290 ACCATCGAATGGGGGTGTTCCAGATCGACGAGAGAGATGCTCTGAGAG 241
17 yCysGlnThrSerAsnAspAlaAlaIaGluAlaLeuAsnAlaSerSertL 34
|||||:|||||
240 TCAGCAACAGCTACGACGACGCGCGAGCATTTGAATTTCTGAAACA 191
34 ySGLuAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeu 50
|||||:|||||
190 AGGAGCATGCACGAAATCATCGAGAGAGAGTTACAGAAAGATTCCTC 141
51 PhcGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
|||||:|||||
140 TTTCAGTATCAGACCTATTCAGTATTCAGTATTCAGTATTCAGTAAGCC 91
67 rProGluPro 70
|||||
90 TCCAGAACCG 81

seq_name: gb_v1:IEI132548

seq_documentation_block:
LOCUS      IEI132548      2763 bp      DNA      circular VRL      01-FEB-1999
DEFINITION Ipomoea yellow vein virus V2, V1, C3 and C2 genes.
ACCESSION  AJ132548
VERSION    AJ132548.1 GI:4210720
KEYWORDS   C2 gene; C2 protein; C3 gene; C3 protein; coat protein; V1 gene; V2
            gene; V2 protein.
SOURCE
ORGANISM   Ipomoea yellow vein virus.
            ssDNA viruses; Geminiviridae; Begomovirus.
REFERENCE  1 (bases 1 to 2763)
            Banks,G.K.
            Direct Submission
            Submitted (26-JAN-1999) Banks G.K., Virus Research, John Innes
            Centre, Norwich Research Park, Colney Lane, Norwich, NR4 6JL, UK
JOURNAL
AUTHORS    Banks,G.K., Bedford,I.D., Beltia,F.J., Cerezo,E.R. and Markham,P.G.
TITLE      A novel geminivirus of Ipomoea indica (Convolvulaceae) from southern
            Spain
JOURNAL    Unpublished
FEATURES
SOURCE
1. 2763
   /organism="Ipomoea yellow vein virus"
   /viroion
   /specific_host="Ipomoea indica"
   /db_xref="taxon:87832"
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gene      995..1390
          /gene="V2"
CDS       995..1390
          /gene="V2"
          /codon_start=1
          /product="V2 protein"
          /protein_id="CA10695.1"
          /db_xref="GI:4210721"
          /translation="MTLLYKDQSDRCRMCSTABMDPLQNPDPDTLXGFCMISVKY
          LQGLIKKYEPTGIFELCSSELIRIFRVKQYDRANSRAEILSLWGTEGKTESELRDSTY
          RALHMECCPNCCPLCPGFKRPDEKEG"
gene      1215..1979
          /gene="V1"
CDS       1215..1979
          /gene="V1"
          /codon_start=1
          /product="coat protein"
          /protein_id="CA10696.1"
          /db_xref="GI:4210722"
          /translation="MTGRIRYSPRFHPYGGROVRSNLLETATVPTGNAPVIAARSY
          VPVSRGYRMKRRGRDRIPKGCVGCKIODEFKADVPRITGTFVCSDFIRGTGLTHRL
          GKRVCIKSMSTIDGVMMDNVAKRDNHNIITWLLRDRPKADPLNEQITMTDNEP
          TTAIRMDLRDMQVLKFSYVSGPYSKQALIRKFFKCLYNHVTYNHKEAKYE
          NQLENALMYSASSHASNPHYQTLRCRAFYDSHKN"
gene      complement(1976..2413)
CDS       complement(1976..2413)
          /gene="C3"
          /codon_start=1
          /product="C3 protein"
          /protein_id="CA10697.1"
          /db_xref="GI:4210723"
          /translation="MDSRTGESISHAOTTRAEPFNPNMSVQOTAPFLRLMYHTNN
          LDSRTYIMKVOLOVNRHNRREIGFQKIFLQFRIIPRLGALPNMTGISNRLKRICNS
          LASTGYSLFNLVYVIRHLPOQCLWEVDVIDCKDKIKELY"
gene      complement(2127..2576)
CDS       complement(2127..2576)
          /gene="C2"
          /codon_start=1
          /product="C2 protein"
          /protein_id="CA10698.1"
          /db_xref="GI:4210724"
          /translation="MSTAPSGYKRRKCPAOPFIHAAKKROKRTPEPRRIYWKGGCS
          AFTINDCKFOHGFTHRGVTKSCPTYESRRIQOSHVCSSDCTISTTIVCYKKQPRLK
          DDHESAASSOPPEDEGNMTPEDLPPIPDHTNASWCYSQLDWTFQSP"
BASE COUNT      734 a      570 c      671 g      788 t
ORIGIN
alignment_scores:
  quality: 274.00      length: 68
  ratio: 4.567      gaps: 0
  percent similarity: 88.235      percent identity: 77.941
Percent Similarity: 88.235      Percent Identity: 77.941
alignment_block:
US-09-289-346A-8 x IYE132548/rev ..
Align seg 1/1 to reverse of: IYE132548 from: 1 to: 2763
1 ThrlenValTrpGlyLualalaValaAspGlyArGserAlaArgIygl 17
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
469 ACCCTCATATGGGGGTGAATTCAGATCGACGGCAGCATCTCTGAGGAGG 420
17 ycySGlThrSerAsnAspAlaAlaIaIaIaIaLeuAsnAlaSerSerl 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
419 TCAGCAGCTCGCTACGACGACCGACGAGGCGCTAAACGATGTTCTA 370
34 yscGlualalaLeuGlnIleIleArgGluLysIleProGluLysTyrLeu 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
369 AAGAACCTGGTGGCAAAATTAATCAGGAGGAACCTCCCTGAAAAATATTTA 320
51 PhcGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67

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|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
319 TTTCATATCATATATTAGTACTAGTAAATTAGATAGCATTTTCTCTCCTCC 270
67 rPro 68
|||
269 TCCT 266
seq_name: gb_v1:MGU75278
seq_documentation_block:
LOCUS      MGU75278      447 bp      DNA      VRL      27-NOV-1996
DEFINITION Macropitillium golden mosaic geminivirus replication-associated
protein (Ac1) gene, partial cds.
ACCESSION      U75278
VERSION      U75278.1      GI:1688188
KEYWORDS
SOURCE
ORGANISM      Macropitillium golden mosaic geminivirus.
                Macropitillium golden mosaic geminivirus
                Viruses: ssDNA viruses; Geminiviridae; Begomovirus.
REFERENCE
  1 (bases 1 to 447)
  Roye,M.E. Diversity and phylogeny of whitefly-transmitted geminiviruses from
  Jamaica
  JOURNAL      Thesis (1996)
  TITLE      2 (bases 1 to 447)
  AUTHORS      Roye,M.E., McLaughlin,W.A. and Maxwell,D.P.
  REFERENCE   Three distinct geminiviruses infecting M. jachyroides from Jamaica
  TITLE      but not BGMV
  JOURNAL      Unpublished (1996)
  REFERENCE   3 (bases 1 to 447)
  AUTHORS      Roye,M.E., McLaughlin,W.A. and Maxwell,D.P.
  TITLE      Direct Submission
  JOURNAL      Submitted (17-OCT-1996) Biochemistry, University of the West
  INDICES      Indies, Mona, Kingston 7, Jamaica
  FEATURES
    source
      1..447
      /organism="Macropitillium golden mosaic geminivirus"
      /strain="Jamaican"
      /isolate="2"
      /db_xref="taxon:51676"
      /clone="PMGJA2"
      complement(1..447)
      /gene="AC1"
      complement(<1..>447)
      /gene="AC1"
      /codon_start=1
      /product="replication-associated protein"
      /protein_id="AAB36919.1"
      /db_xref="GI:1688189"
      /translation="HVLIQFOGKFNCTNRYLPDLVSPSRSAHFHPNIOGAKSSDYKS
      VYEKGDITEMGVETIDGRSARGGQOTSDNAEAALNSGTREAAARIVYEKLPKFLP
      QYHNSSNDRIFEMKDPPEFWAPPPLPSFTFNVDEMOWATVYFGRG"
BASE COUNT      97 a      112 c      110 g      128 t
ORIGIN
alignment_scores:
  quality: 267.00      length: 70
  ratio: 4.306      gaps: 0
  percent similarity: 88.571      percent identity: 70.000
Percent Similarity: 88.571      Percent Identity: 70.000
alignment_block:
US-09-289-346A-8 x MGU75278/rev ..
Align seg 1/1 to reverse of: MGU75278 from: 1 to: 447
1 ThrlenValTrpGlyLualalaValaAspGlyArGserAlaArgIygl 17
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
294 ACCATTCGAATGGGAGGTCTCCACATCGACGGAAGAAGTGTCTGAGGCGG 245
17 ycySGlThrSerAsnAspAlaAlaIaIaIaIaLeuAsnAlaSerSerl 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
244 TCAGCAAAACATCTACGATGACCGCGCAACATTAATTCTGCAACAA 195

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34 YSGluGuaAlaLeuGlnIleIleAArgGluTyrSileProGluTyrLeu 50
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
194 AGAGAGCGGCATGACATAGTCTCAGAGAAAGTTGCCGGAAGTTCTC 145

51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspTyrSth 67
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
144 TTTCATATATCACAACCTATCCAGTAACCTGATAGATTTTCATGAAGGA 95

67 rProGluPro 70
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
94 TCCGGAACCA 85

seq_name: gb_v1:AF098940

seq_documentation block:
LOCUS AF098940 1405 bp DNA VRL 04-MAR-1999
DEFINITION Macropitilium golden mosaic geminivirus strain Jamaica 1
partial cds.
partial cds.
ACCESSION AF098940 GI:4336584
VERSION AF098940.1 GI:4336584
KEYWORDS Macropitilium golden mosaic geminivirus.
Macropitilium golden mosaic geminivirus.
ORGANISM Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
REFERENCE 1 (bases 1 to 1405)
AUTHORS Roye, M.E.
TITLE Genetic diversity and phylogeny of whitefly-transmitted
geminiviruses from Jamaica
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1405)
AUTHORS Roye, M.E., McLaughlin, W.A. and Maxwell, D.P.
TITLE Molecular characterization of two distinct geminiviruses infecting
M. latihyroides from Jamaica
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 1405)
AUTHORS Roye, M.E., McLaughlin, W.A. and Maxwell, D.P.
TITLE Direct Submission
JOURNAL Submitted (14-OCT-1998) Biotechnology Centre, University of the
West Indies, Mona, Kingston 7, Jamaica
FEATURES
source
1..1405
/organism="Macropitilium golden mosaic geminivirus"
/strain="Jamaica strain 1"
/specific host="Macropitilium latihyroides"
/db_xref="taxon:51676"
/country="Jamaica"
/clone="pMGJA2; pMGJA3"
/complement(<1..701)
/gene="rep"
/complement(<1..701)
/gene="rep"
/codon_start=1
/product="replication associated protein"
/protein_id="AAD17850.1"
/db_xref="GI:4336586"
/translation="MPKGSFSIKAKNYFLPYPOCSLTKKEBALSOLTLNLPVKKKFI
KICREFHEDGPHLHVLIQFOGKFNCTNNRLFDLYSPRSAPHPNIOGASSSDYKS
YVERKDGPTEGVCVIDGRSARCGCOOTSNDAALVNLNGSTEAAMRIYKEKLPETFLP
QYHNSMIDRIPIKDPPEPMAPPLFSFTVPDEMOMADYDFERGSAAPPERPMST
IVEGDSRTGKTMAC"
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702..1030
/note="intergenic region"
gene
1031..>1405
/gene="cp"
1031..>1405
/gene="cp"
/codon_start=1
/product="coat protein"
/protein_id="AAD17849.1"
/db_xref="GI:4336585"
/translation="MPKRDGSMRTTPGVAKVSRRLNLSPRGGYGRSNKAOEWNRPM

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RRKPIRYRLTSPDVRPGCEGPKCKVQSYEORHDI SHVGKVMCISDVTGRGVYITHRVGK
RECVFEVYIILKIMDENINCS"
BASE COUNT 328 a 333 c 357 g 386 t 1 others
ORIGIN

alignment_scores:
Quality: 267.00 Length: 70
Ratio: 4.306 Gaps: 0
Percent Similarity: 88.571 Percent Identity: 70.000

alignment_block:
US-09-289-346A-8 x AF098940/rev ..
Align seg 1/1 to reverse of: AF098940 from: 1 to: 1405

1 ThrLeuValTyrPglYgIuaAlaValAspGlyArgSerAlaArgIylgl 17
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
374 ACCATCGAATGGCGGAGTTCACAGATCGACGCAAGAAAGTCTCGAGCGG 325

17 yCysGlnThrSerAsnAspAlaIleAlaGluAlaLeuAsnAlaSerSert 34
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
324 TCAGCAACATCTTAACGATGACGCGCGCAAGCATTTAAATTTGGAACAA 275

34 YSGluGuaAlaLeuGlnIleIleAArgGluTyrSileProGluTyrLeu 50
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
274 AGAGAGCGGCATGACATAGTCTCAGAGAAAGTTGCCGGAAGTTCTC 225

51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspTyrSth 67
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
224 TTTCATATATCACAACCTATCCAGTAACCTGATAGATTTTCATGAAGGA 175

67 rProGluPro 70
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
174 TCCGGAACCA 165

seq_name: gb_v1:AF026553

seq_documentation block:
LOCUS AF026553 1165 bp DNA VRL 03-NOV-1997
DEFINITION Potato yellow mosaic virus Tomato strain AV1 and AC1 genes, partial
cds.
ACCESSION AF026553 GI:2583073
VERSION AF026553.1 GI:2583073
KEYWORDS Geminiviridae.
SOURCE Geminiviridae.
ORGANISM Viruses; ssDNA viruses.
REFERENCE 1 (bases 1 to 1165)
AUTHORS Guzman, P., Arredondo, C.R., Esmatly, D., Portillo, R.J. and
Gibbertson, R.L.
TITLE Partial Characterization of Two Whitefly-Transmitted Geminiviruses
Infecting Tomatoes in Venezuela
JOURNAL Plant Dis. 81, 312-312 (1997)
REFERENCE 2 (bases 1 to 1165)
AUTHORS Guzman, P., Arredondo, C.R., Esmatly, D., Portillo, R.J. and
Gibbertson, R.L.
TITLE Direct Submission
JOURNAL Submitted (24-SEP-1997) Plant Pathology, University of
California-Davis, Department of Plant Pathology, Davis, CA 95616,
USA
FEATURES
source
1..1165
/organism="Geminiviridae"
/strain="Tomato strain"
/db_xref="taxon:10811"
/note="Bipartite genome; whitefly-transmitted; DNA-A
fragment obtained by PCR from tomato sample from State of
Monagas (Venezuela)"
/complement(<1..153)
/gene="capsid protein"
/codon_start=1
/product="AV1"

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CDS
    /protein_id="AAB82606.1"
    /db_xref="GI:2583075"
    /translation="MPKRDAPWMSMAGTSKVSRRNANSPRSSGIGPINKAAEWVNRPM
    YRKPCST"
    464...>1165
    /note="replication-associated protein"
    /codon_start=1
    /product="AC1"
    /protein_id="AAB82605.1"
    /db_xref="GI:2583074"
    /translation="MPKGSFSTKAKNYFLTYPOCSKEDALSQIONLITPVKKRI
    KICRELHENGEPHLVLIQEGFNCTNNRLEFDVSPTRSTHEPNIQAKSSSDVS
    YVRKDDPTLEWGLFQIDGRSARGQOQANDAAEALNSGTKEEAMKIKKRLPKPLF
    QYHNLSGLDIRIFKAPNPWAPPPPLSSFTNVPEHMOEHSDFGRSAARGETISII
    IEGDSRGTGTMACRC"

BASE COUNT      350 a      264 c      256 g      295 t

ORIGIN

alignment_scores:
    Quality: 261.00      Length: 70
    Ratio: 4.078      Gaps: 0
    Percent Similarity: 91.429      Percent Identity: 68.571

alignment_block:
US-09-289-346a-8 x AF026553 ..
Align seg 1/1 to: AF026553 from: 1 to: 1165

1 ThrleuValTrpGlyLualaIaValaAspGlyArgSerAlaArgIylGI 17
||||| ||||| ::||| ||||| ||||| |||||
791 ACCATCGAATGGGATGTTGCCAGATTGACGAGAAAGTCTCGACGTGG 840

17 yCysGlnThrSerAsnAspAlaIaIaIaLualaLeuAsnAlaSerSerL 34
| ||||| ::||| ||||| ||||| ||||| |||||
841 CCACAGACGCGCAACGACGACGCGGAGCATTAACCTCTGGAACAA 890

34 ySGlUGlUaLLeuGlnIleIleArgGluLysIleProGluLysTyrLeu 50
||||| ::||| ||||| ||||| ||||| |||||
891 AGGAAGAACCCATGAATCATTAAGAGAAAGTGGCGGAAAGTTTCTT 940

51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
||||| ::||| ||||| ||||| ||||| |||||
941 TTTCAGTATCATACCTATCATCTCAGTACGCTCGATGATTTTCTGAAGC 990

67 rProGluPro 70
: ||||| ::|||
991 TCCAAATCCG 1000

seq_name: gb_v1:AB001315

seq_documentation_block:
LOCUS      AB001315      570 bp      DNA      VRL      13-FEB-1999
DEFINITION Tobacco leaf curl virus C1 and C4 genes, clone YOKOHAMA3-1, partial
and complete cds.
ACCESSION  AB001315
VERSION    AB001315
KEYWORDS   AB001315.1 GI:3798714

ORGANISM   tobacco leaf curl virus (isolate:YOKOHAMA3,
AUTHORS    specific host:Eupatorium makinoi) DNA, clone:YOKOHAMA3-1.
TITLE      tobacco leaf curl virus
JOURNAL    Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
REFERENCE  1 (bases 1 to 570)
AUTHORS    Ooi,K.
TITLE      Direct Submission
JOURNAL    Submitted (19-FEB-1997) to the DDBJ/EMBL/GenBank databases.
            Kazuyuki Ooi, Kyushu University, Department of Biology, 6-10-1
            Hakozaki Hishiki-ku, Fukuoka, Fukuoka 812, Japan
            (E-mail:kooi@dbmbox.nc.kyushu-u.ac.jp, Tel:+81-92-642-2624,
            Fax:+81-92-642-2645)
            2 (bases 1 to 570)
REFERENCE  Ooi,K., Ohshita,S., Ishii,I. and Yahara,T.
TITLE      Molecular phylogeny of geminivirus infecting wild plants in Japan

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JOURNAL      J. Plant Res. 110, 247-257 (1997)
FEATURES
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            1..570
            /organism="tobacco leaf curl virus"
            /isolate="YOKOHAMA3"
            /specific_host="Eupatorium makinoi"
            /db_xref="taxon:67762"
            /clone="YOKOHAMA3-1"
            complement(1..570)
            /gene="C1"
            complement(<1..570)
            /gene="C1"
            /codon_start=1
            /protein_id="BAA34033.1"
            /db_xref="GI:426541"
            /translation="EPALSQIONITPTNKLVIKICRELHEDSSPHLVLIQEGKKY
            CONRRFDVLSPTRSARHHPNIGAKSSSDVKSITDKDGLTLENGTROIIDRSARGG
            QNANDACAEALNASSKAELALIREKLKDFIFQYHNLSNLDRIFFAPLEVFVCPPT
            ASSPDQVEELEWASERNVMSAARPM"
            complement(231..488)
            /gene="C4"
            complement(231..488)
            /gene="C4"
            /codon_start=1
            /protein_id="BAA34034.1"
            /db_xref="GI:3798715"
            /translation="MEALISMCFCSSKANTAKITDSSTWYPOPDQHSITFRELNL
            APTSSPTSTREIISNGEHSSTEEVELEAARMLTTHVQR"

BASE COUNT      141 a      121 c      126 g      182 t

ORIGIN

alignment_scores:
    Quality: 258.00      Length: 85
    Ratio: 4.161      Gaps: 1
    Percent Similarity: 72.941      Percent Identity: 60.000

alignment_block:
US-09-289-346a-8 x AB001315/rev ..
Align seg 1/1 to reverse of: AB001315 from: 1 to: 570

1 ThrleuValTrpGlyLualaIaValaAspGlyArgSerAlaArgIylGI 17
||||| ||||| ::||| ||||| ||||| |||||
318 ACCCTCGAATGGGAGACATTCGACATCGACGAGAAAGTCTGACAGAG 269

17 yCysGlnThrSerAsnAspAlaIaIaIaLualaLeuAsnAlaSerSerL 34
||||| ::||| ||||| ||||| ||||| |||||
268 CTGCCAGAAATGCTAACGACGATGCGAGGCGTTAAATGCAAGTCTTA 219

34 ySGlUGlUaLLeuGlnIleIleArgGluLysIleProGluLysTyrLeu 50
||||| ::||| ||||| ||||| ||||| |||||
218 AGCCAGAACCATTAAGCAATTAATAGGAAAGCTCCCTAAAGATTWTATA 169

51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIle..... 63
||||| ::||| ||||| ||||| ||||| |||||
168 TTTCATATCATATTAATTAATAGTAATTTAGATGAGATTTTGTCTCTCC 119

64 .....PheAspLysThrP 68
||||| ::|||
118 GTTGAGAGTTTGTGTGTGCTTTACACAGCCTCATCTTTGATCAAGTTTC 69

68 rGlu 69
|||||
68 CAGAA 64

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2216 AGCTAATGATCTGCCGACAGGCTTAATGACAGTTACGTCGAGACAG 2167
37  |a|e|u|g|i|n|l|e|a|r|g|l|u|s|i|l|e|p|r|o|l|u|s|t|y|r|l|e|u|p|h|e| 53
2166 CTTTACCAATTAATGATTAAGGAAATCCCTTAACGATTTTATTTTCAATAT 2117
54  |H|a|s|n|l|e|u|a|n|s|e|r|a|n|l|e|u|a|s|p|a|r|g|i|l|e|p|h|e|a|s|p|l|y|t|h|r|p|r|o 68
2116 CATAATTTAAATGATTAATGATTAAGATTTT.....ACACCT 2078
seq_name: /cgnl_8/gcgdata/geneseq/geneseqn/NA1995.DAT:AAQ84371

seq_documentation_block:
ID      AAQ84371 standard; DNA; 434 BP.
AC      AAQ84371;
XX
XX      19-AUG-1995 (first entry)
XX
XX      Gemini virus-specific polyribozyme-E target sequence.
XX
XX      ribozyme target sequence: polyribozyme-E;
XX      tomato leaf curl virus; RNA cleavage; tomato transgenic plant;
XX      virus disease-resistance; ss.
XX
XX      Tomato leaf curl virus.
XX
XX      Key      location/Qualifiers
XX      misc_feature 13..43
XX      /*tag= a
XX      /note= "ribozyme R1 target sequence"
XX      26..28
XX      /*tag= b
XX      /note= "ribozyme R1 cleavage site"
XX      312..342
XX      /*tag= c
XX      /note= "ribozyme R2 target sequence"
XX      325..327
XX      /*tag= d
XX      /note= "ribozyme R2 cleavage site"
XX      384..414
XX      /*tag= e
XX      /note= "ribozyme R3 target sequence"
XX      397..399
XX      /*tag= c
XX      /note= "ribozyme R3 cleavage site"
XX
XX      W09503404-A.
XX
XX      PD      02-FEB-1995.
XX
XX      PF      22-JUL-1993; 93WO-EP01946.
XX
XX      PR      22-JUL-1993; 93AU-0047014.
XX      PR      22-JUL-1993; 93WO-EP01946.
XX
XX      PA      (BIOC-) BIOCEM SA.
XX      (CSTR) COMMONWEALTH SCI & IND RES ORG.
XX
XX      PI      Baudino S, Comeau D, Dry IB, Gruber V, Lenee P;
XX      Meson J, Rezalan MA, Ridgen JE, Rezanan MA;
XX
XX      DR      WPI: 1995-075232/10.
XX
XX      PT      Synthetic DNA virus ribozyme(s) - reduce replication, infection
XX      and/or assembly of viruses by cleaving target virus sequence,
XX      useful for preparing resistant plants, esp tomatoes.
XX
XX      PS      Example 10: Fig 11b; 90pp; English.
XX
XX      CC      The sequence is a tomato leaf curl virus target sequence for
XX      polyribozyme-E, which hybridizes to and cleaves the sequence and
XX      thereby reduces replication, infection and/or assembly of the virus

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CC      substantially. The ribozyme may be expressed in a transgenic plant,
CC      e.g. tomato, to confer virus disease-resistance.
XX
XX      SQ      Sequence 434 BP; 126 A; 86 C; 91 G; 131 T; 0 other;

alignment_scores:
      Quality: 230.00      Length: 85
      Ratio: 3.770      Gaps: 1
      Percent Similarity: 71.765      Percent Identity: 54.118

alignment_block:
US-09-289-346A-8 x AAQ84371 ..
Align seg 1/1 to: AAQ84371 from: 1 to: 434

1  ThrLeuValTrpGluAlaValAlaValAspGlyArgSerAlaArgGlyG 17
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
95  ACCCTCGAATGGGAGAGATTTCAGATCGATGACGATCGACAGAGGGG 144
17  yCysGlnThrSerAsnAspAlaAlaAlaGluAlaLeuAsnAlaSerSer 34
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
145  ACAACAATCAGCCAAATGACGCTTACGCCAGCGCTTAACACTGGAAGTA 194
34  yScGluAlaLeuGlnIleIleArgGluIysIleProGluIysTyrLeu 50
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
195  AGTCAGAGGCTTACGCTTACGCTTACGATTAACCCCTAAGCATATGCTT 244
51  PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIle..... 63
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
245  TTACAAATTCATATTAATTAATAGTAATTAATGATTAATGATTAATGAT 294
64  .....PheAspIysThrP 68
295  GTTGAGAGCTTATGTTCTTCTTTTATCTTCTTCTTGTGATGAGATTC 344
68  roGlu 69
   |||||
345  CAGAA 349

seq_name: /cgnl_8/gcgdata/geneseq/geneseqn/NA1995.DAT:AAQ84372

seq_documentation_block:
ID      AAQ84372 standard; DNA; 479 BP.
AC      AAQ84372;
XX
XX      19-AUG-1995 (first entry)
XX
XX      DE      Gemini virus-specific polyribozyme-F target sequence.
XX
XX      KM      ribozyme target sequence: polyribozyme-F;
XX      tomato leaf curl virus; RNA cleavage; tomato transgenic plant;
XX      virus disease-resistance; ss.
XX
XX      OS      Tomato leaf curl virus.
XX
XX      FH      Key      location/Qualifiers
XX      misc_feature 46..96
XX      /*tag= a
XX      /note= "ribozyme R4-R5 target sequence"
XX      58..60
XX      /*tag= b
XX      /note= "ribozyme R4 cleavage site"
XX      81..83
XX      /*tag= c
XX      /note= "ribozyme R5 cleavage site"
XX      356..386
XX      /*tag= d
XX      /note= "ribozyme R2 target sequence"
XX      370..372
XX      /*tag= c
XX      /note= "ribozyme R2 cleavage site"

```

```

FT misc_feature 429..459
FT /tag= e
FT /note= "ribozyme R3 target sequence"
FT 442..444
FT /tag= d
FT /note= "ribozyme R3 cleavage site"
XX
XX WO503404-A.
XX
XX 02-FEB-1995.
XX
XX 22-JUL-1993; 93WO-EP01946.
XX
XX 22-JUL-1993; 93AU-0047014.
XX
XX 22-JUL-1993; 93WO-EP01946.
XX
XX (BIOC-) BIOCEM SA.
XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX
XX Baudino S, Comeau D, Dry IB, Gruber V, Lenee P;
XX Mason J, Rezalian MA, Ridden JE, Rezanan MA.
XX
XX WPI: 1995-075232/10.
XX
XX Synthetic DNA virus ribozyme(s) - reduce replication, infection
XX and/or assembly of viruses by cleaving target virus sequence,
XX useful for preparing resistant plants, esp tomatoes.
XX
XX Example 10: Fig 11c; 90pp: English.
XX
XX The sequence is a tomato leaf curl virus sequence for
XX polyribzyme-F, which hybridizes to and cleaves the sequence and
XX thereby reduces replication, infection and/or assembly of the virus
XX substantially. The ribozyme may be expressed in a transgenic plant,
XX e.g. tomato, to confer virus disease-resistance.
XX
XX Sequence 479 BP; 145 A; 95 C; 97 G; 142 T; 0 other:

```

```

alignment_scores:
  Quality: 230.00      Length: 85
  Ratio: 3.770        Gaps: 1
  Percent Similarity: 71.765  Percent Identity: 54.118

```

```

alignment_block:
US-09-289-346a-8 x AA084372 ..

```

```

Align seg 1/1 to: AA084372 from: 1 to: 479

```

```

1 ThrleuValTrpGlyGluAlaAlaValAspGlyArgSerAlaArgGlyGly 17
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
140 ACCCTGGAATGGGGAGATTTCAGATGATGAGACATCTGCCAAGGGGG 189
17 YCysGlnThrSerAsnAspAlaAlaAlaGluAlaLeuAsnAlaSerSerL 34
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
190 ACAACATATCAGCCCATGACGCTTACGCCGCGCTTAACACTGGAAGTA 239
34 YsGluGluAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeu 50
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
240 AGTCAGAGGCTCTTAACGTCCTTAGGCAATTAACCCCTAAGATTATGTT 289
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIle..... 63
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
290 TTTCATATTTCATATTAAATTAATTAATTAATTAATTAATTAATTAATTA 339
64 .....PheAspLysThrP 68
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
340 GTTGAAGTTATGTTCTTCCTTTTATATCTCTCTTTGATGAGACTTC 389
68 roGlu 69
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
390 CAGAA 394

```

```

seq_name: /cgnl_8/gcdata/geneseq/geneseqn/NA1995.DAT:AA084375
seq_documentation_block:
ID AA084375 standard; DNA; 550 BP.
XX
XX AA084375;
XX
XX 19-AUG-1995 (first entry)
XX
XX Tomato leaf curl virus Australian strain DNA sequence.
XX
XX Tomato leaf curl virus; Australia strain; plant disease; ds.
XX
XX Tomato leaf curl virus (Australia).
XX
XX WO503404-A.
XX
XX 02-FEB-1995.
XX
XX 22-JUL-1993; 93WO-EP01946.
XX
XX 22-JUL-1993; 93AU-0047014.
XX
XX 22-JUL-1993; 93WO-EP01946.
XX
XX (BIOC-) BIOCEM SA.
XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX
XX Baudino S, Comeau D, Dry IB, Gruber V, Lenee P;
XX Mason J, Rezalian MA, Ridden JE, Rezanan MA.
XX
XX WPI: 1995-075232/10.
XX
XX Synthetic DNA virus ribozyme(s) - reduce replication, infection
XX and/or assembly of viruses by cleaving target virus sequence,
XX useful for preparing resistant plants, esp tomatoes.
XX
XX Disclosure: Fig 1; 90pp: English.
XX
XX The sequence represents the complementary sense DNA strand of an
XX Australian strain of tomato leaf curl virus. Ribozymes specific
XX for this sequence may be used in generation of transgenic plants
XX with disease-resistance.
XX
XX Sequence 550 BP; 148 A; 120 C; 134 G; 142 T; 6 other:

```

```

alignment_scores:
  Quality: 229.50      Length: 86
  Ratio: 3.762        Gaps: 1
  Percent Similarity: 70.930  Percent Identity: 53.488

```

```

alignment_block:
US-09-289-346a-8 x AA084375 ..

```

```

Align seg 1/1 to: AA084375 from: 1 to: 550

```

```

1 ThrleuValTrpGlyGluAlaAlaValAspGlyArgSerAlaArgGlyGly 17
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
201 ACCCTGGAATGGGGAGATTTCAGATGATGAGACATCTGCCAAGGGGG 250
17 YCysGlnThrSerAsnAspAlaAlaAlaGluAlaLeuAsnAlaSerSerL 34
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
251 ACAACATATCAGCCCATGACGCTTACGCCGCGCTTAACACTGGAAGTA 300
34 YsGluGluAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeu 50
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
301 AGTCAGAGGCTCTTAACGTCCTTAGGCAATTAACCCCTAAGATTATGTT 350
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIle..... 63
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
351 TTACAAATTTCATATTAAATTAATTAATTAATTAATTAATTAATTAATTA 400
64 .....PheAspLysT 67

```

```

401 TCCGTTGAGAGTTTANGTTCCTTTTATCTTCCTTTGATCGAG 450
67 hrProGU 69
   :|||||
451 TTCACGAA 458

```

seq_name: /cgnl_8/gcgdata/geneseq/geneseqn/NA1998.DAT:AAV29761

seq_documentation_block:

```

ID AAV29761 standard; DNA; 2766 BP.
XX
AC AAV29761;
XX
DT 11-AUG-1998 (first entry)
XX
DE Tobacco leaf curling virus gene.
XX
KM Tobacco leaf curling virus gene; TlCV; promoter: ds.
XX
OS Tobacco leaf curling virus.
XX
PN JP10070982-A.
XX
PD 17-MAR-1998.
XX
PF 30-AUG-1996; 96JP-0230394.
XX
PR 30-AUG-1996; 96JP-0230394.
XX
PA (MORO) NORINSUISANSHO KYUSHU NOGYO SHIKENJYO.
XX
DR WPI: 1998-233630/21.
XX
PT Tobacco leaf curling virus gene - useful for inserting into vectors
XX for expression in, e.g. tomato plants
XX
PS Claim 1; Figs 1-3; 9pp; Japanese.
XX
CC This sequence represents the tobacco leaf curling virus (TlCV) gene of
CC the invention. TlCV gene or its promoter can be inserted into a vector
CC for expression in plants, e.g. tobacco and tomato. This sequence is
CC believed to encode the TlCV proteins shown in AAW56493-W56498.
XX
SQ Sequence 2766 BP; 722 A; 576 C; 609 G; 859 T; 0 other;

```

alignment_scores:

```

Quality: 220.00 Length: 84
Ratio: 3.607 Gaps: 1
Percent Similarity: 72.619 Percent Identity: 53.571

```

alignment_block:

US-09-289-346A-8 x AAV29761/rev ..

Align seg 1/1 to reverse of: AAV29761 from: 1 to: 2766

```

2 LeuValTrpGlyGluAlaValAlaSPGlyArgSerAlaArgGlyGly 18
   ||| :||| ||||| ||||| ||||| ||||| |||||
2436 CTTCGATTTCGACTTTCACAGTCGAGCAAGATCACCTAGGCGAGTTG 2387
18 sGlnThrSerAsnAspAlaAlaGluAlaGluAlaAsnAlaSerSerLysG 35
   ||| :||| ||||| ||||| ||||| ||||| |||||
2386 CCAATCTGCCAACGACGACATATGCCGAGCAATCACTCAGATCAAGT 2337
35 LngLualaleuGlnIleIleArgGluLysIleProGluLysTyrLeuPhe 51
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
2336 CACCGGACACTCATATATTAAGGAGAAAGCTCCCAAGATTGTTTGA 2287
52 GlnPheHisAsnLeuAsnSerAsnLeuAsnParGle..... 63
   ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2286 CAATTTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2237

```

```

64 .....PheAspLysThrProG 69
2236 GGAGCTTTTGTTCCTCTTCTAGTCTCTTCATTCATCAAGTTCCTG 2187
69 Lu 69
   ||
2186 AA 2185

```

seq_name: /cgnl_8/gcgdata/geneseq/geneseqn/NA1997.DAT:AAT93291

seq_documentation_block:

```

ID AAT93291 standard; DNA; 1062 BP.
XX
AC AAT93291;
XX
DT 27-APR-1998 (first entry)
XX
DE Bean golden mosaic geminivirus CI mutant ORF BGAC221.
XX
KM Geminivirus; BGWV; CI gene; transdominant mutation;
XX transgenic plant; disease resistance; ss; cyclic; circular.
XX
OS Bean golden mosaic virus type II isolate Guatemala.
XX
PN WO9739110-A1.
XX
PD 23-OCT-1997.
XX
PF 15-APR-1997; 97WO-US06300.
XX
PR 16-APR-1996; 96US-0015517.
XX
PA (SEMI-) SEMINIS VEGETABLE SEEDS INC.
XX (WISC) WISCONSIN ALUMNI RES FOUND.
XX
PI Ahlquist PC, Hanson SF, Luu HT, Maxwell DP, Stout JT;
XX
DR WPI: 1997-526447/48.
XX P-PSDB: AAW34333.
XX
CC Transgenic plants expressing geminivirus AC1 and CI wild-type and
XX mutant genes - have increased resistance to geminivirus infection
XX e.g. tomato mottle virus, tomato yellow leaf curl virus or bean
XX golden mosaic geminivirus
XX
PS Claim 13; Page 107-109; 132pp; English.
XX
CC This DNA sequence comprises construct BGAC221 that codes for a
XX transdominant lethal mutant (see AAW34333) of the CI protein (see
XX AAW34338) of bean golden mosaic virus (BGWV). It was obtained by
XX Kunkel mutagenesis of the wild-type CI gene (see AAT93314). CI is
XX required for replication. The invention involves production of
XX transgenic plants containing DNA comprising geminivirus CI or AC1
XX wild-type or mutant sequences that negatively interfere in trans
XX with geminiviral replication during infection. Such transgenic
XX plants are resistant to viral infection. The AC1/CI genes are
XX especially from BGWV, tomato mottle virus or tomato yellow leaf
XX curl virus (see AAT93282-93) and encode polypeptides (see AAW34324-35)
XX that have mutations in the highly conserved DNA-nicking and/or the
XX NTP-binding domains.
XX
SQ Sequence 1062 BP; 339 A; 245 C; 219 G; 259 T; 0 other;

```

alignment_scores:

```

Quality: 216.00 Length: 70
Ratio: 3.661 Gaps: 0
Percent Similarity: 84.286 Percent Identity: 58.571

```

alignment_block:

US-09-289-346A-8 x AAT93291 ..

Align seg 1/1 to: AAT93291 from: 1 to: 1062

CC This DNA sequence comprises construct BGAC262 that codes for a
CC transdominant lethal mutant (see AAW34335) of the CI protein (see
CC AAW34338) of bean golden mosaic virus (BGMV). It was obtained (see
CC Kunzel mutagenesis of the wild-type CI gene (see AAT93314). CI is
CC required for replication. The invention involves production of
CC transgenic plants containing DNA comprising geminivirus CI or AC1
CC wild-type or mutant sequences that negatively interfere in trans
CC with geminiviral replication during infection. Such transgenic
CC plants are resistant to viral infection. The AC1/CI genes are
CC especially from BGMV, tomato mottle virus or tomato yellow leaf
CC curl virus (see AAT93282-93) and encode polypeptides (see AAW34324-35)
CC that have mutations in the highly conserved DNA-nicking and/or the
CC MTP-binding domains.

XX Sequence 1062 BP; 340 A; 245 C; 219 G; 258 T; 0 other;

alignment_scores:
Quality: 216.00 Length: 70
Ratio: 3.661 Gaps: 0
Percent Similarity: 84.286 Percent Identity: 58.571

alignment_block:
US-09-289-346A-8 x AAT93293 ..

Align seg 1/1 to: AAT93293 from: 1 to: 1062

```
1 ThleuValTrpGlyAlaAlaValAspGlyArgSerIleArgGly17
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
328 ACAATCCAAATGGGACAAATTCACCAAGTCGACGAGATCTCAAGACG 377
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
17 YCysGlnThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSer134
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
378 TCAGCACTCTGCCACGACCTCATATGCAAGGCAATTAAAGCGCATTC 427
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
34 YscGluAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeu 50
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
428 TTGAATCTGCGCTTGACAAATATGACGAGAACACGCAAAAGATTACGTC 477
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
478 CTTCAACATCAACAACATCGCTCTTAATCTCAACGAGATTCGTCAAGT 527
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
67 rProGluPro 70
   |||:|||||:
528 GCCGGAACCA 537
```

seq_name: /cgn1_8/gcgdata/geneseq/geneseqn/NA1996.DAT: AAT12904

seq_documentation_block:

ID AAT12904 standard; DNA; 1080 BP.

XX AAT12904:
XX
XX 07-NOV-1996 (first entry)
XX
XX Sardinian tomato yellow leaf curl virus mutated CI gene (K227A).
DE Sardinian tomato yellow leaf curl virus mutated CI gene (K227A).
XX
XX Nucleotide triphosphate binding site; DNA helicase; RNA helicase;
KW modification; mutation; viral replication; deficient; inhibition;
KW viral resistance; geminivirus; tomato yellow leaf curl virus;
KW Sardinian isolate; SYLVCV; transgenic plant; P-loop; CI gene;
KW All gene; dominant negative phenotype; ss.
XX
XX Sardinian tomato yellow leaf curl virus.

OS Sardinian tomato yellow leaf curl virus.

XX Key Location/Qualifiers

XX Key 1..1080

XX CDS /tag= a

XX FT /product= Rep.(K227A)

XX FT /note= "encodes Rep protein in which wild-type Lys

XX FT at position 227, i.e. within the MTP-

XX FT binding site, is replaced by Ala"

XX W09608573-AL.

XX 21-MAR-1996.

XX 15-SEP-1995; 95WO-FR01192.

XX 15-SEP-1994; 94FR-0011040.

XX (CNRS) CENT NAT RECH SCI.

XX Gronenborn B;

XX WPI: 1996-179947/18.

XX P-PSDB; AAR88870.

XX Prodn. of virus-resistant transgenic plants - using mutated genomic

XX sequence from phytopathogenic DNA virus

XX Disclosure: Fig 13; 93pp; French.

CC Mutation of consensus amino acids in the MTP-binding site of
CC geminivirus Rep protein is used to produce replication deficient
CC viruses. The mutated viral nucleic acid is used for producing
CC transgenic plants that are resistant to, or tolerant of, the native
CC virus. The present sequence encodes a mutant form of the Rep (or CI)
CC protein from the Sardinian isolate of tomato yellow leaf curl virus
CC (SYLVCV) in which the wild-type Lys227 residue has been changed to an
CC Ala residue; transgenic Nicotiana benthamiana plants generated by
CC transformation with the mutated virus were found to be resistant to
CC SYLVCV, i.e. the mutation results in a dominant negative phenotype.

XX Sequence 1080 BP; 355 A; 248 C; 210 G; 267 T; 0 other;

alignment_scores:
Quality: 216.00 Length: 69
Ratio: 3.789 Gaps: 0
Percent Similarity: 82.609 Percent Identity: 56.522

alignment_block:
US-09-289-346A-8 x AAT12904 ..

Align seg 1/1 to: AAT12904 from: 1 to: 1080

```
2 LeuValTrpGlyAlaAlaValAspGlyArgSerIleArgGly18
   ||| |||||:|||||:|||||:|||||:|||||:|||||:
331 CTTGAATGGGCTTCTTCAGATCGACGAGCATCTGCTAGGGGAGGACA 380
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
18 sGlnThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerIysG 35
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
381 ACAGACAGCCACGACGCTTACGCAAAAGCAATTAAAGCGAGGAAGTACT 430
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
35 InGluAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeuPhe 51
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
431 CCCAGGCTTGTGATTAATTAAGCAATTACCGCCTAGACATTCGTTCTA 480
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
52 GlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysThrP 68
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
481 CATTTTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 530
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
68 ogLupro 70
   |||
531 GGCACCT 537
```

seq_name: /cgn1_8/gcgdata/geneseq/geneseqn/NA1996.DAT: AAT12905

seq_documentation_block:

ID AAT12905 standard; DNA; 1080 BP.

XX AAT12905:

XX 07-NOV-1996 (first entry)

```

XX DE Sardinian tomato yellow leaf curl virus mutated C1 gene (K227H).
XX
XX KM Nucleotide triphosphate binding site; DNA helicase; RNA helicase;
XX KM modification; mutation; viral replication; deficient; inhibition;
XX KM viral resistance; geminivirus; tomato yellow leaf curl virus;
XX KM Sardinian isolate; STYLCV; transgenic plant; P-loop; C1 gene;
XX KM All gene: ss.
XX OS Sardinian tomato yellow leaf curl virus.
XX
XX FH Key Location/Qualifiers
XX FT CDS 1..1080
XX FT /*tag= a
XX FT /product= Rep.(K227H)
XX FT /note= "encodes Rep protein in which wild-type Lys
XX FT at position 227, i.e. within the NTP-
XX FT binding site, is replaced by His"
XX
XX PN MO9608573-A1.
XX PD 21-MAR-1996.
XX
XX PF 15-SEP-1995; 95MO-FR01192.
XX PR 15-SEP-1994; 94FR-0011040.
XX PA (CNRS ) CENT NAT RECH SCI.
XX PI Gronenborn B;
XX DR WPI: 1996-179947/18.
XX DR P-PSDB; AAR88871.
XX
XX PT Prodn. of virus-resistant transgenic plants - using mutated genomic
XX PT sequence from phytopathogenic DNA virus
XX PS Disclosure: Fig 13; 93pp; French.
XX
XX CC Mutation of consensus amino acids in the NTP-binding site of
XX CC geminivirus Rep protein is used to produce replication deficient
XX CC viruses. The mutated viral nucleic acid is used for producing
XX CC transgenic plants that are resistant to, or tolerant of, the native
XX CC virus. The present sequence encodes a mutant form of the Rep (or C1)
XX CC protein from the Sardinian isolate of tomato yellow leaf curl virus
XX CC (STYLCV) in which the wild-type Lys227 residue has been changed to a
XX CC His residue; transgenic Nicotiana benthamiana plants generated by
XX CC transformation with the mutated virus were not resistant to STYLCV.
XX CC In contrast, plants transformed with a virus in which Lys227 had been
XX CC replaced by Ala were found to be resistant.
XX
XX SO Sequence 1080 BP; 356 A; 248 C; 208 G; 268 T; 0 other:

alignment_scores:
    Quality: 216.00      Length: 69
    Ratio: 3.789        Gaps: 0
    Percent Similarity: 82.609      Percent Identity: 56.522

alignment_block:
US-09-289-346A-8 x AAT12905 ..

Align seg 1/1 to: AAT12905 from: 1 to: 1080

2 LeuValTTPoLygLuAlaIaValaSpGlyArgSerAlaArgGlyGlyCy 18
   ||| |||||
   ::||| ||||| ||||| ||||| |||||
331 CTTGAATGGGGTCTTCGAGATCGACGAGATCGTGGGAGAGACA 380
   ||||| ||||| ||||| ||||| ||||| |||||
18 sGlnThrSerAsnAspAlaAlaIaGluAlaLeuAsnAlaSerSerLysG 35
   ||||| ||||| ||||| ||||| ||||| |||||
381 ACGACAGCGCAACGACGCTTACGCAAGCAATTAACGCAAGTAAGT 430
   ||||| ||||| ||||| ||||| ||||| |||||
35 InGluAlaLeuGlnIleIleArgGluLysTlleProGluLysTyrLeuPhe 51

```

```

seq_name: /cgn1_8/gcgdata/geneseq/geneseqn/NA1996.DAT:AAT12906
seq_documentation_block:
ID AAT12906 standard; DNA; 1080 BP.
XX
XX AC AAT12906;
XX
XX DT 07-NOV-1996 (first entry)
XX
XX DE Sardinian tomato yellow leaf curl virus mutated C1 gene (K227R).
XX
XX KM Nucleotide triphosphate binding site; DNA helicase; RNA helicase;
XX KM modification; mutation; viral replication; deficient; inhibition;
XX KM viral resistance; geminivirus; tomato yellow leaf curl virus;
XX KM Sardinian isolate; STYLCV; transgenic plant; P-loop; C1 gene;
XX KM All gene: ss.
XX
XX OS Sardinian tomato yellow leaf curl virus.
XX
XX PI Gronenborn B;
XX DR WPI: 1996-179947/18.
XX DR P-PSDB; AAR88872.
XX
XX PT Prodn. of virus-resistant transgenic plants - using mutated genomic
XX PT sequence from phytopathogenic DNA virus
XX PS Disclosure: Fig 13; 93pp; French.
XX
XX CC Mutation of consensus amino acids in the NTP-binding site of
XX CC geminivirus Rep protein is used to produce replication deficient
XX CC viruses. The mutated viral nucleic acid is used for producing
XX CC transgenic plants that are resistant to, or tolerant of, the native
XX CC virus. The present sequence encodes a mutant form of the Rep (or C1)
XX CC protein from the Sardinian isolate of tomato yellow leaf curl virus
XX CC (STYLCV) in which the wild-type Lys227 residue has been changed to an
XX CC Arg residue; transgenic Nicotiana benthamiana plants generated by
XX CC transformation with the mutated virus were not resistant to STYLCV.
XX CC In contrast, plants transformed with a virus in which Lys227 had been
XX CC replaced by Ala were found to be resistant.
XX
XX SO Sequence 1080 BP; 356 A; 247 C; 210 G; 267 T; 0 other:

```

```

alignment_scores:      Quality: 216.00      Length: 69
                       Ratio: 3.789      Gaps: 0
Percent Similarity: 82.609      Percent Identity: 56.522

alignment_block:
US-09-289-346A-8 x AAT12906      ..

Align seg 1/1 to: AAT12906 from: 1 to: 1080

2 LeuValITrpglyGluAlaValaAspGlyArgSerAlaArglyGly 18
   ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
331 CTTCGATCGGCTTCCAGATCGAGCGATCTCTCGAGGAGACA 380
18 sGIuThSerAsnAspAlaIaIaGluAlaLeuAsnAlaSerSerlysg 35
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
381 ACAGACACGACGACGCTTACCGCAAGCAATTAACGCAAGATAGT 430
35 IuGluAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeuPhe 51
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
431 CGCAGGCTTGTGATGTAATTAAGAAATTAAGCATTAAGTCTA 480
52 GlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysThrPr 68
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
481 CATTTTCATATATATAATAGTAATTAAGTATTAAGTTCAGGTCC 530
68 oGIuPro 70
   ||| |||
531 GCGACCT 537

seq_name: /cgn1_8/gcgdata/geneseq/geneseqn/NA1997.DAT:AAT93314
seq_documentation_block:
ID AAT93314 standard; DNA; 1183 BP.
XX
AC AAT93314:
XX
DT 27-APR-1998 (first entry)
XX
DE Bean golden mosaic geminivirus CI open reading frame.
XX
KM Geminivirus; BGMV; CI gene; transdominant mutation;
XX transgenic plant; disease resistance; ss; cyclic; circular.
XX
OS Bean golden mosaic virus type II isolate Guatemala.
XX
FH Key Location/Qualifiers
FT CDS 1..1062
   /*tag= a
PI WO9739110-A1.
PN 23-OCT-1997.
XX
PD 15-APR-1997; 97WO-US06300.
XX
PR 16-APR-1996; 96US-001517.
XX
PA (SEMI-) SEMINIS VEGETABLE SEEDS INC.
XX (WISC ) WISCONSIN ALUMNI RES FOUND.
XX
PI Ahlquist PG, Hanson SF, Luu HT, Maxwell DP, Stout JT;
XX
DR WPI: 1997-526447/48.
DR P-PSDB: AAM34338.
XX
XX Transgenic plants expressing geminivirus AC1 and CI wild-type and
XX PT mutant genes - have increased resistance to geminivirus infection
XX PT e.g. tomato mottle virus, tomato yellow leaf curl virus or bean
XX PT golden mosaic geminivirus
XX
XX Example 5; Page 100-102; 132pp; English.
XX

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CC This genomic DNA sequence includes the open reading frame (ORF) of
CC the wild-type CI gene of bean golden mosaic virus (BGMV), a
CC geminivirus that has a monopartite genome. The CI protein (see
CC AAM34338) is required for replication. The wild-type CI ORF was
CC subcloned to Kunkel mutagenesis (see AAT93290-93). The invention
CC involves production of transgenic plants containing DNA comprising
CC CI or AC1 wild-type or mutant sequences that negatively interfere
CC in trans with geminiviral replication during infection. Such
CC transgenic plants are resistant to viral infection. The AC1/CI
CC genes are especially from BGMV, tomato mottle virus or tomato
CC yellow leaf curl virus (see AAT93282-93) and encode polypeptides
CC (see AAM34324-35) that have mutations in the highly conserved
CC DNA-nicking domain and/or the NTP-binding domains.
XX
SQ Sequence 1183 BP; 372 A; 276 C; 248 G; 287 T; 0 other:

alignment_scores:      Quality: 216.00      Length: 70
                       Ratio: 3.661      Gaps: 0
Percent Similarity: 84.286      Percent Identity: 58.571

alignment_block:
US-09-289-346A-8 x AAT93314      ..

Align seg 1/1 to: AAT93314 from: 1 to: 1183

1 ThrLeuValITrpglyGluAlaValaAspGlyArgSerAlaArglyGly 17
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
328 ACAATCGAATGGGACACATTCCAAGTCGACGCAAGATCTGCAAGAGAGG 377
17 yCysGlnThrSerAsnAspAlaIaIaGluAlaLeuAsnAlaSerSerl 34
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
378 TCAGCAGTCTGCCACGACATATGCAAGCATTAACGCAAGATCA 427
428 TTGAATCTGCCCTTGACATATTCAGAGAGAACGCAAGATTAAGTCTC 477
34 yscIuGluAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeu 50
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
428 TTGAATCTGCCCTTGACATATTCAGAGAGAACGCAAGATTAAGTCTC 477
51 PhcGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysThr 67
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
478 CTTCACATCAATCAACATCCGTTCTAATCTCGAACGATTCCTCAAGT 527
67 rProGluPro 70
   ||||| |||||
528 GCCGGAACCA 537

seq_name: /cgn1_8/gcgdata/geneseq/geneseqn/NA1997.DAT:AAT93290
seq_documentation_block:
ID AAT93290 standard; DNA; 1183 BP.
XX
AC AAT93290:
XX
DT 27-APR-1998 (first entry)
XX
DE Bean golden mosaic geminivirus CI mutant gene.
XX
KM Geminivirus; BGMV; CI gene; transdominant mutation;
XX transgenic plant; disease resistance; ss; cyclic; circular.
XX
OS Bean golden mosaic virus type II isolate Guatemala.
XX
FH Key Location/Qualifiers
FT CDS 1..1062
   /*tag= a
PI WO9739110-A1.
PN 23-OCT-1997.
XX
PD 15-APR-1997; 97WO-US06300.
XX
XX

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1094 GAAAGAACCTTTAAAGAGCTCTTACCTCACAAGAAAGATTGTGA 1143
59 nleuaspargillepheaspilysthrproglu 69
: |||||:||||:|||||:
1144 AGCGGATCGTGTTGTCACCAACACCTGCAC 1174
seq_name: gb_est2:BG595046

seq_documentation_block:
LOCUS BG595046 732 bp mRNA EST 12-APR-2001
DEFINITION EST493724 CSTS Solanum tuberosum cDNA clone csts9019 5' sequence,
ACCESSION BG595046
VERSION BG595046
KEYWORDS BG595046.1 GI:13613186
SOURCE EST.
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
1 (bases 1 to 732)
REFERENCE
AUTHORS van der Hoeven,R., Bezzerides,J., Sun,H., Cho,J., Chiemingo,A.,
Bongri,O., Buell,C.R., Romling,C., Tanksley,S. and Baker,B.
TITLE Generations of ESTs from sprouting potato eyes
JOURNAL Unpublished (2000)
COMMENT Contact: Cathy Romling
The Institute for Genomic Research
For clone info: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com
Seq primer: M13F-R.

FEATURES
Source Location/Qualifiers
1..732
/organism="Solanum tuberosum"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="csts9019"
/clone_lib="csts"
/tissue_type="sprouting eyes from tubers"
/dev_stage="12-14 weeks post harvest"
/lab_host="SOLR"
/notes="vector: pBluescript SK(-); site_1: EcoRI; site_2:
XhoI; Various sizes of sprouting eyes (2mm to 15mm) were
taken from tubers. The tubers were incubated at 26C in the
dark for 2-3 weeks prior to sprouting. The eyes were
frozen in liquid nitrogen immediately upon removal from
tubers."

BASE COUNT 198 a 154 c 164 g 216 t
ORIGIN

alignment_scores:
Quality: 71.50 Length: 54
Ratio: 1.932 Gaps: 3
Percent Similarity: 68.519 Percent Identity: 37.037

alignment_block:
US-09-289-346a-8 x BG595046/rev ..

Align seg 1/1 to reverse of: BG595046 from: 1 to: 732

11 GYAAGSerAlaArgGlyGlyCysGlnThrSerAsnAsp.....AlaAl 25
|||||:|||||:|||||:
408 GGAAGTCGCGCTGCTAGCAGATCTAGACAGATGGAATGGAATGAGACTTC 359
25 aalaGluAlaLeuAsnAlaSerSerLysGluAlaLeuGlnIleLea 42
: |||||:||||:||||:
358 TATTAGAGCGCAAAATAGCAGACTCTTACACTTATTCACAGTAGGAC 309
42 rgGluLysIleProGluLysTyrLeuPheGlnPheHisAsn...IleAsn 57
: |||||:|||||:|||||:
308 AATAAAGATT.....CTTCACTTGTTCAGATTCCACATATGACCTCAG 265

```

```

58 SerAsnLeuAsp 61
: |||||:||||:
264 AACATATATCAAC 253
seq_name: gb_est2:BF506184

seq_documentation_block:
LOCUS BF506184 765 bp mRNA EST 19-APR-2001
DEFINITION At08588.5Prime AT Drosophila melanogaster adult testes potB7
Drosophila melanogaster cDNA clone At08588.5 similar to CG10777:
Fban010777 RNA binding' located on: X 7C8-7C8; 04/07/2001, mRNA
sequence.
ACCESSION BF506184
VERSION BF506184
KEYWORDS BF506184.2 GI:13688762
SOURCE EST.
ORGANISM fruit fly.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 765)
REFERENCE
AUTHORS Stapleton,M., Brokstein,P., Hong,L., Agbayani,A., Baxter,E., Berman
B., Carlson,J., Champe,M., Chavez,C., Chew,M., Dorsett,V., Farfan
D., Frise,E., George,R., Gonzalez,M., Guarin,H., Harris,N., Li,P.,
Liao,G., Miranda,A., Misra,S., Mungall,C.J., Nunco,J., Paclob,J.,
Paragas,V., Park,S., Phouanavong,S., Man,K., Yu,C., Lewis,S.E.,
Celinkner,S. and Rubin,G.M.
BDGP/HMT AT Drosophila EST Project
Unpublished (2000)
JOURNAL On Dec 6, 2000 this sequence version replaced gi:11589485.
COMMENT Contact: Stapleton, M.
BDGP

FEATURES
Source Location/Qualifiers
1..765
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="AT08588"
/clone_lib="AT Drosophila melanogaster adult testes potB7"
/sex="male"
/dev_stage="0-3 day old Ore-R males"
/lab_host="Plates At-10-AT.120: DHS-alpha. Plates
AT.121-AT.319: DHS-alpha Tona"
/notes="Organ: ADULT testes; Vector: potB7; Site_1: EcoRI;
Site_2: XhoI; The mRNA for the testis library was made
from testes and seminal vesicles hand dissected from 0-3
day old Ore-R males. RNA kindly provided by the lab of
Margaret Fuller. Sized fractionated cDNAs were directly
ligated into potB7. Plasmid cDNA library."

BASE COUNT 199 a 205 c 225 g 136 t
ORIGIN

alignment_scores:
Quality: 71.50 Length: 64
Ratio: 2.103 Gaps: 2
Percent Similarity: 53.125 Percent Identity: 34.375

alignment_block:
US-09-289-346a-8 x BF506184 ..

Align seg 1/1 to: BF506184 from: 1 to: 765

10 AspGlyArgSerAlaArgGlyGlyCysGlnThrSerAsnAlaAla 26
: |||||:|||||:|||||:
553 AACGGCGCGAGTCTGCTGCTACCAAGCAATATGACTACATGCTGC 602

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26 agluAlaLeuAsnAlaSerSerlysgluAlaLeuGlnIlelleArg 43
   |||||||  |||||||  |||||||  |||||||  |||||||  |||
603 C...GCCTTAGGCATGCTTCCAAAGAGAGCGCCGAGATCCACG 649
   |||||||  |||||||  |||||||  |||||||  |||||||  |||
43 luLySilePro..... 46
   |||||||
650 AAAAGGCCAAATAATCCCGCGCAATTTAGTGAACCAAGTGGAGAAC 699
   |||||||
47 ...GluLySTyrlleuPheGlnPheHISAsnLeuAsnSerAsn 59
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
700 CTCGAGCCCTTCTCTCAAGATTTCTACACATTCATCCGAA 741

seq_name: gb_est2:BF342302

seq_documentation_block:
LOCUS      BF342302      646 bp      mRNA      EST      22-NOV-2000
DEFINITION 602013083F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4148757
5', mRNA sequence.
ACCESSION  BF342302
VERSION     BF342302.1  GI:11289259
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 646)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Email: cgrabbs-remail.nih.gov
            Tissue Procurement: David N. Louis, M.D.
            cDNA Library Preparation: Life Technologies, Inc.
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LHM9409 row: f column: 22
            High quality sequence stop: 613.
FEATURES             Location/Qualifiers
     source           1..646
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4148757"
                     /clone_lib="NCI_CGAP_Brn64"
                     /tissue_type="glioblastoma with EGFR amplification"
                     /lab_host="DH10B (TI phage-resistant)"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site:1: NCI;
                     Site:2: Salt; Cloned unidirectionally. Primer: Oligo dT.
                     Average insert size 1.57 kb. Constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT      150 a      158 c      197 g      141 t
ORIGIN

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alignment_scores:
  Quality: 71.00      Length: 42
  Ratio: 2.448      Gaps: 2
  Percent Similarity: 69.048      Percent Identity: 42.857
alignment_block:
  US-09-289-346a-8 x BF342302      ..
Align seg 1/1 to: BF342302 from: 1 to: 646

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3 valTrrgLy...GluAlaAlaValAspGlyArgSerAlaArgGlyGly 18
  |||||||  |||  |||||||  |||||||  |||||||  |||
202 GTGTGGGGGTAGAGGAGCGTTGCTGCGAGGAGCGCGGGCGGATG 251
  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
18 sgInThSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerlysg 35
  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

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252 TGAACTCGGGGAGCGGCGCACCCAAAGGCTCAGGGGCCCCAAACCTTG 301
   |||||||  |||||||  |||||||  |||||||  |||||||  |||
35 luGluAlaLeuGlnIlelleArgGlu 43
   |||||||
302 AA.....ATCCGTGA 312

seq_name: gb_gss:AQ906722

seq_documentation_block:
LOCUS      AQ906722      412 bp      DNA      GSS      09-JAN-2001
DEFINITION GSSrC03166 Trypanosoma cruzi random genomic library Trypanosoma
cruzi genomic clone G40C19, DNA sequence.
ACCESSION  AQ906722
VERSION     AQ906722.3  GI:10136203
KEYWORDS    GSS.
SOURCE      Trypanosoma cruzi.
ORGANISM    Trypanosoma cruzi
Eukaryota; Euzlenzoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma; Schizotrypanum.
REFERENCE   1 (bases 1 to 412)
AUTHORS     Aguero,F., Verdun,R., Frasch,A.C.C. and Sanchez,D.O.
TITLE       A random sequencing approach for the analysis of the trypanosoma
cruzi genome: general structure, large gene and repetitive DNA
families, and gene discovery
JOURNAL     Genome Res. 10 (12), 1996-2005 (2000)
COMMENT     On Sep 14, 2000 this sequence version replaced gi:9377231.
            Contact: Sanchez D.O.
            Instituto de Investigaciones Biologicas (Univ. Nac. de Gral
            San Martin)
            Av. Gral Paz entre Albarellos y Constituyentes, INTI edificio 24
            CP(650) San Martin, Prov. de BS AS, Argentina
            Tel: 54-11-4580-7255 ext 309
            Fax: 54-11-4752-9639
            Email: dsanchez@ibb.unsam.edu.ar
            Sequences were basecalled with phred and vector was masked with
            crossmatch (see http://genome.washington.edu). Sequences were then
            trimmed from both ends to remove low quality bases and masked
            vector.
            Seq primer: T7
            Class: Shotgun.
FEATURES             Location/Qualifiers
     source           1..412
                     /organism="Trypanosoma cruzi"
                     /strain="Cl-Brener"
                     /db_xref="taxon:5693"
                     /clone="G40C19"
                     /clone_lib="Trypanosoma cruzi random genomic library"
                     /cell_type="epimastigote"
                     /note="Vector: pBS(-) (Stratagene); T. cruzi DNA was
                     randomly sheared using a nebulizer and the 1 to 2 Kb range
                     was gel purified and cloned into the dephosphorylated
                     HincII site of the vector."
BASE COUNT      113 a      110 c      99 g      90 t
ORIGIN

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alignment_scores:
  Quality: 70.00      Length: 50
  Ratio: 2.121      Gaps: 1
  Percent Similarity: 66.000      Percent Identity: 38.000
alignment_block:
  US-09-289-346a-8 x AQ906722      ..
Align seg 1/1 to: AQ906722 from: 1 to: 412

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10 AspGlyArgSerAlaArgGlyGlyCysGlnThSerAsnAspAlaAla 26
  |||||||  |||  |||||||  |||||||  |||||||  |||
224 GATGCTACCGACAGCAAGCGCCCTCTATCTACAGTTCAGCGCCGACG 273
  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
26 agluAlaLeuAsnAlaSerSerlysgluAlaLeuGlnIlelleArg 42
  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

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274 GTGAGCGAAGAATGCACGACAAAGCATTCATTCTTCCCTACTTGCA 323
43 GtubgllleprocilutystyrtleupnegiclnphiehisAsnleuAnster 58
||||| : :: ||||| : :: :: ||||| : :: :: ||||| : :: :: ||||| :
324 GAACGGCTGCCGACAACGATATCTCCTCCATTAGCAATTTAATTCA 371

seq_name: gb_est1:A1959235

seq_documentation_block:
LOCUS      A1959235          mRNA           EST           20-AUG-1999
DEFINITION gb:f65909.y1 zebrafish Washu MPIMG EST Danio rerio cDNA 5' similar to
VERSION    gb:h69150.405 RIBOSOMAL PROTEIN S18 (HUMAN); mRNA sequence.
KEYWORDS   A1959235
SOURCE     A1959235.1 GI:5751948
            EST.
            zebrafish.
ORGANISM   Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Rasborinae; Danio.
REFERENCE  1 (bases 1 to 560)
AUTHORS   Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy
            ,S., Hillier,L., Knab,T., Martin,J., Beck,C., Wyllie,T., Underwood
            ,K., Stepien,M., Theising,B.B., Allen,M., Bowers,Y., Person,B.,
            Swaller,T., Gibbons,M., Page,D., Harvey,N., Schurk,R., Riltter,E.,
            Korn,S., Shih,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R.
            and Wilson,R.
TITLE      Washu Zebrafish EST Project 1998
JOURNAL    Unpublished (1998)
COMMENT    Contact: Stephen L. Johnson
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel.: 314 286 1800
            Fax: 314 286 1810
            Email: zbrafish@watson.wustl.edu
            CDNA Library Preparation by: Matthew Clark, CDNA Library Arrayed by:
            Matthew Clark, DNA Sequencing by: Washington University Genome
            Sequencing Center Clone distribution: Genome Systems, St. Louis,
            Missouri (web address: www.genomesystems.com) (email contact:
            info@genomesystems.com) and Research Genetics, Huntsville, Alabama
            (web address: www.resgen.com) (email contact: info@resgen.com) and
            ResourceCenter@umprimar Datenbank, Berlin, Germany (web address:
            www.rzp.de)
            Seq primer: T3 ET from Amersham
            High quality sequence stop: 491.

FEATURES             Source
         location/Qualifiers
         1..560
         /organism="Danio rerio"
         /db_xref="taxon:7955"
         /clone_lib="Zebrafish Washu MPIMG EST"
         /sex="mixed"
         /tissue.type="26 somite embryos, adult livers, shield
stage embryos"
         /lab_host="XLI-blue MRF"
         /note="Vector: pSPORT1; Site_1: NotI; Site_2: SalI; 1st
strand cDNA was primed with a Not I - oligo(dT)15 primer
15'GACAGCTTCAGATCGGAGCGAGCGCCGCTTTTTTTTTTTTTT3';
double-stranded cDNA was ligated to Sal I adaptors (BRL),
digested with Not I and cloned into the Not I and Sal I
sites of the pSPORT1 vector (BRL). Library was constructed
by Matthew Clark (Lehrnach lab; ICRR, London and Max Planck
Institut fuer Molekulare Genetik,Berlin). cDNAs for EST
analysis were selected following oligonucleotide
hybridization fingerprinting of arrayed clones from
zebrafish late somitogenesis (26 ss), adult liver or
embryonic shield stage (5.6 h) libraries. Fingerprint
data were used to computationally cluster cDNAs, and a
single cDNA from each cluster was chosen for sequencing.
In some cases multiple members of the same cluster were
sequenced to assess clustering parameters or single clones
were sequenced additional times to assess quality
control."

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ORIGIN
Alignment_scores:
  Quality: 70.00      Length: 61
  Ratio: 1.944      Gaps: 2
  Percent Similarity: 59.016      Percent Identity: 31.148

Alignment_block:
  US-09-289-346A-8 x AI959235 ..

Align seg 1/1 to: AI959235 from: 1 to: 560

1 ThrleValTrrpGlyAlaAlaValAlaSpGlyArgSerAlaArgGlyG1 17
||||| ||||| |||||
22 ACATTGTCTGTGGGGGGGGGTGTG.....GGCGG 50
17 yCysGlnThrSerAsnAspAlaAlaAlaGluAlaLeuAsnAlaSerSert 34
||||| ||||| ||||| |||||
51 GTGTGACCCCTCTCTCTCCACACGCGTCCGCCACGCCGTCGCCACCGATC 100
34 yAGGluAlaLeuGlnIleIleArgGlyIuLysIleArgIuLysTyrLeu 50
||||| ||||| ||||| |||||
101 AAGATGTCTCTCTC.....GTCTATCCGACAGAGTTTCAG 135
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAsp 61
||||| ||||| ||||| |||||
136 CACATCTCTGTCTCTCAACACGAACATTCAT 168

seq_name: gb_est2:BG472323

seq_documentation_block:
LOCUS      BG472323      789 bp      mRNA      EST      21-MAR-2001
DEFINITION 602513970F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:4645793 5',
mRNA sequence.
ACCESSION  BG472323
VERSION    BG472323.1  GI:13404598
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 789)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaps@email.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: Image.lnl.gov
Plate: L1CM419 row: 1 column: 18
High quality sequence stop: 745.
Location/Qualifiers
1..789
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4645793"
/clone_1lb="NIH_MGC_16"
/tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adapter: GGCAAGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
Note: This is a NIH_MGC Library."

BASE COUNT      162 a      265 c      211 g      151 t

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ORIGIN

alignment_scores:

Quality:	70.00	Length:	78
Ratio:	1.591	Gaps:	2
Percent Similarity:	56.410	Percent Identity:	26.923

alignment_block:

US-09-289-346a-8 x BG472323 ..

Align seg 1/1 to: BG472323 from: 1 to: 789

```

1 ThrLeuValTrpGlyAlaIleAlaValAspGlyArgSerAlaArgGlyGly 17
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
480 ACCCTGCACTGGGGGGAGACCCGGAATTGACCCGACGGCTGTAGGACGAC 529
17 yGsglnThrSerAsnAspAlaIleAlaIleAlaLeuAsn..... 30
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
530 ACCGTACACGACGACACTTGCAGCCGCGCGGAGCTTCACATTGTCATT 579
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
31 .....AlaSerSerlysgluGlu 36
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
580 AFAACTCAGACCTTATTCCTGACGCCGACACTGCCAGCAACAAGTCAGAA 629
37 AlAlaLeuGlnIleIleArgGlyIleProGlyIleTyfLeupheGlnPh 53
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
630 GGCCTCGCTGCTCTG.....GCTGTTCTCTATTGAGAT 661
53 ghIsAsnLeuAsnSerAsnLeuAsnParGlyIlePhe 64
: ||||| ||||| ||||| ||||| ||||| ||||| |||||
662 GGGCTCTTCATTCCTCTATGACAGATCTTC 695

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seq_name: gb_est2:BG113520

seq_documentation_block:

LOCUS BG113520 1142 bp mRNA EST 30-JAN-2001

DEFINITION 602283979P1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:4371642 5', mRNA sequence.

ACCESSION BG113520

VERSION BG113520.1 GI:12607026

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1142)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LHAM10030 row: m column: 19
High quality sequence stop: 326.
Location/Qualifiers
1..1142
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4371642"
/clone_id="NIH_MGC_86"
/tissue_type="osteosarcoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: bone; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.533 kb. Library enriched for full-length clones and constructed by Life Technologies.

BASE COUNT 351 a 275 c 272 g 244 t

ORIGIN

alignment_scores:

Quality:	69.50	Length:	60
Ratio:	1.986 <td>Gaps:</td> <td>2 </td>	Gaps:	2
Percent Similarity:	58.333 <td>Percent Identity:</td> <td>35.000 </td>	Percent Identity:	35.000

alignment_block:

US-09-289-346a-8 x BG113520 ..

Align seg 1/1 to: BG113520 from: 1 to: 1142

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3 ValTrp.....GlyAlaIleAlaValAspGlyArgSerAlaArgGlyGly 17
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
464 GTGTGCATCTCCGAGACCGGAGCTGTAAGAGTCCCTCCGATACGAGCG 513
17 yGsglnThrSerAsnAspAlaIleAlaIleAlaLeuAsnAlaSerSer 34
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
514 TTGCCAGGAGTCTGGGAAAGTGTCTCTCTCACAACGAGACACCGAGGC 563
34 ysgluGlnAlaLeuGlnIleIleArgGlyIleProGlyIleTyf 49
: ||||| ||||| ||||| ||||| ||||| ||||| |||||
564 AAGTGTACACAGCTCGAGATTATCTGTTAAAGTGCCTCCGATACGATAC 613
50 LeupheGlnPheHisAsnLeuAsnSerAsn 59
||||| ||||| ||||| ||||| ||||| ||||| |||||
614 AGATACCAACACAAACACAAACAAAC 643

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seq_name: gb_est1:AV369952

seq_documentation_block:

LOCUS AV369952 216 bp mRNA EST 14-NOV-1999

DEFINITION AV369952 RIKEN full-length enriched, adult male colon Mus musculus cDNA clone 9030203124 3', mRNA sequence.

ACCESSION AV369952

VERSION AV369952.1 GI:6417599

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 216)

AUTHORS Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Horii, F., Ishii, Y., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Owa, C., Ozawa, Y., Saito, H., Sano, M., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Takahashi, F., Tateo, M., Tomihaga, N., Tsunoda, Y., Watanabe, S., Yamamura, T., Yasunishi, A., Yokota, T., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.

JOURNAL RIKEN Mouse ESTs (Konno, H., et al. 1999)

COMMENT Unpublished (1999)
Contact: Yoshinori Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Saitama-cho, Tsunumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/,
Sasaki, N., Izawa, M., Watanabe, M., Okazaki, Y. and Hayashizaki, Y., Matsuyama, S., Carninci, P., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.,
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)
Itoh, M., Katsunari, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki


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ACCESSION      A2208697
VERSION        A2208697.1  GI:8421822
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
COMMENT
FEATURES
    source
        1. 910
            /organism="Strongylocentrotus purpuratus"
            /db_xref="taxon:7668"
            /clone="Plate=150 Col=4 Row=E"
            /clone_lib="Strongylocentrotus purpuratus, purple sea
            urchin, sperm genomic BAC library"
            /note="Organ: sperm; Vector: BAC3.6; BAC Clones in E.Coli
            DH10B"
BASE COUNT      248 a      255 c      170 g      237 t
ORIGIN
alignment_scores:
    Quality:      68.50      Length:      56
    Ratio:        1.957      Gaps:      3
    Percent Similarity: 62.500      Percent Identity: 35.714
alignment block:
US-09-289-346A-8 x A2208697  ...
Align seg 1/1 to: A2208697 from: 1 to: 910
18  CysGlnThrSerAsnAPLaAlaIaGlu...AlaLeuAsnAlaSerSe 33
||||| ||||| ||||| ||||| ||||| ||||| |||||
604  TGCACACTCTCTACCGGGCGCATCCCGGAAATGTTTAAACAATCTAT 653
33  rlysgtuglualaleuGlnIlelle....ArgGluLysIleProGluL 48
::: |||||::: ::: |||||:::
654  CTTTACTCCACACAGACACTACTAGCAATATATGCAAAACTGCGGAAA 703
48  ystYrIleupheGlnpHehIsaLnleuAsnSerIsaLnleuAspArgIle 64
||||| ||||| ||||| ||||| ||||| ||||| |||||
704  AATGG.....CACACTATTGGAAAAAATATACCCGAGCATTTGG 741
65  AspLysThrProGluPro 70
||||| ||||| ||||| ||||| ||||| ||||| |||||
742  GGTAAACCCCTTCGCCG 759
seq_name: gb_gss:AQ950848
seq documentation block:
LOCUS      AQ950848      572 bp      DNA      GSS      27-JAN-2000
DEFINITION      Sheared DNA-S1M3.TF Sheared DNA Trypanosoma brucei genomic clone
                  Sheared DNA-S1M3. DNA sequence.

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ACCESSION      A0950848
VERSION        A0950848.1 GI:6774113
KEYWORDS       GSS.
SOURCE         Trypanosoma brucei.
ORGANISM       Trypanosoma brucei
               Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
REFERENCE      1 (bases 1 to 572)
AUTHORS        El-Sayed,N., Zhao,S., Zhao,H., Gill,S., Suh,E., Malek,J., Fujii,C.,
               Gerrard,C., Leech,V., de Jong,P., Ullu,E., Melville,S., Doneison,J.,
               Frazer,C. and Adams,M.
TITLE          Determination of clone end sequences from Trypanosoma brucei GUTat
               10.1 sheared DNA library
JOURNAL        Unpublished (1999)
COMMENT        Other_GSSs: Sheared DNA-51M3.TR
               Contact: Najib M. El-Sayed
               Department of Eukaryotic Genomics
               The Institute for Genomic Research
               9712 Medical Center Dr., Rockville, MD 20850, USA
               Tel: 301 838 0200
               Fax: 301 838 0208
               Email: nelsayed@tigr.org
               Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared
               DNA library constructed at TIGR. Clones will be available for
               distribution through ATCC. Sheared DNA end sequences search page:
               http://www.tigr.org/tdb/mdb/tbdb/.
               Seq primer: M13-Forward
               Class: shotgun.
FEATURES       location/Qualifiers
SOURCE         1..572
               /organism="Trypanosoma brucei"
               /strain="TREU927/4 GUTat 10.1"
               /db_xref="taxon:5691"
               /clone="Sheared DNA-51M3"
               /clone.lib="Sheared DNA"
               /note="Vector: pUC18. Site.1: SmaI. Constructed at The
               Institute for Genomic Research (TIGR), Rockville, MD.
               Genomic DNA isolated from a cloned population of
               Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically
               sheared to give a tight size distribution (approx 2 kb).
               The v + i method used for the library construction is
               described in detail in Smith, H.O. and Venter, J.C.
               (Making small insert libraries for whole genome shotgun
               sequencing projects. In Genome Sequencing: A Practical
               Approach, eds. M. Vaundin and B. Barrell, Oxford University
               Press, 1999)."
BASE COUNT     115 a 118 c 180 g 159 t
ORIGIN
alignment_scores:
Quality:      68.00           Length:      31
Ratio:        2.519          Gaps:        0
Percent Similarity: 87.097    Percent Identity: 38.710
alignment_block:
US-09-289-346A-8 x A0950848 ..
Align seg 1/1 to: A0950848 from: 1 to: 572
11 GlyArgSerAlaArgGlyCysGlnThrSerAsnAspAlaAlaIacI 27
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
291 GGTCGTCTCCGGCATGCGCGTTGCCAAAGCAAGATGAGTGATGTGA 340
27 uAlaLeuAsnAlaSerSerLyScIncluaLalenglinlelle 41
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
341 AGGTGTCTCGCGAGACATCTCCGACGCACATTGACGTGATG 383
seq_name: gb_gss:A0947513
seq_documentation_block:
LOCUS      A0947513              567 bp      DNA                      GSS
DEFINITION Sheared DNA-19m17.1F Sheared DNA Trypanosoma brucei genomic clone

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VERSION      BG593614.1  GI:13611754
KEYWORDS     EST.
SOURCE       Solanum tuberosum
ORGANISM     potato.
Eukaryota:  Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
REFERENCE    1 (bases 1 to 603)
AUTHORS      van der Hoeven,R., Bezzerides,J., Sun,H., Cho,J., Chiemingo,A.,
              Bougri,O., Bell,C.R., Romning,C., Tanksley,S. and Baker,B.
TITLE        The Institute for Genomic Research
JOURNAL      Generations of ESTs from sprouting potato eyes
COMMENT      Unpublished (2000)
              Contact: Cathy Romning
              For clone info: please contact Research Genetics, Libraries
              Division tel 1-800-711-6195, email cdna@esgen.com
              Seq primer: M13F-R.
FEATURES     Location/Qualifiers
              1..603
               /organism="Solanum tuberosum"
               /cultivar="Kennebec"
               /db_xref="taxon:4113"
               /clone_csts4p4
               /clone_id="cSTS"
               /russie_type="sprouting eyes from tubers"
               /dev_stage="12-14 weeks post harvest"
               /lab_host="SOLR"
               /note="Vector: pluescript SK(-); Site_1: EcoRI; Site_2:
              XhoI; Various sizes of sprouting eyes (2mm to 15mm) were
              taken from tubers. The tubers were incubated at 26C in the
              dark for 2-3 weeks prior to sprouting. The eyes were
              frozen in liquid nitrogen immediately upon removal from
              tubers."
BASE COUNT   160 a      131 c      135 g      177 t
ORIGIN
alignment_scores:
      Quality: 67.50      Length: 54
      Ratio: 1.929      Gaps: 3
      Percent Similarity: 64.815      Percent Identity: 38.889
alignment_block:
US-09-289-346A-8 x BG593614/rev ..
Align seg 1/1 to reverse of: BG593614 from: 1 to: 603
11 GYATGSeTAlaTgTlYcSgInTrSeAsAsp.....AlAaL 25
|||||
393 GCAAGCTCGGCTGCTTGACAGATGCTGACAGATGAATGAATAGACGCTG 344
25 aAaGuaTAlaLeuSAnAseSeTlYcSgInGuaTAlaLeuGInTleL 42
: |||||
343 TATTAGAACCAAAATAGCAGAGCTCTTTACATCTTATACCAAGTT... 298
42 rGtIuLsIlleProGluTysTYrLeuPhcGInDhehIsAn...LeuAsn 57
:::|||||
297 ..AGCAAAATAAGATTCTTCACTGTGTGACAGATTCCACAAATAGCTCAAC 250
58 SeTAsnLeuAsp 61
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249 AACCAATATCAAC 238

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2216 AGCTAAATGATGCTCCGACAGAGGCGCTTAATGACAGTTCCAGTGAAGCAG 2167
37 lalencunlllellarlgulysllleproglulystyleuheglnp 53
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2166 CTTTGGACAAATTAATGAGMAAACCTCCCTAAAGATTTATTTTTCATAT 2117
54 HlsasnlousSersAsnlueAsparllleheAsplyThPro 68
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seq_name: /cgnl_7/pdata/1/lna/GB_COMB.seq:US-08-838-151A-48

seq_documentation_block:
Sequence 48, Application US/08838151A
Patent No. 6291743
GENERAL INFORMATION:
APPLICANT: Strout, John T
APPLICANT: Lou, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Gemlinivirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Dressler, Rocky, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3601P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 1062 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bean Golden Mosaic Gemlinivirus
STRAIN: Type II
INDIVIDUAL ISOLATE: Guatemala
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1059
US-08-838-151A-48

alignment_scores:
Quality: 216.00 Length: 70
Ratio: 3.661 Gaps: 0
Percent Similarity: 84.286 Percent Identity: 58.571

alignment_block:
US-09-289-346A-B x US-08-838-151A-48

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1059
; US-08-838-151A-51
;
alignment_scores:
    Quality: 216.00      Length: 70
    Ratio: 3.661         Gaps: 0
    Percent Similarity: 84.286   Percent Identity: 58.571
;
alignment_block:
US-09-289-346A-8 x US-08-838-151A-51
;
Align seg 1/1 to: US-08-838-151A-51 from: 1 to: 1062
;
1 ThrLeuValTrpGlyGluAlaAlaValAspGlyArgSerAlaArgGlyG1 17
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
328 ACAATCGATGGGACATTCACAGATCGACGACGATTCGACAGAGAG 377
;
17 yCysGlnThrSerAsnAspAlaAlaAlaGluAlaLeuAsnAlaSerSert 34
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
378 TCAGCAGTCTGCCACGACTCATATGCAAGGCAATTAACGCGATTCAA 427
;
34 ysgIuglAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeu 50
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
428 TTGAATCTGCTTGACATATTCAGAGAACAGAACGAAAGTTACGTC 477
;
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
478 CTCACATCATCACAAATCCGTTCTTAATCTCGAACGATCTTCGCAAGT 527
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528 GCCGGAACCA 537
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seq_name: /cgnl_7/ptodata/1/ina/6A_COMB.seq:US-08-838-151A-54
;
seq_documentation_block:
; Sequence 54, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/838.151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
;
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; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1062 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bean Golden Mosaic Geminivirus
; STRAIN: Type II
; INDIVIDUAL ISOLATE: Guatemala
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1059
; US-08-838-151A-54
;
alignment_scores:
    Quality: 216.00      Length: 70
    Ratio: 3.661         Gaps: 0
    Percent Similarity: 84.286   Percent Identity: 58.571
;
alignment_block:
US-09-289-346A-8 x US-08-838-151A-54
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Align seg 1/1 to: US-08-838-151A-54 from: 1 to: 1062
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1 ThrLeuValTrpGlyGluAlaAlaValAspGlyArgSerAlaArgGlyG1 17
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328 ACAATCGATGGGACAAATTCACAGATCGACGACGATTCGACAGAGAG 377
;
17 yCysGlnThrSerAsnAspAlaAlaAlaGluAlaLeuAsnAlaSerSert 34
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
378 TCAGCAGTCTGCCACGACTCATATGCAAGGCAATTAACGCGATTCAA 427
;
34 ysgIuglAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeu 50
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
428 TTGAATCTGCTTGACATATTCAGAGAACAGAACGAAAGTTACGTC 477
;
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
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478 CTCACATCATCACAAATCCGTTCTTAATCTCGAACGATCTTCGCAAGT 527
;
67 rProGluPro 70
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528 GCCGGAACCA 537
;
seq_name: /cgnl_7/ptodata/1/ina/6A_COMB.seq:US-08-809-103B-7
;
seq_documentation_block:
; Sequence 7, Application US/08809103B
; Patent No. 6133505
; GENERAL INFORMATION:
; APPLICANT: CRONENBORN, Bruno
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/809.103B
;
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FILING DATE: 17-MAR-1997
CLASSIFICATION: 800
PRIORITY APPLICATION DATA: FR 94.11040
FILING DATE: 15-SEP-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR95/01192
FILING DATE: 15-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: PATCH, Andrew J.
REGISTRATION NUMBER: 32,925
REFERENCE/DOCKET NUMBER: US94AL CNR TOM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 521-2297
TELEFAX: (703) 685-0573
TELEX: 248425 EMBON
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1145 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1077
US-08-809-103B-7

alignment_scores:
Quality: 216.00 Length: 69
Ratio: 3.789 Gaps: 0
Percent Similarity: 82.609 Percent Identity: 56.522

alignment_block:
US-09-289-346A-8 x US-08-809-103B-7 ..

Align seg 1/1 to: US-08-809-103B-7 from: 1 to: 1145

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2 LeuValTrpGlyGluAlaValAspGlyArgSerAlaArgGlyCys 18
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331 CTGGAATGGGGTACTTCCAGATCGACGCGCATCTGCTAGGGGAGACA 380
18 sGlnTrpSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerLys 35
||||| ..... ||||| ..... ||||| ..... ||||| .....
381 ACAGACGCCACGACGCTTACGCCAAGCAATTACCGCAGGAAGTACT 430
35 LucAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeuPhe 51
::::: ||||| ..... ||||| ..... ||||| ..... ||||| .....
431 CGCAGGCTCTGATGTAATTAAGAATTACGCCCTAGCATTTACGTTCTA 480
52 GlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysThrP 68
::::: ||||| ..... ||||| ..... ||||| ..... ||||| .....
481 CATTTCATATATATAATAGTAATTAGATACGTTTCCAGGTGCTCC 530
68 oGluPro 70
| |||
531 GGCACCT 537

seq_name: /cgn1_7/ptodata/1/ina/6A_COMB.seq:US-08-809-103B-1
seq_documentation_block:
; Sequence 1, Application US/08809103B
; Patent No. 6133505
; GENERAL INFORMATION:
; APPLICANT: GRONENBORN, Bruno
; TITLE OF INVENTION: PHYTOGENIC DNA VIRUS RESISTANT
; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
```

STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,103B
FILING DATE: 17-MAR-1997
CLASSIFICATION: 800
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: FR 94.11040
FILING DATE: 15-SEP-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR95/01192
FILING DATE: 15-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: PATCH, Andrew J.
REGISTRATION NUMBER: 32,925
REFERENCE/DOCKET NUMBER: US94AL CNR TOM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 521-2297
TELEFAX: (703) 685-0573
TELEX: 248425 EMBON
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1148 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1077
US-08-809-103B-1

alignment_scores:
Quality: 216.00 Length: 69
Ratio: 3.789 Gaps: 0
Percent Similarity: 82.609 Percent Identity: 56.522

alignment_block:
US-09-289-346A-8 x US-08-809-103B-1 ..

Align seg 1/1 to: US-08-809-103B-1 from: 1 to: 1148

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2 LeuValTrpGlyGluAlaValAspGlyArgSerAlaArgGlyCys 18
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331 CTGGAATGGGGTACTTCCAGATCGACGCGCATCTGCTAGGGGAGACA 380
18 sGlnTrpSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerLys 35
||||| ..... ||||| ..... ||||| ..... ||||| .....
381 ACAGACGCCACGACGCTTACGCCAAGCAATTACCGCAGGAAGTACT 430
35 LucAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeuPhe 51
::::: ||||| ..... ||||| ..... ||||| ..... ||||| .....
431 CGCAGGCTCTGATGTAATTAAGAATTACGCCCTAGCATTTACGTTCTA 480
52 GlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysThrP 68
::::: ||||| ..... ||||| ..... ||||| ..... ||||| .....
481 CATTTCATATATATAATAGTAATTAGATACGTTTCCAGGTGCTCC 530
68 oGluPro 70
| |||
531 GGCACCT 537

seq_name: /cgn1_7/ptodata/1/ina/6A_COMB.seq:US-08-809-103B-3
seq_documentation_block:
; Sequence 3, Application US/08809103B
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Patent No. 6133505
GENERAL INFORMATION:
APPLICANT: GRONENBORN, Bruno
TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: YOUNG & THOMPSON
STREET: 745 South 23rd Street
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,103B
FILING DATE: 17-MAR-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94.11040
FILING DATE: 15-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR95/01192
FILING DATE: 15-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: PATCH, Andrew J.
REGISTRATION NUMBER: 32,925
REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 521-2297
TELEFAX: (703) 685-0573
TELEX: 248425 EMBON
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1150 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1077
US-08-809-103B-3

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alignment_scores:
Quality: 216.00      Length: 69
Ratio: 3.789         Gaps: 0
Percent Similarity: 82.609      Percent Identity: 56.522

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alignment_block:
us-09-289-346a-8 x US-08-809-103B-3

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2 LeuValTrpGlyGluAlaAlaValAspGlyArgSerAlaArgGlyGlyC 18
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331 CTGAATGGGCTACTTCAGATCGACGACGATCTCTAGGGAGGACA 380
18 sGlnThSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerIysG 35
|||||
381 ACAGACGACACGACGCTTACGCAAGCAATTACGACGAGTAAGT 430
35 InGluAlaLeuGlnIleLeuArgGluLysIleProGluLysTyrLeuPhe 51
|||||
431 CGCAGGCTCTTGATGTAATTAAGATTACGCGCTACAGATTACGTTCTA 480
52 GluPheIAsnLeuAsnSerAsnLeuAspArgIlePheAspLysThrPr 68
|||||

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481 CATTTCATATAATATAAGTAATTAGATTAGGTTTCCAGGTGCTCC 530
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531 GGCACCT 537

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seq_name: /cgn1-7/plodata/1/lna/6A.COMB.seq:US-08-809-103B-5

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seq_documentation_block:
Sequence 5, Application US/08809103B

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Patent No. 6133505
GENERAL INFORMATION:

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APPLICANT: GRONENBORN, Bruno
TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT

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```

NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:

```

```

ADDRESSEE: YOUNG & THOMPSON
STREET: 745 South 23rd Street

```

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CITY: Arlington
STATE: Virginia

```

```

COUNTRY: U.S.A.
ZIP: 22202

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/08/809,103B
FILING DATE: 17-MAR-1997

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CLASSIFICATION: 800
PRIOR APPLICATION DATA:

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APPLICATION NUMBER: FR 94.11040
FILING DATE: 15-SEP-1994

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR95/01192

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FILING DATE: 15-SEP-1995
ATTORNEY/AGENT INFORMATION:

```

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NAME: PATCH, Andrew J.
REGISTRATION NUMBER: 32,925

```

```

REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
TELECOMMUNICATION INFORMATION:

```

```

TELEPHONE: (703) 521-2297
TELEFAX: (703) 685-0573

```

```

TELEX: 248425 EMBON
INFORMATION FOR SEQ ID NO: 5:

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SEQUENCE CHARACTERISTICS:
LENGTH: 1150 base pairs

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TYPE: nucleic acid
STRANDEDNESS: double

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TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

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FEATURE:
NAME/KEY: CDS

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LOCATION: 1..1077
US-08-809-103B-5

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alignment_scores:
Quality: 216.00      Length: 69
Ratio: 3.789         Gaps: 0
Percent Similarity: 82.609      Percent Identity: 56.522

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alignment_block:
us-09-289-346a-8 x US-08-809-103B-5

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Align seg 1/1 to: US-08-809-103B-5 from: 1 to: 1150

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2 LeuValTrpGlyGluAlaAlaValAspGlyArgSerAlaArgGlyGlyC 18
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331 CTGAATGGGCTACTTCAGATCGACGACGATCTCTAGGGAGGACA 380

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AUTHORS: Morales, FJ
AUTHORS: Ahlquist, P
AUTHORS: Lontello, AO
AUTHORS: Maxwell, D
TITLE: Bean Golden Mosaic Geminivirus Type II
TITLE: Isolates from the Dominican Republic and
TITLE: Guatemala: Nucleotide Sequences, Infections
TITLE: Pseudorecombinants, and Phylogenetic Relationships
JOURNAL: Phytopathology
VOLUME: 84
ISSUE: 3
PAGES: 321-329
DATE: 1994
US-08-838-151A-43

alignment_scores:
    Quality: 216.00      Length: 70
    Ratio: 3.661        Gaps: 0
Percent Similarity: 84.206 Percent Identity: 58.571

alignment_block:
US-09-289-346A-8 x US-08-838-151A-43    ..

Align seg 1/1 to: US-08-838-151A-43 from: 1 to: 1183

1 ThrleuValTTPGlyGluAlaAlaValAspLyArgSerAlaArgGlyI 17
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328 ACAATCGAATGGGGAGCAATTCACAGTCGACGCGAGATCTCGAACAGCAGC 377
17 YCysGlnThrSerAsnSpAlaAlaAlaGluAlaLeuAsnAlaSerI 34
I |||||:|||||: |||||: |||||: |||||: |||||: |||||:
378 TCAGCAGCTGCCAACGACGCTCATGTGCMAAGCATTTAAACGACGATTCAA 427
34 YSGluGluAlaLeuGlnIleLeuArgGluIlyIleProGluIySTyrLeu 50
||||| ||||||| ||||||| ||||||| ||||||| |||||||
428 TTGATCTTCGCTTGACATATTGAAGGAGAACACCGAAGATTTACGTC 477
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspIySTh 67
||||| |||||||:|||||:|||||:|||||:|||||: |||||:
478 CTTCAACATCAACAACATCCCTTTCAATCTCGAACGAGATCTTCTGCAACGT 527
67 rProGluPro 70
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528 GCCGGAGACCA 537

seq_name: /cgnl_7/ptodata/1/ina/0B_COMB.seq:US-08-838-151A-45
seq_documentation_block:
; Sequence 45, Application US/08838151A
; Patent No. 6291743
GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rocky, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
City: Chicago
STATE: Illinois
COUNTRY: U.S.A.
Zip: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 1183 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bean Golden Mosaic Geminivirus
STRAIN: Type II
INDIVIDUAL ISOLATE: Guatemala
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1059
US-08-838-151A-45
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alignment_scores:
Quality: 216.00      Length: 70
Ratio: 3.661         Gaps: 0
Percent Similarity: 84.286   Percent Identity: 58.571
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alignment_block:

US-09-289-346A-8 x US-08-838-151A-45 ..

Align seg 1/1 to: US-08-838-151A-45 from: 1 to: 1183

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1 ThrleuValTrpGlyGluAlaAlaValAspGlyArgSerAlaArgGly 17
||||| ||||||| ||||||| ||||||| ||||||| |||||||
328 ACATCGAATGGGGACAAATTCGAAGTCGACGCGAGATCTCAAGAGAGG 377
17 yCysGlnThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerL 34
| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
378 TCAGCAGCTGCGCAACGACTATGCAAGGCTTTAAACGACGATTCAA 427
34 ySgIguAlaLeuGlnIleIleArgGluIysIleProGluIysTyrLeu 50
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
428 TTGAATCTGCTTGACAATATTGAAGAGAACACCGAAGATTACGTC 477
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLys 67
:::| | | | | | | | | | | | | | | | | | | | | | | |
478 CTTCAACATTCACAACATCCGTTTAATCTCGAACGATCTTCGCAAGT 527
67 rProGluPro 70
:::| | | | | | | | | | | | | | | | | | | | | | | |
528 GCCGGAAACCA 537
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seq_name: /cgnl_7/ptodata/1/lna/6A_COMB.seq:US-09-065-999-5

seq_documentation_block:

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; Sequence 5, Application US/09065999
; Patent No. 6118048
; GENERAL INFORMATION:
; APPLICANT: Hanson, Stephen F.
; APPLICANT: Maxwell, Douglas P.
; TITLE OF INVENTION: TRANS-DOMINANT INHIBITION OF GEMINIVIRAL
; TITLE OF INVENTION: DNA REPLICATION BY GEMINIVIRUS REP GENE MUTANTS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Quarles & Brady
; STREET: One South Pinckney Street
```

```
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA: 999
APPLICATION NUMBER: US/09/065,999
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 960296.94754
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1651 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-065-999-5
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alignment_scores:
Quality: 216.00      Length: 70
Ratio: 3.661         Gaps: 0
Percent Similarity: 84.286   Percent Identity: 58.571
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alignment_block:

US-09-289-346A-8 x US-09-065-999-5 ..

Align seg 1/1 to: US-09-065-999-5 from: 1 to: 1651

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1 ThrleuValTrpGlyGluAlaAlaValAspGlyArgSerAlaArgGly 17
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796 ACATCGAATGGGGACAAATTCGAAGTCGACGCGAGATCTCAAGAGAGG 845
17 yCysGlnThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerL 34
| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
846 TCAGCAGCTGCGCAACGACTATGCAAGGCTTTAAACGACGATTCAA 895
34 ySgIguAlaLeuGlnIleIleArgGluIysIleProGluIysTyrLeu 50
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
896 TTGAATCTGCTTGACAATATTGAAGAGAACACCGAAGATTACGTC 945
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLys 67
:::| | | | | | | | | | | | | | | | | | | | | | | |
946 CTTCAACATTCACAACATCCGTTTAATCTCGAACGATCTTCGCAAGT 995
67 rProGluPro 70
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996 GCCGGAAACCA 1005
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seq_name: /cgnl_7/ptodata/1/lna/6A_COMB.seq:US-09-065-999-6

seq_documentation_block:

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; Sequence 6, Application US/09065999
; Patent No. 6118048
; GENERAL INFORMATION:
; APPLICANT: Hanson, Stephen F.
; APPLICANT: Maxwell, Douglas P.
; TITLE OF INVENTION: TRANS-DOMINANT INHIBITION OF GEMINIVIRAL
; TITLE OF INVENTION: DNA REPLICATION BY GEMINIVIRUS REP GENE MUTANTS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Quarles & Brady
```



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34 yscgluualaleuglnlleleargclulysilleproglulyslytleu 50
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2171 AGAAGAACCCCGCAGATATATTAGAGAGAAATCCACAGAAATATTTA 2122
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysThr 67
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2121 TTTCAGTTCACAACTAAATAGCAATTTAGATAGATATTTGATTAAGAC 2072
67 rProgluPro 70
|||||
2071 TCCTGACCA 2062

seq_name: gb_v1:AY029750
seq_documentation_block: 2588 bp DNA circular VRL 08-MAY-2001
LOCUS AY029750 Tomato severe rugose virus DNA-A, complete sequence.
DEFINITION AY029750
ACCESSION AY029750
VERSION AY029750.1 GI:14009278
KEYWORDS
SOURCE
ORGANISM
Virus; ssDNA viruses; Geminiviridae; Begomovirus.
Tomato severe rugose virus.
REFERENCE
AUTHORS Rezende,W.L., Goulart,L.R., Parreira,K.S. and Figueiredo,J.E.F.
TITLE The full-length DNA-A nucleotide sequence of a novel tomato-infecting begomovirus, Tomato severe rugose virus, in Brazil
JOURNAL
REFERENCE
AUTHORS Rezende,W.L., Goulart,L.R., Parreira,K.S. and Figueiredo,J.E.F.
TITLE Direct Submision
JOURNAL
REFERENCE
AUTHORS Rezende,W.L., Goulart,L.R., Parreira,K.S. and Figueiredo,J.E.F.
TITLE Submitted (03-APR-2001) Instituto de Genetica e Bioquimica,
Universidade Federal de Uberlandia, Av. Amazonas s/o, Bloco 2E,
Sala 24, Campus Umuarama, Uberlandia, Minas Gerais 38.400-000,
Brazil
FEATURES
source
Location/Qualifiers
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/strain="Minas Gerais"
/db_xref="taxon:158463"
/country="Brazil"
/note="segment: DNA-A"
305..1060
/gene="AV1"
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/db_xref="GI:14009282"
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RECVKSLYITCKVMDESILKNTNSVMVLVDRRPYCTPMDPGVPMFDEPST
ATYKNDLRDRQVHMFTAKVTGGVTSNEQALVKKRWKNNNVYTHQEGKIENHT
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/db_xref="GI:14009280"
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/product="trap"

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/db_xref="GI:14009279"
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FOHNLNSNLDRIARAPDERPAPYPLSSFTNVRKQMDADYFGQARPERPISI
IIEGDSRTGKTMMARAFCAHNYLSGHLDFNRYVSNHVEYVNDIDIAHYLTKHKE
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/db_xref="GI:14009281"
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/note="common region"

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BASE COUNT 660 a 525 c 598 g 805 t
ORIGIN

alignment_scores:
Quality: 307.00 Length: 70
Ratio: 4.723 Gaps: 0
Percent Similarity: 92.857 Percent Identity: 81.429

alignment_block:
US-09-289-346a-9 x AY029750/rev ..
Align seg 1/1 to reverse of: AY029750 from: 1 to: 2588
1 ThrLeuValTrpGlygluPheGlnValAlaGlyArgSerAlaArgGlycl 17
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2258 ACTATCGAATGGGCGCAATTCAGACGACGCGAGTGTAGAGCGCG 2209
17 yscglnthrserasnaspalalalalaglualaleuasnaliserserl 34
|||||
2208 TTGGCCGACAGCTAACGATGCTGCCGACAGACCTTGAAACGACCTTCA 2159
|||||
34 yscgluualaleuglnlleleargclulysilleproglulyslytleu 50
|||||
2158 AACAGCTCCCTTCGACATATCCGGAGAACGTAACCGGAAAGTTTAA 2109
|||||
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysThr 67
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2108 TTTCAGTTCACAACTAAATAGCAATTTAGATAGATATTTGCAAGGGC 2059
67 rProgluPro 70
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2058 TCCTGACCA 2049

seq_name: gb_v1:AF291705
seq_documentation_block: 2622 bp DNA circular VRL 25-SEP-2000
LOCUS AF291705 Tomato rugose mosaic virus DNA-A, complete sequence.
DEFINITION AF291705
ACCESSION AF291705
VERSION AF291705.1 GI:10281644

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         /protein_id="Agi1547.1"
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STGSFQSLSQLPNDIDPESEFMDIER"
complement(join(1570..2622,1..6))
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complement(join(1570..2622,1..6))
/gene="Rep"
/note="Rep"
/codon_start=1
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/protein_id="Agi1546.1"
/db_xref="GI:10281646"
/translation="MEPATFRRPOTKANKYFLTYPKGISKEEALISLTKNLNTPPTNI
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SYVDKDSDTTEMGEFFQIDGSRARCGCTPADDAEAENASFKDIALDI TEKKPER
FOEPNLNSDLDIRPARAPEWAPTEFTSTNTYNPREMDADDPFGGAARPERR
IIIEGDSRTGKTMMARAIGAHHNVLSGHILDNPBYSSHVEYINVIDIAPYLKLK
ELICARDMSNCNKYCKRPVOIKGGIIPCIVLCPREGCASYSKCFLDKENSALSMT
AQFIINSPILOSSTSCG"

BASE COUNT    684 a     562 c     600 g     776 t
ORIGIN

alignment_scores:
        Quality:   305.00          Length:       70
        Ratio:     4.692           Gaps:        0
Percent Similarity: 92.857      Percent Identity: 81.429

Alignment_block:
US-09-289-346A-9 x AF291705/rev ..

Align seg 1/1 to reverse of: AF291705 from: 1 to: 2622

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2298 ACTATGCAGATTGGGGGCAATTCCAATAVICAGACGGAGAAGTGCTAGAGCGG 2249

                17 yCySGlnThrSerAsnAspAlaIAlaIacLualaleuAnaIsaSerSeL 34
                   |||||||::::|::::|::::|::::|::::|::::|
2248 TTGCCAGACAGCTAACGACGCTGCCCCACAAGACTTTGAACGACACCTTCOA 2199

                34 ygslLuJalaleugInlIleIarGgluLySllepProGUlystyrlEu 50
                   ||::: |::::|::::|::::|::::|::::|::::|
2198 AAGACATCGCCTTGcAgATTA TC GGGAAGATGCGGAAAGATTCCTTA 2149

                51 PhgGlPhhHisAnLeuAnsSerfaNleuAsparGIlIpheasplysth 67
                   |||||||::::|::::|::::|::::|::::|::::|
2148 TTTCACTTTCACATCTAATACTATTAGTAGATAGCATATTTCACAAggcc 2099

                67 rProGUlpuro 70
                   ::|||::|::|

2098 TCCGAGAGCCA 2089

seq_name: gb_v1:LMDU92532

seq_documentation_block:
LOCUS      LMDU92532      1193 bp      DNA               VRL      01-Apr-1997
DEFINITION Leonurus mosaic virus Rep protein (rep) and coat protein (cp)
genes, partial cds.
ACCESSION U92532
VERSION   U92532.1 GI:1916344
KEYWORDS
SOURCE
 ORGANISM Leonurus mosaic virus.
            Leonurus musci virus.
            Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
REFERENCE Faria,J.C., and Maxwell,I.D.P.
TITLE      Variability in geminivirus associated with Phaseolus vulgaris in
Brazil
```

JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1193)
 AUTHORS Farla,J.C. and Maxwell,D.P.
 TITLE Direct Submission
 JOURNAL Submitted (08-MAR-1997) Plant pathology, University of Wisconsin,
 1630 Linden Dr, Madison, WI 53706-1598, USA
 FEATURES
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 /strain="LemV_Brazil_1"
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 /gene="rep"
 /complement(<1. .678)
 /gene="rep"
 /note="AC1: replication associated protein"
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 /db_xref="GI:1916345"
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 IKIRRELHDDQPHLHVLOIEGKVOITNNRFLPVLVTTSSAHFHPNQAKSSDYK
 SYIDKDDIVEMGEYVDGRSSRGQGVNDAAEAUNADPKRTALQIIIEKLPKYL
 FQFNILNSNLDRIFAKAPERPVPPLSFTNVDPDEQWADVEYFGSSAARPLRPM
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 /db_xref="Locus:58177"
 /note="origin of replication: common region"
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 Quality: 288.00 Length: 70
 Ratio: 4.571 Gaps: 0
 Percent Similarity: 90.000 Percent Identity: 80.000
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 US-09-289-346a-9 x LMU92532/rev ..
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 1 TTTTLeuValTTPrGlyGluPhgGlnValAlaGlyArgSerAlaArgGlyL 17
 348 ACGAGTTGAATGGGGTGAATTCACGCGAGCGAGAACTTCTAGAGAGAG 299
 17 yCYGlnThrSerAsnAspAlaAlaIaGluAlaLeuAsnAlaSerSerL 34
 298 CCAACGACGAGTTAATGACGCTGACGCTGAGCGCTTAAATGCTCCGACAT 249
 34 yscGluAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeu 50
 248 AACGACGCGCTCTCAATTAATTAAGAGAAATGCGGAGAAATATCTT 199
 51 pHeGlnPhhHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
 198 TTTTCATTTCAATTAATTAATTTGATTTGATTAATTTGCAAGGC 149
 67 rProGluPro 70
 148 TCCGAGAGCCA 139
 seq_name: gb_vl:AF131071

seq documentation block:
 LOCUS AF131071 1345 bp DNA VRL 17-JUN-1999
 DEFINITION Tomato mild mottle geminivirus segment A replication associated
 protein (rep) and coat protein (CP) genes, partial cds.
 ACCESSION AF131071
 VERSION AF131071.1 GI:4928223
 KEYWORDS
 SOURCE
 ORGANISM
 tomato mild mottle geminivirus.
 Viruses; ssDNA viruses: Geminiviridae; Unclassified Geminiviridae.
 1 (bases 1 to 1345)
 /db_xref="taxon:92943"
 /chromosome="segment A"
 /clone="pNH5ak"
 /country="Honduras: Comayagua Valley"
 /note="Obtained from a tomato plant collected in Dec. 1996
 by M.K. Nakha and D.P. Maxwell"
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 /note="rep protein"
 /codon_start=1
 /product="replication-associated protein"
 /protein_id="AAB33471.1"
 /db_xref="GI:4928224"
 /translation="MPLPKKFLINSKVFLEYPHCSLSKEETLEQLRLNTPNNKY
 IKIARELHEDGEYHIVLIOEGKFKTONRFPFLVSTSTHHPHVOGAKSSTDYK
 SYVDKDDTIVEMGEYVDGRSSRGQGVNDAAEAUNADPKRTALQIIIEKLPKYL
 FQFNILNSNLDRIFAKAPERPVPPLSFTNVDPDEQWADVEYFGSSAARPLRPM
 LIVEGGR"
 /db_xref="Locus:58177"
 /note="ori"
 /complement(<1. .678)
 /gene="cp"
 /note="av1"
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 /gene="cp"
 /note="capsid protein"
 /codon_start=1
 /product="coat protein"
 /protein_id="AAB33472.1"
 /db_xref="GI:4928225"
 /translation="MPKRDAPWRMSATPRVSRSSNVPPDGLGRKFDKSSAANRPM
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 BASE COUNT 329 a 289 c 313 g 414 t
 ORIGIN
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 Quality: 288.00 Length: 70
 Ratio: 4.364 Gaps: 0
 Percent Similarity: 94.286 Percent Identity: 75.714
 alignment_block:
 AF131071

US-09-289-346a-9 x AF131071/rev ..

Align seg 1/1 to reverse of: AF131071 from: 1 to: 1345

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348 ACAATCGATGCGGAGAAATTCAGATCGACGCGAGATCTGCTAGAGAGG 299
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
17 YCysGlnThrSerAsnAspAlaAlaGlnAlaLeuAsnAlaSerSerL 34
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
298 TCAGCAACAGCTAACAGAGCGTCCGCGAGGCGCTAAATGCTCTCGA 249
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
34 YSGlGluAlaLeuGlnIleIleArgGluLysIleProGluLysThrLeu 50
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
248 AAGAGAGAGCCATGCGATTTATTAAGAGAGCTCCCAAGAGATTTCCT 199
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51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
198 TTTTCATATTCACACACCTGCTGTAGTACCTAGACAGAGATTTGCTAAGC 149
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
67 rProGluPro 70
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148 TCCGGAGACCG 139
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seq_name: gb_v1:MBGARAL

seq_documentation_block:
LOCUS      MBGARAL             2617 bp ss-DNA   circular   VRL       02-AUG-1993
DEFINITION Bean golden mosaic geminivirus viral coat protein (ARI) gene,
complete cds; putative replicative protein (AL1) gene, putative
cds; AL2 gene, complete cds; and AL3 gene, complete cds.
ACCESSION   M88686
VERSION     M88686.1 GI:331462
KEYWORDS    Bean golden mosaic protein.
SOURCE      Bean golden mosaic virus (individual isolate Brazil, strain Type I)
            Replicative form DNA.
ORGANISM    bean golden mosaic virus
            Viruses: ssDNA viruses; Geminiviridae; Begomovirus.
REFERENCE   1 (sites)
AUTHORS     Gilbertson,R.L., Faria,J.C., Hanson,S.F., Morales,F.J.,
            Alquist,P.G., Maxwell,D.P. and Russell,D.R.
TITLE       Cloning of the Complete DNA Genomes of Four Bean-infecting
            Geminiviruses and Determining Their Infectivity by Electric
            Discharge Particle Acceleratio
            Phytopathology 81, 980-985 (1991)
JOURNAL     2 (sites)
REFERENCE   Gilbertson,R.L., Hidayat,S.H., Martinez,R.T, Leong,S.A, Faria,J.C.,
AUTHORS     Morales,F.J. and Maxwell,D.P.
TITLE       Differentiation of bean-infecting geminiviruses by nucleic acid
            hybridization probes and aspects of bean golden mosaic in Brazil
            plant Dis. 75, 336-342 (1991)
JOURNAL     3 (bases 1 to 2617)
REFERENCE   Gilbertson,R.L., Faria,J.C., Alquist,P.G. and Maxwell,D.P.
AUTHORS     Genetic diversity in geminiviruses causing bean golden mosaic
TITLE       disease: The nucleotide sequence of the infectious cloned DNA
            components of a Brazilian isolate of bean golden mosaic geminivirus
            unpublished (1992)
JOURNAL     Location/Qualifiers
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            /dev_stage="Replicative form"
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            358..1113

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RCKVKSYYITGKTIMDENIKIKNTNSVMFVLVDRRPYGTGPMDFGVPMFDPENST
ATYKNDLRDRFOVMHKEFYGVVGGVANSNDALVKRRKVNMYVYVNHQBAGYENHT
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/db_xref="GI:331465"
/translation="MDSRTGERTARQAEKVYIWEISNPLYEKMYNVEDLOYYTTRY
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GHGTRGTHGHTSSGEMRYLADIKSPFDQVDRKSTIHNDSITPPNTPVQPOPE
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OYHNLSSNDRIFTKAPDPPSPYHLSSFTVPREMEADYDGRGAAAPERPISI
IIEEDSRGTGMARALGTNHYLSGHLDFNSKVSNAEYVDDIDIAPHYLIKHKME
LMQAKVMOSNCKRKRPVQIKGCIPISYVLCNPGRCASYKCPLDKEENALKNWTIHNA
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BASE COUNT 677 a 491 c 592 g 857 t
ORIGIN

alignment_scores:
Quality: 286.00 Length: 67
Ratio: 4.469 Gaps: 0
Percent similarity: 95.522 Percent identity: 79.104

alignment_block:
US-09-289-346a-9 x MBGARAL/rev ..

Align seg 1/1 to reverse of: MBGARAL from: 1 to: 2617

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   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
20 rSerAsnAspAlaAlaGlnAlaLeuAsnAlaSerSerLySGluGluA 37
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2255 ACCTAATGATTCGCGCATTCGAGACATTTGAAATGCTTCTCAAGAGAGAG 2206
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CDS      complement(815..1072)
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         /product="AC4"
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         /db_xref="GI:9858127"
         /translation="MGRLTSMCMWCCSSKANSSAOIADSIWHSRDRITFTPTSHLNP
         APMSSPSIRTGIPSPGVNSRSTADLLEFASRLITTPORL"

BASE COUNT      359 a      296 c      327 g      401 t
ORIGIN

alignment_scores:
      Quality: 284.00      Length: 68
      Ratio: 4.581      Gaps: 0
      Percent similarity: 91.176      Percent identity: 82.353

alignment_block:
US-09-289-346A-9 x AF288227/rev ..

Align seg 1/1 to reverse of: AF288227 from: 1 to: 1383

1   ThrLeuValTrpGlyGluPheGlnValAlaGlyArgSerAlaArgGlyG1 17
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
902 ACCATCACCTGGGGTGAATTCAGGTCGACGCGACAGTCTGCTAGAGGAGG 853

17  YcysGlnThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerL 34
    |   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
852 CCAGCAGACTGCTACGACGACGCGACGAGGCTCAAGCAGAGGTTCTA 803

34  YGluGluAlaLeuGlnIleIleArgGluLysIleProGluLysTryLeu 50
    |||||   |||||:|||||:|||||:|||||:|||||:|||||:|||||
802 AAGAGAGCTGGCTTGCAATATATCAGGAGAACTCCCTAAAAAATTTTA 753

51  PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
752 TTTCATTTTCATTAATTTAGTAGTAATTTAGATAGCATTTTTCCTCCTCC 703

67  rPro 68
    |||
702 ACCT 699

seq_name: gb_vt:AF104036

seq_documentation_block:
LOCUS      AF104036      2828 bp      DNA      circular      VRL      05-AUG-1999
DEFINITION Sweet potato leaf curl virus DNA A, complete sequence.
ACCESSION  AF104036
VERSION    AF104036.1 GI:5702158
KEYWORDS
SOURCE     .
ORGANISM   Sweet potato leaf curl virus.
            Sweet potato leaf curl virus
            Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
REFERENCE  1 (bases 1 to 2828)
            Lotrakul,P., Valverde,R.A., Clark,C.A., Slim,J. and De la Torre,R.
            Detection of a geminivirus infecting sweet potato in the United
            States
JOURNAL    Plant Dis. 82, 1253-1257 (1998)
REFERENCE  2 (bases 1 to 2828)
            Lotrakul,P. and Valverde,R.A.
            Cloning of a DNA-A-like genomic component of sweet potato leaf curl
            virus : nucleotide sequence and phylogenetic relationships
JOURNAL    Molecular Plant Pathology On-Line (1999)
REMARK     http://www.dssp.org.uk/mpool/1999/0422lotrakul/
AUTHORS    Lotrakul,P. and Valverde,R.A.
TITLE      Direct Submission
JOURNAL    Submitted (02-NOV-1998) Plant Pathology and Crop Physiology,
            Louisiana State University, 302 Life Sciences Bldg., LSU, Baton
            Rouge, LA 70803, USA
FEATURES
source     1..2828
            Location/Qualifiers

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gene      /organism="sweet potato leaf curl virus"
         /db_xref="taxon:100755"
         /chromosome="DNA A"
         /country="USA"
         132..476
         /gene="AV2"
         132..476
         /gene="AV2"
         /note="AR2"
         /codon_start=1
         /product="precoat protein AV2"
         /protein_id="AAD47169.1"
         /db_xref="GI:5702159"
         /translation="MAELMDPLONPLDPTLGFRCMLSVKYLQSLKKYBERGTLPFL
         CSELIRIPRVNQYDANARAFRISISINGETKTAELRDSYRALHMECCPCCKRLCP
         GFRPRDEKRG"
         301..1065
         /gene="AV1"
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         /gene="AV1"
         /note="AR1"
         /codon_start=1
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         /protein_id="AAD47170.1"
         /db_xref="GI:5702160"
         /translation="MTGRMYSPRFHYGGRPVRRRLNFEATIVPTGNAPVIAARSY
         VPVSRGVBMKRRRGDRIPKCGVCPCKVODIEFKNDVPRITGFFVYSDFTRGTLTHRL
         GKRVCVASMGI DGKVMMDNDYAKRDRHNIITYYWLIRODRPKKDLNFGQITPMQNEP
         TTAKLRMDLRDMQVLKRFVTVSGGPEYSHKEQALIRKFEKLYNHVYNNHKEAKE
         NQLENALMLYSSASHASNPPYQTLRCRAYFYDSHNN"
         complement(1081..1515)
         /gene="AC3"
         complement(1081..1515)
         /gene="AC3"
         /note="AL3"
         /codon_start=1
         /product="AC3"
         /protein_id="AAD47171.1"
         /db_xref="GI:5702161"
         /translation="MDSRTGESISHAQTTRAVERDTPNMSVGRAPPHLRIMYHEST
         OGRTILKPOLVANYRERROLGPHKIFLOFRILTLRLGALISWGIILRLKWLRCNEL
         ANLGFFSLNVLVFIIVRYLRVCSNIDELDTVDCCDDVYLLY"
         complement(1232..1678)
         /gene="AC2"
         complement(1232..1678)
         /gene="AC2"
         /note="AL2"
         /codon_start=1
         /product="transactivator protein AC2"
         /protein_id="AAD47172.1"
         /db_xref="GI:5702162"
         /translation="MSNPLSGYKKRRCPIQERLHTBEAKKAKKRVBQRTRIYWKGGCS
         AFITTTCKYQGHGTFHRCINKSCSYESSRIHQHVCSDCTVPSQNVNCPREHTGEN
         HPQIPABCELOGKEATGIPDLPPIPIDDPSNMCYSQLDYFGFP"
         complement(1587..2681)
         /gene="AC1"
         complement(1587..2681)
         /gene="AC1"
         /note="AL1; REP gene"
         /codon_start=1
         /product="replication initiation protein AC1"
         /protein_id="AAD47173.1"
         /db_xref="GI:5702163"
         /translation="MAPPKRFKIQAKNFTIYPRCSLSKEKCLAQALNLTQPSKKYI
         HVAERLDHDEPHLVLVQFEGKRFVCTNSRFDLVSPKRSNHPHNIQGAKSSDVYS
         VYDKDDGITWGEFOVDGRSARGGQGTANDAAALNKSKEAALQITREKIPEDYLR
         QFHNLVSNLDRIFSPSPSYSSPSSSFNAVPDIIISMALENWDSAAARDPRISIV
         IEGPSRIGKTVWARSIGPHNYLCGHLDSPKVYSNMAVNIIDVNPQYLKHPFEMG
         AOKDMQSNCKYKGRVRIKGIPTIPLCPGGSSPKLMLDPRBOGALKMNAITANAIRC
         DVQSPFWOEVSNSGATAHNGECOEBS"
         complement(2267..2524)
         /gene="AC4"
         complement(2267..2524)

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/gene="AC4"
/ncore="A14"
/codon_start=1
/product="AC4"
/protein_id="AAB47174.1"
/db_xref="GI:5702164"
/translation="MGNTITMCMCCKSSKANSQAQIADSSISWHTDRITFTPTSRRLNP
APMSSPTIRTGIPSPGVNSRSTADLLEFASRLITTPORL"
BASE COUNT      741 a      606 c      675 g      806 t
ORIGIN

alignment_scores:
  Quality: 284.00      Length: 68
  Ratio: 4.581      Gaps: 0
  Percent Similarity: 91.176      Percent Identity: 82.353

alignment_block:
US-09-289-346a-9 x AF104036/rev ..

Align seg 1/1 to reverse of: AF104036 from: 1 to: 2828

1 ThrLeuValTrpGlyGluPheGlnValAlaGlyArgSerAlaArgGlyC1 17
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2354 ACCATCACCCTGGCGTGAATTCACGACGACGCTCTAAACGACGAGTCTCA 2305
17 yCysGlnTrpSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerL 34
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2304 CCAGCAGACTGCTAAACGACGACGACGCTCTAAACGACGAGTCTCA 2255
34 yGluGluAlaLeuGlnIleIleArgGluLysIleProGluLysTrpLeu 50
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2254 AAGAAAGCTGCGTTGCATAATATCAGGACGAACTCCCTGAAAAATATTTA 2205
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2204 TTTCATATTCAATTAATTAGTTAGTAATTAGATGATTTTTCCTCC 2155
67 rPro 68
|||
2154 ACCT 2151

seq_name: gb_v1:SGU67926

seq_documentation_block:
LOCUS SGU67926 554 bp DNA VRL 28-JAN-1998
DEFINITION Sida golden mosaic geminivirus Rep protein (AC1) gene, partial cds.
ACCESSION U67926
VERSION U67926.1 GI:1546801
KEYWORDS
SOURCE
ORGANISM
sida golden mosaic virus.
sida golden mosaic virus.
viruses: ssDNA viruses: Geminiviridae; Begomovirus.
1 (bases 1 to 554)
REFERENCE
AUTHORS
Royer,M.E., McLaughlin,W.A., Nakhla,N.K. and Maxwell,D.P.
TITLE
Genetic Diversity among geminiviruses associated with the weed
species Sida spp, Macroptilium lathyroides, and Wissadula
amplissima from Jamaica
Plant Dis. 81, 1251-1258 (1997)
2 (bases 1 to 554)
REFERENCE
AUTHORS
Royer,M.E., McLaughlin,W.A. and Maxwell,D.P.
TITLE
Direct Submission
JOURNAL
Submitted (23-NOV-1996) Plant Pathology, University of Wisconsin,
1630 Linden Drive, Madison, WI 53706-1598, USA
FEATURES
FEATURES
1..554
Location/Qualifiers
/organism="sida golden mosaic virus"
/strain="Jamaica"
/isolate="Jamaica, May 1993"
/db_xref="taxon:51034"
/note="DNA A component"
complement(1..554)
/gene="AC1"
gene
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CDS
complement(<1..>554)
/gene="AC1"
/note="Replication-associated protein"
/codon_start=1
/product="Rep protein"
/protein_id="AAB97865.1"
/db_xref="GI:1546802"
/translation="SISKERALSQLOTLKTPVNNKFKICRELDNCEPHULVIOFE
GKYNCTNRFEDVSPTRSVHFPHFIOGAKSSSVKSVKEDGPTIEGVFOIDGRSA
RGGOQTANDAAAEALNNGCTEKDAIKIIREALPERYLTQYINLSNIDRITSKPEPMS
HPPPLBSFTAVPGQMEWADGYFER"
BASE COUNT      121 a      127 c      139 g      167 t
ORIGIN

alignment_scores:
  Quality: 281.00      Length: 70
  Ratio: 4.323      Gaps: 0
  Percent Similarity: 92.857      Percent Identity: 72.857

alignment_block:
US-09-289-346a-9 x SGU67926/rev ..

Align seg 1/1 to reverse of: SGU67926 from: 1 to: 554

1 ThrLeuValTrpGlyGluPheGlnValAlaGlyArgSerAlaArgGlyC1 17
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
290 ACCATCAGATGGGGGCTTCCAGATCGACGACGAGTCTCTGGACG 241
17 yCysGlnTrpSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerL 34
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
240 TCAGCAACAGCTAACGACGACGACGACGACGATGATTCGAAACAA 191
34 yGluGluAlaLeuGlnIleIleArgGluLysIleProGluLysTrpLeu 50
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
190 AGCAGATGCTGAAATCATCATCAGACAGAGATTCACGAAAGATATCTC 141
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
140 TTTCATATCACACCTATCCAGTATATGATAGGATTTTCATGACGCC 91
67 rProGluPro 70
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90 TCCAGAACCG 81

seq_name: gb_v1:IEI132548

seq_documentation_block:
LOCUS IEI132548 2763 bp DNA circular VRL 01-FEB-1999
DEFINITION Ipomoea yellow vein virus V2, V1, C3 and C2 genes.
ACCESSION A1132548
VERSION A1132548.1 GI:4210720
KEYWORDS
SOURCE
ORGANISM
Ipomoea yellow vein virus.
Ipomoea yellow vein virus.
viruses: ssDNA viruses: Geminiviridae; Begomovirus.
1 (bases 1 to 2763)
REFERENCE
AUTHORS
Banks,G.K.
TITLE
Direct Submission
JOURNAL
Submitted (26-JAN-1999) Banks G.K., Virus Research, John Innes
Centre, Norwich Research Park, Colney Lane, Norwich, NR4 6JL, UK
2 (bases 1 to 2763)
REFERENCE
AUTHORS
Banks,G.K., Bedford,I.D., Beilte,F.J., Cerezo,E.R. and Markham,P.G.
TITLE
A novel geminivirus of Ipomoea indica (Convolvulaceae) from southern
Spain
JOURNAL
Unpublished
FEATURES
FEATURES
1..2763
Location/Qualifiers
/organism="Ipomoea yellow vein virus"
/virion
/specific_host="Ipomoea indica"
/db_xref="taxon:87832"
/gene="AC1"
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gene      995..1390
          /gene="V2"
CDS        995..1390
          /gene="V2"
          /codon_start=1
          /product="V2 protein"
          /protein_id="CAI0695.1"
          /db_xref="GI:4210721"
          /translation="MTLLYKDSQSDRCAPGCSSTAEMDPLONPLDPLLYGPRCMISYKY
          LAGILKKYEPGTGFEICSELRIFRYRQYDRANSRAETISLMGETGKTESLRDSTY
          RALHMCCPCCKRCLCPGFKRPDEKEG"
gene      1215..1979
          /gene="V1"
          /gene="V1"
          /db_xref="GI:4210722"
          /translation="MTGRIRVSPRPHPGYGGROYRBSLNTETATPYTNGNAVPIAARSY
          VPSRCVBMRRRGDPRKCVGPKTODEEFKMDVPHCTGTCVSPDFIGTGILTHL
          GKAVCIKSMIDCKVMDNDVAKRDHNTITWLIIRDNRKDFLNFGLPTMDNBP
          TTKIRMDLDRMQVLKFSVTVSGSPYSHKEGALLKFEKCLYNHVTYNHKEAKYE
          MOLENAIMLYSASSHSNPYQTLRCRAYFYDSHKN"
          complement(1976..2413)
CDS        /gene="C3"
          /complement(1976..2413)
          /gene="C3"
          /codon_start=1
          /product="C3 protein"
          /protein_id="CAI0697.1"
          /db_xref="GI:4210723"
          /translation="MDSRTGESLSHAQITRAAEFNNPMSVGGTAPFHLRLMYHTNN
          LSKRTIMKVDLQVHNRRREIGOKTIFLQPIITRLIGAIPTMTGISNRLKMKICNS
          LAGLYFSLENLVYIRHLPOQLWEVEVDVIOCKDOIKVLY"
          complement(2127..2576)
gene      /gene="C2"
          /complement(2127..2576)
          /gene="C2"
          /codon_start=1
          /product="C2 protein"
          /protein_id="CAI0698.1"
          /db_xref="GI:4210724"
          /translation="MSTAPSGYKRCPCAPOEPIHAARKRQKTPPEPRLVWKGCGCS
          APTINDCKRQHGFTHRGVTSCTDYESRILQDSHYGSDCTIPSTTDVCPYKQPRLK
          DDHSSAASSQPPDEGMWIPEDLPPIPDHNASDWCYSQLDWTFQSP"
BASE COUNT 734 a 570 c 671 g 788 t
ORIGIN

alignment_scores:
  Quality: 280.00      Length: 68
  Ratio: 4.590        Gaps: 0
  Percent Similarity: 89.706   Percent Identity: 79.412

alignment_block:
US-09-289-346a-9 x IYEL32548/rev ..

Align seg 1/1 to reverse of: IYEL32548 from: 1 to: 2763

1 ThrLeuValTrpGlyGluPheGlnValAlaGlyAyrSerAlaArgIylGI 17
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469 ACCCTCATATGGGGTGATTCAGATCCAGCGCAGATCTCGCTAGAGGAGG 420

17 yCysGlnThrSerAsnAspAlaAlaAlaGluAlaLeuAsnAlaSerSerL 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
419 TCAGCAGTCTGCTAACGACGACGCCGACAGGCGCTAAACGCATCTTCA 370

34 yGluGluAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeu 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
369 AAGAAAGCTCGTTGCAAAATATCAGAGGAGAACTCCCTGAAAAAATATTTA 320

51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67

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|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
319 TTTCATATCATATATTAGTATAGTATAGATATTTTCTGCTGCC 270

67 rPro 68
|||||
269 TCCT 266

seq_name: gb_v1:MGU75278

seq_documentation_block:
LOCUS      MGU75278      447 bp      DNA
DEFINITION Macrotellium golden mosaic geminivirus replication-associated
protein (AC1) gene, partial cds.
ACCESSION  U75278.1
VERSION    U75278.1
KEYWORDS   GI:1688188
SOURCE     Macrotellium golden mosaic geminivirus.
ORGANISM   Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
REFERENCE  1 (bases 1 to 447)
AUTHORS    Royle,M.E.
TITLE      Diversity and phylogeny of whitefly-transmitted geminiviruses from
Jamaica
JOURNAL    Thesis (1996)
REFERENCE  2 (bases 1 to 447)
AUTHORS    Royle,M.E., McLaughlin,W.A. and Maxwell,D.P.
TITLE      Three distinct geminiviruses infecting M. lachryoides from Jamaica
but not BCMV
JOURNAL    Unpublished (1996)
REFERENCE  3 (bases 1 to 447)
AUTHORS    Royle,M.E., McLaughlin,W.A. and Maxwell,D.P.
TITLE      Direct Submission
JOURNAL    Submitted (17-OCT-1996) Biochemistry, University of the West
Indies, Mona, Kingston 7, Jamaica
FEATURES   Location/Qualifiers
source     1..447
            /organism="Macrotellium golden mosaic geminivirus"
            /strain="Jamaican"
            /isolate="2"
            /db_xref="taxon:51676"
            /clone="pmcJ2"
            complement(1..447)
            /gene="AC1"
            complement(<1..>447)
            /gene="AC1"
            /codon_start=1
            /product="replication-associated protein"
            /protein_id="AAB36919.1"
            /db_xref="GI:1688189"
            /translation="HVLIOFGKFCNTNNRLFDLVPSRAHFHPNIOGAKSSSDVKS
            YVEKDGTIEGVQIDGRSARGGCOQTSNDAAALASGTREAMRIYKELPKFLF
            OYHNLSSNLDLIFMKDPEPPWAPPPPLSSFTNVDPDEKOWATNYFGRG"
BASE COUNT 97 a 112 c 110 g 128 t
ORIGIN

alignment_scores:
  Quality: 273.00      Length: 70
  Ratio: 4.333        Gaps: 0
  Percent Similarity: 90.000   Percent Identity: 71.429

alignment_block:
US-09-289-346a-9 x MGU75278/rev ..

Align seg 1/1 to reverse of: MGU75278 from: 1 to: 447

1 ThrLeuValTrpGlyGluPheGlnValAlaGlyAyrSerAlaArgIylGI 17
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
294 ACCATGAATGGGAGCTGTCCAGATCGACGAGAGAGTGTGAGAGCGG 245

17 yCysGlnThrSerAsnAspAlaAlaAlaGluAlaLeuAsnAlaSerSerL 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
244 TCAGCAACATCTAACGATGCAACCGCCGACGACATTAATTTTCGANAAC 195

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34 ysglgluAlaleuGlnIleIleAArgGluLysIleProGluLysTyrLeu 50
||||| |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
194 AGAGCGCGCCATGACATATGTCAGAGAGAAGTTGCCGAAAGTTTCTC 145

51 pHeGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
144 TTTCATATCACAACCTATCAGTACCTCGATAGATTTTCATGAGAAGA 95

67 rProGluPro 70
|||||
94 TCCGGAAACA 85

seq_name: gb_v1:AF098940

seq_documentation_block:
LOCUS AF098940 1405 bp DNA VRL 04-MAR-1999
DEFINITION Macropittium golden mosaic geminivirus strain Jamaica strain 1
partial cds.
replication associated protein (rep) and coat protein (cp) genes,
partial cds.
ACCESSION AF098940 GI:4336584
VERSION AF098940.1 GI:4336584
KEYWORDS
SOURCE Macropittium golden mosaic geminivirus.
ORGANISM Macropittium golden mosaic geminivirus.
REFERENCE 1 (bases 1 to 1405)
AUTHORS Roye,M.E.
TITLE Genetic diversity and phylogeny of whitefly-transmitted geminiviruses from Jamaica
JOURNAL 2 (bases 1 to 1405)
AUTHORS Roye,M.E., McLaughlin,W.A. and Maxwell,D.P.
TITLE Molecular characterization of two distinct geminiviruses infecting M. lathyroides from Jamaica
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 1405)
AUTHORS Roye,M.E., McLaughlin,W.A. and Maxwell,D.P.
TITLE Direct Submission
JOURNAL Submitted (14-OCT-1998) Biotechnology Centre, University of the West Indies, Mona, Kingston 7, Jamaica
FEATURES
source
1..1405
/organism="Macropittium golden mosaic geminivirus"
/strain="Jamaica strain 1"
/specific_host="Macropittium lathyroides"
/db_xref="taxon:51676"
/country="Jamaica"
/clone="pmGJA2; pmGJA3"
complement(<1..701)
/gene="rep"
complement(<1..701)
/gene="cp"
/codon_start=1
/product="replication associated protein"
/protein_id="AA017850.1"
/db_xref="GI:4336586"
/translatiion="MPKRSFSIKAKYVFLYPOCSITKEPALSQLTNLMPVKKRI
KICREHEDQPHLHVLIQFOGKNCNNRFLDVSFRRSHFRPNIOGAKSSDYKS
YVEKDGDTFVGVFQIDGRSARQOQTSNDAAPALNSGTKEAMRIYKELPKPLF
OYNLSSNLTORIEFKDPEPMAPEPLSSFTNVPEQEMADDDYFGRSARPERPMSI
IVEGDSRTGKTMMAC"
702..1030
/feature="intergenic region"
1031..>1405
/gene="cp"
1031..>1405
/gene="cp"
/product="coat protein"
/protein_id="AA017849.1"
/db_xref="GI:4336585"
/translatiion="MPKRDGSWRTTPGAVKVSRLNYSPPGYGPRSNKAQEWVNRPM

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RRKPRIVLTSPDPVPRGCEGPKVQVSQEQRHDISHGVKWCISDTRGYVITRWCK
RFCKVFYIIIGKIMDENINQSC"
BASE COUNT 328 a 333 c 357 g 386 t 1 others
ORIGIN

alignment_scores:
Quality: 273.00 Length: 70
Ratio: 4.333 Gaps: 0
Percent Similarity: 90.000 Percent Identity: 71.429

alignment_block:
US-09-289-346a-9 x AF098940/rev ..

Align seg 1/1 to reverse of: AF098940 from: 1 to: 1405

1 ThrLeuValTrpPolYgLuPheGlnValAlaGlyArgSerAlaArgLysI 17
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374 ACCATCGAATGGGAGTGTCCAGATCGACGAGAGAAAGTGTGAGAGCG 325

17 yCysGlnThrSerAsnAspAlaAlaIaGluAlaLeuAsnAlaSerSerL 34
| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
324 TCAGCAAAACATCTAACGATGACGCCCGCAGACGATTAAATCTGGAACA 275

34 ysglgluAlaleuGlnIleIleAArgGluLysIleProGluLysTyrLeu 50
||||| |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
274 AGAGCGCGCCATGACATATGTCAGAGAGAAGTTGCCGAAAGTTTCTC 225

51 pHeGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
224 TTTCATATCACAACCTATCAGTACCTCGATAGATTTTCATGAGAAGA 175

67 rProGluPro 70
|||||
174 TCCGGAAACA 165

seq_name: gb_v1:AF026553

seq_documentation_block: 1165 bp DNA VRL 03-NOV-1997
LOCUS AF026553
DEFINITION Potato yellow mosaic virus tomato strain AV1 and AC1 genes, partial
cds.
ACCESSION AF026553 GI:2583073
VERSION AF026553
KEYWORDS
SOURCE Geminiviridae.
ORGANISM Geminiviridae.
REFERENCE 1 (bases 1 to 1165)
AUTHORS Guzman,P., Arredondo,C.R., Emmaty,D., Portillo,R.J. and
Gilbertson,R.L.
TITLE Partial Characterization of Two Whitefly-Transmitted Geminiviruses
Infecting Tomatoes in Venezuela
JOURNAL 2 (bases 1 to 1165)
REFERENCE Guzman,P., Arredondo,C.R., Emmaty,D., Portillo,R.J. and
AUTHORS Gilbertson,R.L.
TITLE Direct Submission
JOURNAL Submitted (24-SEP-1997) Plant Pathology, University of
California-Davis, Department of Plant Pathology, Davis, CA 95616,
USA
FEATURES
source
1..1165
/organism="Geminiviridae"
/strain="Tomato strain"
/db_xref="taxon:10811"
/feature="Bipartite genome: whitefly-transmitted; DNA-A
fragment obtained by PCR from tomato sample from State of
Monagas (Venezuela)"
complement(<1..153)
/feature="capsid protein"
/codon_start=1
/product="AV1"

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CDS
    /protein_id="AA82606.1"
    /db_xref="GI:2583075"
    /translation="MPKRDAPMRSMAGTSKVSNNANYSRPSGIGPRLNKAAEWNRP
    YRPSI"
    464..>1165
    /note="replication-associated protein"
    /codon_start=1
    /product="AC1"
    /protein_id="AA82605.1"
    /db_xref="GI:2583074"
    /translation="MPKSGSFSTKAKNYLTTPQSLSKEDALSOTONLTTPVKKFI
    KICRELHENGEPHLVLIQIEGKFNCTNNRLFDVSPSTRHFNPIQKSSDVKS
    YVEKDDITLWGLFQIDGSRAGCOTANDAALNSGTFKEAMKIIKKLPEKLF
    OYHNLSSDLDRIFMKAPNPWAPPPPLSFTNVPHQEMSHDYFGSSAARGETISII
    IEGDSRTGRTMACRC"

BASE COUNT      350 a      264 c      256 g      295 t

ORIGIN
alignment_scores:
    Quality: 267.00      Length: 70
    Ratio: 4.108      Gaps: 0
    Percent Similarity: 92.857      Percent Identity: 70.000

alignment_block:
US-09-289-346A-9 x AF026553 ..

Align seg 1/1 to: AF026553 from: 1 to: 1165

1   ThrLeuValTTPGlyGluPheGlnValAlaGlyArgSerAlaArgGlyG1 17
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
791 ACCATCGAATGGGATGTGTCGATGTCGAGAGAGAGTGTCTCGAGGTGG 840

17  YCysGlnThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerL 34
    | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
841 CCAACAGACCGCAACAGACGAGCGAGCGCATTAACCTCGAACAA 890

34  YsGluGluAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeu 50
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
891 AGGAAGAGCCATGAAATCATTAAGAGAGAGTCCCGGAAAAGTTTCTT 940

51  PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
941 TTTCAGTATCATTAACCTATCCAGTGACCTCGATAGATTTTTCATGAGGC 990

67  rProGluPro 70
    :|||:|:|:|
991 TCCAAATCCG 1000

seq_name: gb_v1:AB001315

seq_documentation_block:
LOCUS      AB001315      570 bp      DNA      VRL      13-FEB-1999
DEFINITION Tobacco leaf curl virus C1 and C4 genes, clone YOKOHAMA3-1, partial
and complete cds.
ACCESSION  AB001315
VERSION    AB001315.1 GI:3798714
KEYWORDS
SOURCE     tobacco leaf curl virus (isolate:YOKOHAMA3,
            specific host:Eupatorium makinoi) DNA, clone:YOKOHAMA3-1.
            tobacco leaf curl virus
            Viruses: ssDNA viruses; Geminiviridae; Begomovirus.
            1 (bases 1 to 570)
ORGANISM   Ooi,K.
REFERENCE  1 Direct Submission
            Submitted (19-FEB-1997) to the DDBJ/EMBL/Genbank databases.
            Kazuyuki Ooi, Kyushu University, Department of Biology; 6-10-1
            Hakozaki Higashi-ku, Fukuoka 812, Japan
            (E-mail:koosic@box.nc.kyushu-u.ac.jp, Tel: +81-92-642-2624,
            Fax: +81-92-642-2645)
            2 (bases 1 to 570)
AUTHORS    Ooi,K., Ohshita,S., Ishii,I. and Yahara,T.
TITLE      Molecular phylogeny of geminivirus infecting wild plants in Japan

```

```

JOURNAL      J. Plant Res. 110, 247-257 (1997)
FEATURES
SOURCE
    /organism="tobacco leaf curl virus"
    /isolate="YOKOHAMA3"
    /specific_host="Eupatorium makinoi"
    /db_xref="taxon:67762"
    /clone="YOKOHAMA3-1"
    complement(1..570)
    /gene="C1"
    complement(<1..>570)
    /codon_start=1
    /gene="C1"
    /protein_id="BAA34033.1"
    /db_xref="GI:4426541"
    /translation="EEALSQLQINPTNKLTKICRELHEDSGPHLVLIQREGKK
    QNNRRFDLVSPTRSAHFHPNIQAKSSSDVKSITDDGDTLEMGTFQIDGSRAGGC
    QNANDACAEALNASSKAELALIIREKLPRKDFIOYHNLNSLDRIFAPLPEVFCPT
    ASSFDQVPEELEWASENSEVMSAARPRP"
    complement(231..488)
    /gene="C4"
    complement(231..488)
    /gene="C4"
    /codon_start=1
    /protein_id="BAA34034.1"
    /db_xref="GI:3798715"
    /translation="MEALISMCFSSKANTNAKITDSSSTWYPOPDHISIRFRELN
    APITSSPTSTETELRSNGEHSRSTEEVEEARMLTHVQR"

BASE COUNT      141 a      121 c      126 g      182 t

ORIGIN
alignment_scores:
    Quality: 264.00      Length: 85
    Ratio: 4.190      Gaps: 1
    Percent Similarity: 74.118      Percent Identity: 61.176

alignment_block:
US-09-289-346A-9 x AB001315/rev ..

Align seg 1/1 to reverse of: AB001315 from: 1 to: 570

1   ThrLeuValTTPGlyGluPheGlnValAlaGlyArgSerAlaArgGlyG1 17
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
318 ACCCTCGAATGGGAGACATTCCAGATCGACGAGAGAGTGTCTAGAGAGG 269

17  YCysGlnThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerL 34
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
268 CTGCCAGATGCTAACGACGATGTGCAAGCGGTAAATGCAAGTTCYA 219

34  YsGluGluAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeu 50
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
218 AGCGAGAGCCATTAGCAATATTAGGAAACCTCCCTAAGATTATTAYA 169

51  PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIle..... 63
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
168 TTTCATATCATTAATTAAATAGTATTAGATGAGATTTTGCTCTCTC 119

64  .....
118 GTTGAGAGTTTGTGTTGTCCTTTCACAGCTCATGCTTGTGATCAAGTTC 69

68  rGlu 69
    |||||
68  CAGAA 64

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```

2216 ACCTAATGATGCTGCCGACAGCCCTTAATGACGCTTCAGCTGAGCAG 2167
37 lalcuGlnlleIleargGluLysIleProGluLysIleuheGlnp 53
||||| ||||||||| ||||||| : : : : |||||||
2166 CTTTAGCAATTAATTAAGGAAACCTCCCTAAAGATTATTTTCAATAT 2117
54 HisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysThrPro 68
||||| : : : ||||||||| |||||
2116 CATTAAATTAAATGTAAATTAGATAGATTTT.....ACACCT 2078

seq.name: /cgnl_8/gcgdata/geneseq/geneseq/NA1995.DAT:AA084371

seq_documentation_block:
ID AA084371 standard; DNA: 434 BP.
XX
AC AA084371;
XX
DT 19-AUG-1995 (first entry)
XX
DE Gemini1 virus-specific polyribozyme-E target sequence.
XX
KW ribozyme target sequence; polyribozyme-E;
KM tomato leaf curl virus; RNA cleavage; tomato transgenic plant;
KW virus disease-resistance; ss.
XX
OS Tomato leaf curl virus.
XX
FH Key location/qualifiers
FT misc_feature 13..43
FT /*tag= a
FT /note= "ribozyme R1 target sequence"
FT 26..28
FT misc_feature
FT /*tag= b
FT /note= "ribozyme R1 cleavage site"
FT 312..342
FT misc_feature
FT /*tag= c
FT /note= "ribozyme R2 target sequence"
FT 325..327
FT misc_feature
FT /*tag= d
FT /note= "ribozyme R2 cleavage site"
FT 384..414
FT /*tag= e
FT /note= "ribozyme R3 target sequence"
FT 397..399
FT misc_feature
FT /*tag= c
FT /note= "ribozyme R3 cleavage site"
XX
PN WO9503404-A.
XX
PD 02-FEB-1995.
XX
PF 22-JUL-1993; 93WO-EP01946.
XX
PR 22-JUL-1993; 93AU-0047014.
XX
PR 22-JUL-1993; 93WO-EP01946.
XX
PA (BIOC-) BIOCEM SA.
XX
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX
PI Baudino S, Comeau D, Dry IB, Gruber V, Ienee P;
PI Mason J, Rezaiian MA, Rlyden JE, Rezaiian MA;
XX
XX WPI: 1995-075232/10.
XX
XX Synthetic DNA virus ribozyme(s) - reduce replication, infection
XX and/or assembly of viruses by cleaving target virus sequence,
XX useful for preparing resistant plants, esp tomatoes.
XX
XX Example 10; Fig 11b; 90pp; English.
XX
XX The sequence is a tomato leaf curl virus target sequence for
XX polyribozyme-E, which hybridizes to and cleaves the sequence and
XX thereby reduces replication, infection and/or assembly of the virus

```

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CC substantially. The ribozyme may be expressed in a transgenic plant,
CC e.g. tomato, to confer virus disease-resistance.
XX
SQ Sequence 434 BP; 126 A; 86 C; 91 G; 131 T; 0 other;

alignment_scores:
Quality: 236.00 Length: 85
Ratio: 3.806 Caps: 1
Percent Similarity: 72.941 Percent Identity: 55.294

alignment_block:
US-09-289-346a-9 x AA084371 ..
Align seg 1/1 to: AA084371 from: 1 to: 434

1 ThrLeuValTrpGlyGluPheGlnValAlaGlyArgSerAlaArgGly 17
||||| ||||||||| : : : ||||||||| |||||||
95 ACCCTCGAATGCGGAGAGCTTCAGATCGATCGATCGCAAGAGGGGG 144
17 ycgsglnThrSerAspAlaAlaAlaGluAlaLeuAsnAlaSerL 34
||||| : : : ||||||||| : : : |||||||||
145 ACACACATACGCAATGACGCTTACGCGCGGCTTAACACTGGAAGTA 194
34 ysglucGlnAlaLeuGlnIleIleArgGluLysIleProGluLysTrpLeu 50
||||| : : : ||||||||| : : : |||||||
195 AGTCAGAGGCTCTTAACGCTTAGGGAATTAGCCCTTAGGATTATGCTT 244
51 pheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIle..... 63
: : : ||||||||| ||||||||| |||||||
245 TTACAAATTTCATTAATTAAATAGTAATTAGATAGATTTTACACCTCC 294
64 ..... PheAspLysThrP 68
295 GTTGGAGGTTTATGTTCTCTTTTATTACTTCTTTTGATCGAGTTC 344
68 roGlu 69
|||||
345 CAGAA 349

seq.name: /cgnl_8/gcgdata/geneseq/geneseq/NA1995.DAT:AA084372

seq_documentation_block:
ID AA084372 standard; DNA: 479 BP.
XX
AC AA084372;
XX
DT 19-AUG-1995 (first entry)
XX
DE Gemini1 virus-specific polyribozyme-F target sequence.
XX
KW ribozyme target sequence; polyribozyme-F;
KM tomato leaf curl virus; RNA cleavage; tomato transgenic plant;
KW virus disease-resistance; ss.
XX
OS Tomato leaf curl virus.
XX
FH Key location/qualifiers
FT misc_feature 46..96
FT /*tag= a
FT /note= "ribozyme R4-R5 target sequence"
FT 58..60
FT misc_feature
FT /*tag= b
FT /note= "ribozyme R4 cleavage site"
FT 81..83
FT /*tag= c
FT /note= "ribozyme R5 cleavage site"
FT 356..386
FT misc_feature
FT /*tag= d
FT /note= "ribozyme R2 target sequence"
FT 370..372
FT /*tag= c
FT /note= "ribozyme R2 cleavage site"

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FT	misc_feature	429..459	/*tag= e
FT		/note= "ribozyme R3 target sequence"	
FT	misc_feature	442..444	/*tag= d
FT		/note= "ribozyme R3 cleavage site"	
FT			
PN	W09503404-A.		
PD	02-FEB-1995.		
PF	22-JUL-1993;	93WO-EP01946.	
PR	22-JUL-1993;	93AU-0047014.	
PR	22-JUL-1993;	93WO-EP01946.	
PA	(BIOC-) BIOCEM SA.		
PA	(CSIR) COMMONWEALTH SCI & IND RES ORG.		
P1	Baudino S, Comeau D, Dry IB, Gruber V, Lenée P;		
P1	Mason J, Rezaiian MA, Rigen JE, Rezanan MA;		
DR	WPI; 1995-075232/10.		
XX			
XX	Synthetic DNA virus ribozyme(s) - reduce replication, infection		
PT	and/or assembly of viruses by cleaving target virus sequence,		
PT	useful for preparing resistant plants, esp tomatoes.		
XX			
PS	Example 10; Fig 11c; 90pp; English.		
XX			
CC	The sequence is a tomato leaf curl virus target sequence for		
CC	polyribozyme-F, which hybridizes to and cleaves the sequence and		
CC	thereby reduces replication, infection and/or assembly of the virus		
CC	substantially. The ribozyme may be expressed in a transgenic plant		
CC	e.g. tomato, to confer virus disease-resistance.		
XX			
SO	Sequence 479 BP; 145 A; 95 C; 97 G; 142 T; 0 other;		

alignment_scores:		Length:
Quality:	236.00	85
Ratio:	3.806	Gaps: 1
Percent Similarity:	72.941	Percent Identity: 55.294
alignment_block:		
US-09-289-346A-9 ..		
Align seg 1/1 to: AAQ84372 from: 1 to: 479		
1	ThleuValITrpglyGluPhcglInValAlagIaYrGSeRAlaArglycl 17	
	::	
140	ACCCCTCAATCGGAGAGATTTCAGATCGATGGACCATTCGCAGAGGGG 189	
17	YcysGlnThSerAsnAspAlaAlaAlaGluAlaLeuAsnAlaSerSerL 34	
	:: ::	
190	ACAACATCAGCCCATGACGCTTACGCCAGGCGCTTACACTGGAGAT 239	
34	ysgluGluAlaLeuGlnIleIleArGgLUlYsIlleProGluYsTYrleu 50	
	::	
240	AGTCAGAGGCTCTTAACCTCCTTAGGGAATTAGCCCTTAAGCATTTATGTT 289	
51	PhcglInPhcHISAsnLeuAsnSerAsnLeuAspArgIle 63	
	:::	
290	TTACAAATTTCAATTAAATTAAATAGTAATTTAGATGATTTTACACCTCC 339	
64PheAspLysThrP 68	
	::	
340	GTTGGAGTTATGTTCTCCTTTTAACTCTTCTTTGATCGAGTTC 389	
68	roGlu 69	
390	CAGAA 394	

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seq_name: /cpgl_8/gcgdata/geneseq/geneseqn/NA1995.DAT:AA084375
seq_documentation_block:
ID   AA084375 standard; DNA; 550 BP.
XX
XX   AA084375;
AC
XX
XX   19-AUG-1995 (first entry)
DT
XX
XX   Tomato leaf curl virus Australian strain DNA sequence.
DE
XX
XX   Tomato leaf curl virus; Australia; strain; plant disease; ds.
XX
XX   Tomato leaf curl virus (Australia).
XX
XX   WC9503404-A.
XX
XX   WC9503404-A.
XX
XX   02-FEB-1995.
XX
XX   22-JUL-1993; 93WC-EP01946.
XX
XX   22-JUL-1993; 93AU-0047014.
XX
XX   22-JUL-1993; 93WC-EP01946.
XX
XX   (BIOC-) BIOCEM SA.
XX
XX   (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX
XX   Baudino S, Comeau D, Dry IB, Gruber V, Lenee P;
XX
XX   Mason J, Rezaiian MA, Ridgen JE, Rezanan MA;
XX
XX   MPI; 1995-075232/10.
XX
XX   Synthetic DNA virus ribozyme(s) - reduce replication, infection
XX
XX   and/or assembly of viruses by cleaving target virus sequence,
XX
XX   useful for preparing resistant plants, esp tomatoes.
XX
XX   Disclosure; Fig 1; 90pp; English.
XX
XX   The sequence represents the complementary sense DNA strand of a
XX
XX   Australian strain of tomoato leaf curl virus. Ribozymes specific
XX
XX   for this sequence may be used in generation of transgenic plants
XX
XX   with disease-resistance.
XX
XX   Sequence 550 BP; 148 A; 120 C; 134 G; 142 T; 6 other.

```

```

alignment_scores:
    Quality: 235.50
    Ratio: 3.798
    Percent Similarity: 72.093
    Percent Identity: 54.651

alignment_block:
    US-09-289-346A-9 x AAG84375 ..

Align seg 1/1 to: AAG84375 from: 1 to: 550

1 ThrLeuVal1TrpGlyGluPheGluValAlaGlyArgSerAlaArgGlyc1 17
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
201 ACCCTCGAATGGGAGAGATTTCAGATTCAGTCAGATTCGCAAGAGGGG 250
||||| ||||| ||||| ||||| ||||| ||||| |||||

17 yCysGlnThrSerAsnSpAlaAlaIleGluAlaLeuAsnAlaSerSerL 34
| ||||| ||||| ||||| ||||| ||||| ||||| |||||
251 ACAACATCAATGACCAATGACGCTTACGCCAGCCGCTTAACACTGCAAGTA 300
||||| ||||| ||||| ||||| ||||| ||||| |||||

34 ySgIuGluAlaLeuGlnIleIleArgGluLysIleProGluLysTryLeu 50
||||| ||||| ||||| ||||| ||||| ||||| |||||
301 AGCTAGAGGGCTTAACTCCCTTACGGGAATTAGCCCTTAAGGATTATGTT 350
||||| ||||| ||||| ||||| ||||| ||||| |||||

51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIle..... 63
:::||||| ||||| ||||| ||||| ||||| ||||| |||||
351 TTACAAATTTCATTATTTAAATAGTAAATTAGATTCAGATTTTNNNTACACC 400
||||| ||||| ||||| ||||| ||||| ||||| |||||

64 .....PheAspLysT 67

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```

401 TCCGTTGAGGTTTATGTTTCCTTTTACTTCTTTGATGAG 450
67 hrProglu 69
:::|||||
451 TTCAGAA 458

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seq_name: /cgn1_8/gcgdata/geneseq/geneseqn/NA1998.DAT:AAV29761

seq_documentation_block:

ID AAV29761 standard: DNA: 2766 BP.

AAV29761:

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11-AUG-1998 (first entry)
xx
DE Tobacco leaf curling virus gene.
xx
KM Tobacco leaf curling virus gene; TLCV; promoter; ds.
xx
OS Tobacco leaf curling virus.
xx

```

JP10070982-A.

17-MAR-1998.

30-AUG-1996; 96JP-0230394.

30-AUG-1996; 96JP-0230394.

(NORO) NORINSUISANSO KYUSHU NOGO SHIKENJO.

WPI: 1998-233630/21.

Tobacco leaf curling virus gene - useful for inserting into vectors for expression in, e.g. tomato plants

Claim 1: Figs 1-3; 9pp; Japanese.

This sequence represents the tobacco leaf curling virus (TLCV) gene of the invention. TLCV gene or its promoter can be inserted into a vector for expression in plants, e.g. tobacco and tomato. This sequence is believed to encode the TLCV proteins shown in AAM56493-W56498.

Sequence 2766 BP: 722 A; 576 C; 609 G; 859 T; 0 other:

alignment_scores:

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Quality: 226.00 Length: 84
Ratio: 3.645 Gaps: 1
Percent Similarity: 73.810 Percent Identity: 54.762

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alignment_block:

US-09-289-346a-9 x AAV29761/rev ..

Align seg 1/1 to reverse of: AAV29761 from: 1 to: 2766

2 LeuValTTRGlgylupheglvalAlaGlyArgSerAlaArgIglylcy 18

2436 CTTGATTGAGCTTTCACGACGAGGAGATCAGCTAGCGAGCTTG 2387

18 sglThrSerAsnAspAlaAlaIaGluAlaLeuAsnAlaSerSerlysg 35

2386 CCAATCTCCACGACGACATATGCCAGGCAATCACTCAGATCAAGT 2337

35 IuGluAlaLeuGlnIleIleArgIuLysIleProGluIuTyLeuphe 51

2336 CAVCGGACACTCATATTATTAAGGAGAAAGCTCCAAAGATTGTTTA 2287

52 GluPheHisIuLeuAsnSerAsnLeuAspArgIle..... 63

2286 CAATTCATTAATTAAATTCAAATTAGATGATTTTGCCTCCATTT 2237

```

64 .....PheAspLysThrProG 69
2236 GGAGGTTTGTGTTGCTTTTCTAGTCTTCTTCATTTGATCAAGTTCCG 2187
69 Iu 69
2186 AA 2185

```

seq_name: /cgn1_8/gcgdata/geneseq/geneseqn/NA1997.DAT:AAT93291

seq_documentation_block:

ID AAT93291 standard: DNA: 1062 BP.

AAT93291:

27-APR-1998 (first entry)

DE Bean golden mosaic geminivirus CI mutant ORF BGAC221.

Geminivirus; BGW; CI gene; transdominant mutation;

transgenic plant; disease resistance; ss; cyclic; circular.

OS Bean golden mosaic virus type II isolate Guatemala.

W09739110-A1.

23-OCT-1997.

15-APR-1997; 97WO-US06300.

16-APR-1996; 96US-0015517.

(SEMI-) SEMINIS VEGETABLE SEEDS INC.

(WISC) WISCONSIN AIDUMI RES FOUND.

Abiquist PG, Hanson SF, Luu HT, Maxwell DP, Stout JT.

WPI: 1997-526447/48.

P-PSDB: AAM34333.

Transgenic plants expressing geminivirus AC1 and CI wild-type and

mutant genes - have increased resistance to geminivirus infection

e.g. tomato mottle virus, tomato yellow leaf curl virus or bean

golden mosaic geminivirus

Claim 13: Page 107-109; 132pp; English.

This DNA sequence comprises construct BGAC221 that codes for a

transdominant lethal mutant (see AAM34333) of the CI protein (see

AAM34338) of bean golden mosaic virus (BGW). It was obtained by

Kunkel mutagenesis of the wild-type CI gene (see AAT93314). CI is

required for replication. The invention involves production of

transgenic plants containing DNA comprising geminivirus CI or AC1

wild-type or mutant sequences that negatively interfere in trans

with geminiviral replication during infection. Such transgenic

plants are resistant to viral infection. The AC1/CI genes are

especially from BGW, tomato mottle virus or tomato yellow leaf

curl virus (see AAT93292-93) and encode polypeptides (see AAM34324-35)

that have mutations in the highly conserved DNA-nicking and/or the

NTP-binding domains.

alignment_scores:

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Quality: 222.00 Length: 70
Ratio: 3.700 Gaps: 0
Percent Similarity: 85.714 Percent Identity: 60.000

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alignment_block:

US-09-289-346a-9 x AAT93291 ..

Align seg 1/1 to: AAT93291 from: 1 to: 1062

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:1 ThrLeuValTrpGlyUpheGlnValAlaGlyArgSerAlaArgGlyG1 17
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
328 ACAATGCAATGGGGACAAATTCAGTCAGCGCAATCTGCAAGAGGAGG 377
17 yCysGlnThrSerAsnAspAlaAlaAlaGlnValAlaLeuAsnAlaSerSerL 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
378 TCAGCAGCTGTGCCACGACTCATATGCAAAAGCATTAACGCGATTCAA 427
34 ySgLUAlaLeuGlnIleIleArgGlnLysIleProGlnLysTyrLeu 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
428 TTGAATCTGCTGACAAATATGAAAGAGAACACCAAGCAATACGTAC 477
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
478 CTTCACATCTGCACACATCCGCTCTAATCTGAAACGGATCTTCGTCAA 527
67 rProGluPro 70
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
528 GCCGGAACCA 537

seq_name: /cgnl_8/gcgdata/geneseq/geneseqn/NA1997.DAT:AA193292

seq_documentation_block:
ID AAT93292 standard; DNA; 1062 BP.
XX
AC AAT93292;
XX
DT 27-APR-1998 (first entry)
XX
DE Bean golden mosaic geminivirus C1 mutant ORF BGAC228.
XX
KW Geminivirus; BGW; C1 gene; transdominant mutation;
XX
KW Transgenic plant; disease resistance; ss; cyclic; circular.
XX
OS Bean golden mosaic virus type II isolate Guatemala.
XX
PN WO9739110-A1.
XX
PD 23-OCT-1997.
XX
PF 15-APR-1997; 97WO-US06300.
XX
PR 16-APR-1996; 96US-0015517.
XX
PA (SEMI-) SEMINIS VEGETABLE SEEDS INC.
XX
PA (MISC) WISCONSIN ALUMNI RES FOUND.
XX
PI Ahlquist PG, Hanson SF, Luu HT, Maxwell DP, Stout JT;
XX
WP1: 1997-526447/48.
XX
P-PSDB; AAW34334.
XX
PT Transgenic plants expressing geminivirus AC1 and C1 wild-type and
PT mutant genes - have increased resistance to geminivirus infection
PT e.g. tomato mottle virus, tomato yellow leaf curl virus or bean
PT golden mosaic geminivirus
XX
PS Claim 13; Page 111-112; 132pp; English.
XX
CC This DNA sequence comprises construct BGAC228 that codes for a
CC transdominant lethal mutant (see AAW34334) of the C1 protein (see
CC AAW34338) of bean golden mosaic virus (BGW). It was obtained by
CC Kunkel mutagenesis of the wild-type C1 gene (see AAT93314). C1 is
CC required for replication. The invention involves production of
CC transgenic plants containing DNA comprising geminivirus C1 or AC1
CC wild-type or mutant sequences that negatively interfere in trans
CC with geminiviral replication during infection. Such transgenic
CC plants are resistant to viral infection. The AC1/C1 genes are
CC especially from BGW, tomato mottle virus or tomato yellow leaf
CC curl virus (see AAT93282-93) and encode polypeptides (see AAW34324-35)
CC that have mutations in the highly conserved DNA-nicking and/or the
CC NTP-binding domains.

```

```

XX
SQ Sequence 1062 BP; 338 A; 247 C; 218 G; 259 T; 0 other;

alignment_scores:
Quality: 222.00 Length: 70
Ratio: 3.700 Gaps: 0
Percent Similarity: 85.714 Percent Identity: 60.000

alignment_block:
US-09-289-346A-9 x AAT93292 ..
Align seg 1/1 to: AAT93292 from: 1 to: 1062

1 ThrLeuValTrpGlyUpheGlnValAlaGlyArgSerAlaArgGlyG1 17
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
328 ACAATGCAATGGGGACAAATTCAGTCAGCGCAATCTGCAAGAGGAGG 377
17 yCysGlnThrSerAsnAspAlaAlaAlaGlnValAlaLeuAsnAlaSerSerL 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
378 TCAGCAGCTGTGCCACGACTCATATGCAAAAGCATTAACGCGATTCAA 427
34 ySgLUAlaLeuGlnIleIleArgGlnLysIleProGlnLysTyrLeu 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
428 TTGAATCTGCTGACAAATATGAAAGAGAACACCAAGCAATACGTAC 477
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
478 CTTCACATCTGCACACATCCGCTCTAATCTGAAACGGATCTTCGTCAA 527
67 rProGluPro 70
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
528 GCCGGAACCA 537

seq_name: /cgnl_8/gcgdata/geneseq/geneseqn/NA1997.DAT:AA193293

seq_documentation_block:
ID AAT93293 standard; DNA; 1062 BP.
XX
AC AAT93293;
XX
DT 27-APR-1998 (first entry)
XX
DE Bean golden mosaic geminivirus C1 mutant ORF BGAC262.
XX
KW Geminivirus; BGW; C1 gene; transdominant mutation;
XX
KW Transgenic plant; disease resistance; ss; cyclic; circular.
XX
OS Bean golden mosaic virus type II isolate Guatemala.
XX
PN WO9739110-A1.
XX
PD 23-OCT-1997.
XX
PF 15-APR-1997; 97WO-US06300.
XX
PR 16-APR-1996; 96US-0015517.
XX
PA (SEMI-) SEMINIS VEGETABLE SEEDS INC.
XX
PA (MISC) WISCONSIN ALUMNI RES FOUND.
XX
PI Ahlquist PG, Hanson SF, Luu HT, Maxwell DP, Stout JT;
XX
WP1: 1997-526447/48.
XX
P-PSDB; AAW34335.
XX
PT Transgenic plants expressing geminivirus AC1 and C1 wild-type and
PT mutant genes - have increased resistance to geminivirus infection
PT e.g. tomato mottle virus, tomato yellow leaf curl virus or bean
PT golden mosaic geminivirus
XX
PS Claim 13; Page 115-116; 132pp; English.
XX

```

FT binding site, is replaced by Ala"

DT 07-NOV-1996 (first entry)

```

XX DE Sardinian tomato yellow leaf curl virus mutated C1 gene (K227H).
XX
XX Nucleotide triphosphate binding site; DNA helicase; RNA helicase;
XX modification; mutation; viral replication; deficient; inhibition;
XX vital resistance; geminivirus; tomato yellow leaf curl virus;
XX Sardinian isolate; STYLCV; transgenic plant; P-loop; C1 gene;
XX AL1 gene; ss.
XX
XX Sardinian tomato yellow leaf curl virus.
XX
XX Key Location/Qualifiers
XX CDS 1..1080
XX /*tag= a
XX /product= Rep.(K227H)
XX /note= "encodes Rep protein in which wild-type Lys
XX at position 227, i.e. within the NTP-
XX binding site, is replaced by His"
XX
XX PN W09608573-A1.
XX
XX PD 21-MAR-1996.
XX
XX PE 15-SEP-1995; 95WO-FR01192.
XX
XX PR 15-SEP-1994; 94FR-0011040.
XX
XX PA (CNRS ) CENT NAT RECH SCT.
XX
XX PI Gronenborn B;
XX
XX DR WPI: 1996-179947/18.
XX P-PSDB: AAR88871.
XX
XX PT prodn. of virus-resistant transgenic plants - using mutated genomic
XX sequence from phytopathogenic DNA virus
XX
XX PS Disclosure: Fig 13; 93pp; French.
XX
XX CC Mutation of consensus amino acids in the NTP-binding site of
XX geminivirus Rep protein is used to produce replication deficient
XX viruses. The mutated viral nucleic acid is used for producing
XX transgenic plants that are resistant to, or tolerant of, the native
XX virus. The present sequence encodes a mutant form of the Rep (or C1)
XX protein from the Sardinian isolate of tomato yellow leaf curl virus
XX (STYLCV) in which the wild-type Lys227 residue has been changed to a
XX His residue; transgenic Nicotiana benthamiana plants generated by
XX transformation with the mutated virus were not resistant to STYLCV.
XX In contrast, plants transformed with a virus in which Lys227 had been
XX replaced by Ala were found to be resistant.
XX
XX SQ Sequence 1080 BP; 356 A; 248 C; 208 G; 268 T; 0 other;

alignment_scores:
Quality: 222.00 Length: 69
Ratio: 3.828 Gaps: 0
Percent Similarity: 84.058 Percent Identity: 57.971

alignment_block:
US-09-289-346a-9 x AAT12905 ..

Align seg 1/1 to: AAT12905 from: 1 to: 1080

2 LeuValTrpPglYgluPheGlnValAlaGlyArgSerAlaArgGlyGlyC 18
||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
331 CTGATGATGGGACTTCCGATCGACGACGATCTCTGACGGAGACACA 380
18 sGlnThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerLysG 35
||||| ||||| ||||| ||||| ||||| ||||| |||||
381 ACAGACAGCGCACGACGCTTACGCAAGCAATTAACGACGAGTAAGT 430
35 InGluAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeuPhe 51

```

```

431 CGCAGCGCTCTGATGATTAATAAGAAATAGCGCGTAGATGCTTCGA 480
52 GlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysThrP 68
||||| ||||| ||||| ||||| ||||| ||||| |||||
481 CATTTCATTAATATTAATATGATTAATTAAGTTTCCAGCTGCCGCC 530
68 oGluPro 70
|||
531 GGCACCT 537

seq_name: /cgn1_8/gcgdata/geneseq/geneseqn/NA1996.DAT: AAT12905
seq_documentation_block:
ID AAT12906 standard; DNA; 1080 BP.
XX AC AAT12906;
XX
XX DT 07-NOV-1996 (first entry)
XX
XX DE Sardinian tomato yellow leaf curl virus mutated C1 gene (K227R).
XX
XX KW Nucleotide triphosphate binding site; DNA helicase; RNA helicase;
XX modification; mutation; viral replication; deficient; inhibition;
XX viral resistance; geminivirus; tomato yellow leaf curl virus;
XX Sardinian isolate; STYLCV; transgenic plant; P-loop; C1 gene;
XX AL1 gene; ss.
XX
XX OS Sardinian tomato yellow leaf curl virus.
XX
XX Key Location/Qualifiers
XX CDS 1..1080
XX /*tag= a
XX /product= Rep.(K227R)
XX /note= "encodes Rep protein in which wild-type Lys
XX at position 227, i.e. within the NTP-
XX binding site, is replaced by Arg"
XX
XX PN W09608573-A1.
XX
XX PD 21-MAR-1996.
XX
XX PE 15-SEP-1995; 95WO-FR01192.
XX
XX PR 15-SEP-1994; 94FR-0011040.
XX
XX PA (CNRS ) CENT NAT RECH SCT.
XX
XX PI Gronenborn B;
XX
XX DR WPI: 1996-179947/18.
XX P-PSDB: AAR88872.
XX
XX PT prodn. of virus-resistant transgenic plants - using mutated genomic
XX sequence from phytopathogenic DNA virus
XX
XX PS Disclosure: Fig 13; 93pp; French.
XX
XX CC Mutation of consensus amino acids in the NTP-binding site of
XX geminivirus Rep protein is used to produce replication deficient
XX viruses. The mutated viral nucleic acid is used for producing
XX transgenic plants that are resistant to, or tolerant of, the native
XX virus. The present sequence encodes a mutant form of the Rep (or C1)
XX protein from the Sardinian isolate of tomato yellow leaf curl virus
XX (STYLCV) in which the wild-type Lys227 residue has been changed to an
XX Arg residue; transgenic Nicotiana benthamiana plants generated by
XX transformation with the mutated virus were not resistant to STYLCV.
XX In contrast, plants transformed with a virus in which Lys227 had been
XX replaced by Ala were found to be resistant.
XX
XX SQ Sequence 1080 BP; 356 A; 247 C; 210 G; 267 T; 0 other;

```

```

alignment_scores:      Quality: 222.00      Length: 69
                       Ratio: 3.828      Gaps: 0
                       Percent Similarity: 84.058      Percent Identity: 57.971

alignment_block:
US-09-289-346A-9 x AAT12906 ..

Align seg 1/1 to: AAT12906 from: 1 to: 1080

2 LeuValATrPcLyGluPheGlnValAlaGlyARgSerAlaArgLyGlyC 18
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
331 CTGATGAGGCTGCTTCCAGATCGACGACGATCTGCTGAGGAGACCA 380
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
18 sGlnTrSerAsnAspAlaAlaGlnAlaLeuAsnAlaSerSerLyG 35
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
381 ACGACAGCGCCACGACGCTTACGCAAGCAATTAACGCGAGATAGCT 430
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
35 LngLAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeuPhe 51
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
431 CGCAGGCTCTGTGATGTATTAAGAAATTAGCGGCTAGACATTACGTTCTA 480
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
52 GlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysThrPr 68
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
481 CATTTTCATATATATAATAGTATTAGATAAGCTTTTCCAGGCTCC 530
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
68 oGluPro 70
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
531 GGCACCT 537

seq_name: /cgnl_8/gcgdata/geneseq/geneseqn/NA1997.DAT: AAT93314

seq_documentation_block:
ID AAT93314 standard; DNA: 1183 BP.
XX
AC AAT93314;
XX
AC AAT93314;
XX
DT 27-APR-1998 (first entry)
XX
DE Bean golden mosaic geminivirus CI open reading frame.
XX
KW Geminivirus; BGWV; CI gene; transdominant mutation;
KW transgenic plant; disease resistance; ss; cyclic; circular.
XX
OS Bean golden mosaic virus type II isolate Guatemala.
XX
FH Key Location/Qualifiers
FT CDS 1..1062
FT /*tag= a
XX
PN WO9739110-A1.
XX
PD 23-OCT-1997.
XX
PE 15-APR-1997; 97WO-US06300.
XX
PR 16-APR-1996; 96US-0015517.
XX
PA (SEMI-) SEMINIS VEGETABLE SEEDS INC.
PA (WISC ) WISCONSIN ALUMNI RES FOUND.
XX
PI Ahlquist PG, Hanson SF, Luu HT, Maxwell DP, Stout JT;
XX
DR WPI: 1997-526447/48.
DR P-PSDB: AAM34338.
XX
XX Transgenic plants expressing geminivirus AC1 and CI wild-type and
XX mutant genes - have increased resistance to geminivirus infection
XX e.g. tomato mottle virus, tomato yellow leaf curl virus or bean
XX golden mosaic geminivirus
XX
XX Example 5; Page 100-102; 132pp; English.
XX

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CC This genomic DNA sequence includes the open reading frame (ORF) of
CC the wild-type CI gene of bean golden mosaic virus (BGWV). a
CC geminivirus that has a monopartite genome. The CI protein (see
CC AAM34338) is required for replication. The wild-type CI ORF was
CC subjected to Kunkel mutagenesis (see AAT93290-93). The invention
CC involves production of transgenic plants containing DNA comprising
CC CI or AC1 wild-type or mutant sequences that negatively interfere
CC in trans with geminiviral replication during infection. Such
CC transgenic plants are resistant to viral infection. The AC1/CI
CC genes are especially from BGWV, tomato mottle virus or tomato
CC yellow leaf curl virus (see AAT93282-93) and encode polypeptides
CC (see AAM34324-35) that have mutations in the highly conserved
CC DNA-nicking domain and/or the NTP-binding domains.
XX
SQ Sequence 1183 BP; 372 A; 276 C; 248 G; 287 T; 0 other;

alignment_scores:      Quality: 222.00      Length: 70
                       Ratio: 3.700      Gaps: 0
                       Percent Similarity: 85.714      Percent Identity: 60.000

alignment_block:
US-09-289-346A-9 x AAT93314 ..

Align seg 1/1 to: AAT93314 from: 1 to: 1183

1 ThrLeuValTrPcLyGluPheGlnValAlaGlyARgSerAlaArgLyG 17
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
328 ACATTCGAATCGGCGGACAAATTCGAAGTCAGCGGATCTGCAAGAGAGG 377
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
17 yCySGlnTrSerAsnAspAlaAlaGlnAlaLeuAsnAlaSerSerL 34
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
378 TCAGCAGCTCTGCCACGACTCATATGCAAAAGCATTAACGCCGATTCNA 427
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
34 ySGlnLAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeu 50
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
428 TTGAATCTGCGCTTGACAAATATGAAAGCAAGAACGAAAGATACGTC 477
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysThr 67
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
478 CTTCAACATCTACCAACATCCCTTCTAATCTCGAACGAGATCTCTCAAAAG 527
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
67 rProGluPro 70
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
528 GCGGAACCA 537

seq_name: /cgnl_8/gcgdata/geneseq/geneseqn/NA1997.DAT: AAT93290

seq_documentation_block:
ID AAT93290 standard; DNA: 1183 BP.
XX
AC AAT93290;
XX
AC AAT93290;
XX
DT 27-APR-1998 (first entry)
XX
DE Bean golden mosaic geminivirus CI mutant gene.
XX
KW Geminivirus; BGWV; CI gene; transdominant mutation;
KW transgenic plant; disease resistance; ss; cyclic; circular.
XX
OS Bean golden mosaic virus type II isolate Guatemala.
XX
FH Key Location/Qualifiers
FT CDS 1..1062
FT /*tag= a
XX
PN WO9739110-A1.
XX
PD 23-OCT-1997.
XX
PE 15-APR-1997; 97WO-US06300.
XX

```



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XX 16-APR-1996: 96US-0015517.
XX (SEM-) SEMINIS VEGETABLE SEEDS INC.
XX (WISC ) WISCONSIN ALUMNI RES FOUND.
XX
XX Ahlquist PG, Hanson SF, Luu HT, Maxwell DP, Stout JT:
XX
XX WPI, 1997-526447/48.
XX P-PSDB; AAM34332.
XX
XX Transgenic plants expressing geminivirus AC1 and CI wild-type and
XX mutant genes - have increased resistance to geminivirus infection
XX e.g. tomato mottle virus, tomato yellow leaf curl virus or bean
XX golden mosaic geminivirus
XX
XX Claim 13; Page 103-105; 132pp; English.
XX
XX This DNA sequence comprises construct BGAC190 that codes for a
XX control mutant (see AAM34332) of the CI protein (see AAM34338) of bean
XX golden mosaic virus (BGMV). It was obtained by Kunzel mutagenesis
XX of the wild-type CI gene (see AAT93314). CI is required for
XX replication. The invention involves production of transgenic
XX plants containing DNA comprising geminivirus CI or AC1 wild-type or
XX mutant sequences that negatively interfere in trans with
XX geminiviral replication during infection. Such transgenic plants
XX are resistant to viral infection. The AC1/CI genes are especially
XX from BGMV, tomato mottle virus or tomato yellow leaf curl virus (see
XX AAT93382-93) and encode polypeptides (see AAM3324-35) that have
XX mutations in the highly conserved DNA-nicking and/or the NTP-binding
XX domains.
XX
XX Sequence 1183 BP, 371 A; 277 G; 249 G; 286 T; 0 other;
XX
XX alignment_scores:
XX      quality: 222.00      length: 70
XX      Ratio: 3.700      Gaps: 0
XX Percent Similarity: 85.714      Percent Identity: 60.000
XX
XX alignment_block:
XX US-09-289-346A-9 x AAT93290 ..
XX
XX Align seg 1/1 to: AAT93290 from: 1 to: 1183
XX
XX 1 ThrLeuValTyrPglYgluPhgInValaIaGlyArSeraIlaArgIylg1 17
XX      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX 328 ACATCGAATGGGACCAATTCAGTGCAGCGCGAGATCTCGAAGAGAGG 377
XX
XX 17 yCysGlnThrSerAsnAspAlaIaAlaGluAlaLeuAsnAlaSerSer1 34
XX      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX 378 TCAGCAAGCTGTCCAACGACATCATGCAAAAGCGATTAAACGCGAGATTCA 427
XX
XX 34 ySgIuGluAlaLeuGlnIleIleArgIuGluYsIleProGluYsTyrLeu 50
XX      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX 428 TTGAATCGCCCTTGACATATTGAAGGAAGAACACCGAAGAATTACGTC 477
XX
XX 51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
XX      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX 478 CTTCACACATCCACACATCCGTTCTTAATCTGCACAGCATCTTCGCAAAAGT 527
XX
XX 67 rProGluPro 70
XX      :|||||:
XX 528 GCCGGAAACCA 537
XX
XX seq_name: /cgnl_8/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA94700
XX
XX seq_documentation_block:
XX ID AAA94700 standard; DNA: 1651 BP.
XX
XX AC AAA94700:
XX
XX DT 15-JAN-2001 (first entry)
XX

```

```

DE pMRC 2288 35S-rep gene cassette
XX
KW Geminivirus; DNA-A; geminivirus replication inhibition; ac3 gene;
KW transgenic plant; antiviral; gene library; bean golden mosaic virus;
KM BGWV; alfalfa mosaic virus; AMV; cauliflower mosaic virus; CaMV; ds.
XX
OS Bean golden mosaic virus.
OS Cauliflower mosaic virus.
OS Alfalfa mosaic virus.
OS Synthetic.
XX
XX US6118048-A.
XX
PD 12-SEP-2000.
XX
XX 24-APR-1998; 98US-0065999.
XX
PR 25-APR-1997; 97US-0044925.
XX
PA (WISC ) WISCONSIN ALUMNI RES FOUND.
XX
DR WP1; 2000-610861/58.
XX
PT Genetic construct comprising a mutant geminiviral rep gene, useful for
PT producing a plant resistant to geminiviral infection -
XX
XX Example: Column 15-16; 14pp: English.
XX
PS The present sequence is a 35S-rep gene cassette comprising the rep gene
CC of bean golden mosaic virus (BGMY)-GA cloned downstream of the CaMV
CC 35S promoter and an alfalfa mosaic virus (AMV) leader sequence. The
CC sequence was integrated into pBS11-KS+ to produce a rep gene expression
CC vector. DNA-nicking domain mutations may be incorporated into rep gene
CC to produce a genetic construct that acts as a trans-dominant inhibitor
CC of geminiviral replication. When expressed in a plant cell, this
CC inhibitor is able to dramatically reduce replication of geminivirus.
CC Genetic constructs that include sequences containing a portion of the
CC ac3 gene in addition to the trans-dominant inhibitor exhibit increased
CC efficiency and broadened specificity of inhibition of geminiviral
CC replication. Geminiviruses are one of the greatest constraints on
CC production of important crops, including cassava, beans, cowpeas,
CC peppers, tomatoes and cotton. The effects of the virus can be overcome
CC by using the genetic construct.
XX
SQ Sequence 1651 BP; 517 A; 393 C; 342 G; 399 T; 0 other;

alignment_scores:
    Quality: 222.00      Length: 70
    Ratio: 3.700        Gaps: 0
Percent Similarity: 85.714   Percent Identity: 60.000

alignment_block:
US-09-289-346A-9 x AAA94700 ..

Align seg 1/1 to: AAA94700 from: 1 to: 1651

1 ThrlenuValtrpglygUpheginValaIagIYArseriaIarnglygl 17
| | | | | | | | | | | | | | | | | | | | | | | | | | |
796 ACATCATCAATGGGACACATTCCAAGTCGACGCCAGATCTCAGAAGAG 845
17 yCySGInThSerASnAspaIaaIaaIaIaIaIaLeuaSnalSeSertl 34
| . | | | | | | | | | | | | | | | | | | | | | | | | |
846 TCAGACACTGTGCACACGATCATATTCGAAGCGAATTAACGACATTCAA 895
34 ysGlugIualaleuGlnlleleArGslubylSlperogluIySTYleu 50
| | | | | | | | | | | | | | | | | | | | | | | | | | |
896 TTGAATCTGGCTTGCACAATATTCGAAGGAGAACCAACGAAAGATTACGTC 945
51 PheGInPheHisanleuAnSerASnleuAspargllepHeAsplySTH 67
| | | | | | | | | | | | | | | | | | | | | | | | | | |
946 CTTCACATCATCAACATCCGTTCTAAATCTCGAAGCGATTTCCGCAAGT 995

```


Fri Jan 4 09:39:55 2002

us-09-289-346a-9.p2n.rng

Page 11

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OM of: US-09-289-346a-9 to: EST:* out_format : pfs
Date: Jan 3, 2002 6:16 PM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

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-Q/cgml1/USPTO.pool/US09289346/rnatc_03012002_153303_16354/app_query.fasta_1.1163  
-DB=EST -QPM=fastap -SUFFIX=p2n.rst -GAPOP=12.000 -GAPEXT=4.000  
-MINMATCH=0.100 -LOOPEL=0.000 -LOOPEXT=0.000 -OGAPOP=4.500  
-OGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000  
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELDP=6.000  
-DLEXT=7.000 -STAR=1 -MATRIX=blomsm62 -TRANS=human4.0.cst  
-LIST=45 -DOCALLIGN=200 -THR_SCORE=ptc -THR_MAX=100 -THR_MIN=0  
-ALIGN=15 -MODE=LOCAL -OUTPMT=pfs -NORM=ext -MINLEN=0  
-MAXLEN=2000000000 -USER=US09289346_@CGML1_1.6788 -NCPU=6  
-ICPU=3 -LONGLOG -NO_XLPHY -WAIT -THREADS=1
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Search information block:

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Query Length: 70
Database: EST:*
Database sequences: 11351937
Database length: 107921985
Search time (sec): 8697.120000

score list:

Sequence	Strd Orig	ZScore	EScore	Len	Documentation
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gb_est2:BG595046	-	71.50	153.97	20.63	732 BG595046 EST493724 cSTS Solanum
gb_est1:AT731422	-	70.50	154.24	19.91	546 AT731422 BNGH19563 six-day Cot
gb_est2:BF506184	+	70.50	151.22	29.35	765 BF506184 AT08588.Sprtime AT Dros
gb_est2:BG594992	+	70.50	149.11	64.25	1512 BG594992 601658769F1 NIH MGC 6
gb_est2:BG580771	+	69.00	151.73	32.45	487 BG580771 EST482499 GYN Medicago
gb_est1:AT599225	+	69.00	150.48	27.26	560 AT599225 f025909.Y1 Zebrafish W
gb_gss:AO950848	+	69.00	150.29	33.04	572 AO950848 Sheared DNA-51M3.TF SF
gb_gss:AO947513	-	69.00	149.06	34.04	587 AO947513 Sheared DNA-49M17.TF S
gb_est2:BF646894	+	69.00	149.15	38.28	567 BF646894 NF07707EC1F1061 Ellic
gb_est2:BF649762	+	69.00	149.09	38.55	654 BF649762 NF08306EC1F1058 Ellic
gb_gss:AZ208697	+	68.50	144.95	65.55	910 AZ208697 SP_0150_A2_C02.SP6E ST
gb_est2:W89594	+	68.00	143.13	82.82	978 W89594 mf73d09.r1 Soates mouse
gb_est1:AA29185	+	67.50	150.40	32.57	381 AA29185 my339h09.r1 Barstead mc
gb_gss:AZ26150	-	67.50	146.56	41.27	468 AZ26150 476.dio41h11.s1 Saccha
gb_est1:AA388642	+	67.50	146.90	51.04	563 AA388642 EST492292 cSTS Solanum
gb_est2:BG593614	+	67.50	146.29	55.23	603 BG593614 EST492292 cSTS Solanum
gb_est2:BG599652	-	67.50	144.68	67.83	721 BG599652 EST504547 cSTS Solanum
gb_est2:BI406561	-	67.50	144.49	69.57	737 BI406561 171B01 Mature tuber 1a
gb_est1:AA486985	-	67.00	151.25	29.22	304 AA486985 abd4c01.r1 Striatogene
gb_gss:AO906722	+	67.00	146.52	41.45	412 AO906722 GSTC03166 Trypanosoma
gb_est2:BG275828	+	67.00	146.74	52.14	503 BG275828 NXS1_148.D05.F NXS1 (N
gb_gss:AO367423	+	67.00	146.71	76.88	705 AO367423 tox0001E09r CUG1 Tomat
gb_est1:AA863354	+	66.50	148.99	39.04	343 AA863354 oth04e07.s1 NCL_CGAP_Ki
gb_est1:AA950726	+	66.50	143.71	76.84	618 AA950726 LD30829.Sprtime LD Dros
gb_est2:BI236878	+	66.50	143.54	78.56	630 BI236878 REB33007.Sprtime RE Dros
gb_est2:BG236868	+	66.00	149.14	38.33	256 BG236868 nat81b01.x1 NCL_CGAP_H
gb_est1:AA729475	+	66.00	148.22	43.13	328 AA729475 nsc06d09.s1 NCL_CGAP_H
gb_est1:AA742525	+	66.00	145.60	60.30	439 AA742525 AV742525 CB Homo sapi
gb_est1:AA744255	+	66.00	144.19	73.30	514 AA744255 AV744255 CB Homo sapi
gb_est1:AA737185	+	66.00	143.01	84.06	585 AA737185 AV737185 CB Homo sapi
gb_est1:AA736552	+	66.00	143.01	84.06	586 AA736552 AV736552 CB Homo sapi
gb_gss:AO449424	+	66.00	142.97	84.56	589 AO449424 mg5b0023008f CUG1 R16c
gb_est1:AA741448	+	66.00	142.86	85.71	596 AA741448 AV741448 CB Homo sapi
gb_est1:AA738839	+	66.00	142.58	88.86	615 AA738839 AV738839 CB Homo sapi
gb_gss:AO902899	+	66.00	139.57	130.68	860 AO902899 Tetradodon nigroviridis
gb_gss:AO902899	+	66.00	137.61	168.01	1070 AL351960 Tetradodon nigroviridis
gb_est2:HG37423	-	65.50	143.03	83.89	513 HG37423 15552 Lambda-Put2 Arabid
gb_est1:AT1728017	-	65.50	142.39	91.08	551 AT1728017 BNGH19608 six-day Cot
gb_est1:BE547392	-	65.50	137.45	171.64	956 BE547392 60107962F1 NIH_MGC_12
gb_gss:AO904MBO	-	65.50	137.23	176.40	979 AL297213 Tetradodon nigroviridis

gb_gss:AO904MBO - 65.50 136.32 198.33 1084 | AL297213 Tetradodon nigroviridis
gb_est2:HG37423 - 65.00 147.09 49.83 286 | HG37423 15552 Lambda-Put2 Arabid
gb_est1:AT1728017 + 65.00 143.03 83.89 513 | AT1728017 BNGH19608 six-day Cot
gb_est2:BF488298 + 65.00 143.69 77.09 418 | BF488298 AT23536.Sprtime AT D

seq_name: gb_est2:BF342302

seq_documentation_block:

LOCUS BF342302 646 bp mRNA 22-NOV-2000
DEFINITION 602013083F1 NCL_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4148757
5', mRNA sequence.
ACCESSION BF342302
VERSION BF342302.1 GI:11289259
KEYWORDS EST.
SOURCE human
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 646)
NIR-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
AUTHORS Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgaabs-remail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMNL at:
http://image.llnl.gov
Plate: LAM9409 row: f column: 22
High quality sequence stop: 613.

FEATURES

source

1..646
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4148757"
/clone_lib="NCL_CGAP_Brn64"
/tissue_type="glio/blastoma with EGFR amplification"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: brain; Vector: pCMV-Sport6; Site: 1; NotI;
Site: 2; SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.57 kb. Constructed by Life
Technologies. Note: this is a NCL_CGAP Library."
BASE COUNT 150 a 158 c 197 g 141 t
ORIGIN

alignment_scores:

Quality: 74.00 Length: 42
Ratio: 2.467 Gaps: 2
Percent Similarity: 71.429 Percent Identity: 45.238

alignment_block:

US-09-289-346a-9 x BF342302 ..

Align seg 1/1 to: BF342302 from: 1 to: 646

3 ValTrpGly...GluPheGlnValAlaGlyArgSerAlaArgGlyGlyCys 18
||||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
18 sGlnThrSerAsnAspAlaAlaGluAlaGluAlaGluAlaSerSerIysG 35
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
202 GTGTGGGGGTACAGGAGACGCTTGGCGGACGGGAGCGGGGGGATG 251
252 TGAACCTCGGAGCGGACCCACCAAGGGCTCAAGGGGCCCAACCTTG 301
35 luGluAlaGluGlnIleIleArgGlu 43
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
302 AA.....ATCCGTGAA 312
seq_name: gb_est2:BG595046

seq_documentation_block:
 LOCUS BG595046 732 bp mRNA EST 12-APR-2001
 DEFINITION EST93724 csts Solanum tuberosum cDNA clone csts9019 5' sequence,
 mRNA sequence.
 ACCESSION BG595046
 VERSION BG595046.1 GI:13613186
 KEYWORDS EST.
 SOURCE potato.
 ORGANISM Solanum tuberosum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
 REFERENCE 1 (bases 1 to 732)
 AUTHORS Van der Hoeven,R., Bezzerides,J., Sun,H., Cho,J., Chiemingo,A.,
 Buehl,O., Buehl,C.R., Ronning,C., Tankeley,S. and Baker,B.
 TITLE Generations of ESTs from sprouting potato eyes
 JOURNAL Unpublished (2000)
 COMMENT Contact: Cathy Ronning
 The Institute for Genomic Research
 For clone info: please contact Research Genetics, Libraries
 Division tel 1-800-711-6195, email cdna@resgen.com
 Seq primer: M13p-R.
 FEATURES
 source Location/Qualifiers
 1..732
 /organism="Solanum tuberosum"
 /cultivar="Kennebec"
 /db_xref="taxon:4113"
 /clone="csts9019"
 /clone_lib="csts"
 /tissue_type="sprouting eyes from tubers"
 /dev_stage="12-14 weeks post harvest"
 /lab_host="SOLR"
 /note="Vector: pBluescript SK(-); Site1: EcoRI; Site2:
 XhoI; Various sizes of sprouting eyes (2mm to 15mm) were
 taken from tubers. The tubers were incubated at 26C in the
 dark for 2-3 weeks prior to sprouting. The eyes were
 frozen in liquid nitrogen immediately upon removal from
 tubers."
 alignment_scores:
 Quality: 71.50 Length: 54
 Ratio: 1.932 Gaps: 3
 Percent Similarity: 68.519 Percent Identity: 37.037
 alignment_block:
 US-09-289-346a-9 x BG595046/rev ..
 Align seg 1/1 to reverse of: BG595046 from: 1 to: 732
 11 GYAAGSerAlaArgGlyGlyCysGlnThrSerAsnASP.....AlaAl 25
 |||||
 408 GGAAGGTCGGCTCGTAGCAGATGCTAGACGAGTAATGAATGAGCTTG 359
 25 aaAGlualaleuAsnAlaSerSerIysGluGluAlaLeuGlnIleIla 42
 :|||
 358 TATTAAAGCAAAATAGCAGAACTTTTACAACTTTATCCAAATGATGCA 309
 42 rGgluIysIleProGluIysTyrLeuPheGlnPheHisAsn...LeuAsn 57
 :|||
 308 AATAAAGATT.....CTTCACTTGTTCAGATTCACCAATGACCTCAAC 265
 58 SerAsnLeuASP 61
 :|||
 264 AACCAATATCAAC 253
 seq_name: gb_est1:A1731422
 seq_documentation_block:
 LOCUS A1731422 546 bp mRNA EST 11-JUN-1999
 DEFINITION BNGH19563 six-day Cotton fiber Gossypium hirsutum cDNA 5' similar

to mitochondrial processing peptidase (EC 3.4.99.41) alpha-II chain
 precursor - potato g11587562 (X80236) mitochondrial processing
 peptidase [Solanum tuberosum], mRNA sequence.
 ACCESSION A1731422
 VERSION A1731422.1 GI:5050274
 KEYWORDS EST.
 SOURCE upland cotton.
 ORGANISM Gossypium hirsutum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
 REFERENCE 1 (bases 1 to 546)
 AUTHORS Blewitt,M., Matz,E.C., Davy,D.F. and Burr,B.
 TITLE ESTs from developing cotton fiber
 JOURNAL Unpublished (1999)
 COMMENT Contact: Ben Burr
 Biology Department
 Brookhaven National Laboratory
 Upton, NY 11973, USA
 Tel: 516-344-3396
 Fax: 516-344-3407
 Email: burrb@nsl.bnl.gov
 Seq primer: T3 Primer.
 FEATURES
 source Location/Qualifiers
 1..546
 /organism="Gossypium hirsutum"
 /cultivar="Acala Maxxa"
 /db_xref="taxon:3635"
 /clone_lib="Six-day Cotton fiber"
 /tissue_type="Immature fiber"
 /dev_stage="Six days post anthesis"
 /lab_host="XLI-Blue"
 /note="Vector: pBluescript II KS+"
 BASE COUNT 151 a 93 c 134 g 160 t 2 others
 ORIGIN
 alignment_scores:
 Quality: 70.50 Length: 62
 Ratio: 1.720 Gaps: 1
 Percent Similarity: 66.129 Percent Identity: 32.258
 alignment_block:
 US-09-289-346a-9 x A1731422/rev ..
 Align seg 1/1 to reverse of: A1731422 from: 1 to: 546
 9 ValAlaGlyArgSerAlaArgGlyGlyCysGlnThrSerAsnASPAlaAl 25
 :|||
 475 ATATTGGCAAGATCTGACGAAAGTGTTCTGCACACGATTAACATTCTTC 426
 25 aaLa...GluAlaLeuAsnAlaSerSerIysGluGluAlaLeuGlnIle 41
 :|||
 425 ATGTTTACACCGAGTTCGTCGACATCCAGACAGACGATTAATAATT 376
 41 laArgGluIysIleProGluIysTyrLeuPheGlnPheHisAsnLeuAsn 57
 :|||
 375 TTGCACAAAAATCCCTCCAAACTGTAAGTTCACACATATTAACTGACAG 326
 58 SerAsnLeuASPArgIlePheASPlysrThrProGlu 69
 :|||
 325 TCTGGGCGTAAAGAGGATTTCCAATGCACACGAA 220
 seq_name: gb_est2:BF506184
 seq_documentation_block:
 LOCUS BF506184 765 bp mRNA EST 19-APR-2001
 DEFINITION AT08588 5prime AT Drosophila melanogaster adult testes por7
 Drosophila melanogaster cDNA clone AT08588 5 similar to CG107777:
 Fban010777 'RNA binding' located on: X 7C8-7C8;: 04/07/2001, mRNA
 sequence.
 ACCESSION BF506184
 VERSION BF506184.2 GI:13688762

KEYWORDS EST.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
REFERENCE Eukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
AUTHORS 1 (bases 1 to 765)
Stapleton, M., Broksstein, P., Hong, L., Agbayan, A., Baxter, E., Berman, B., Carlson, J., Champe, M., Chavez, C., Chew, M., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Miranda, A., Misra, S., Mungall, C. J., Nunoo, J., Pacleb, J., Paragas, V., Park, S., Phouanavong, S., Wan, K., Yu, C., Lewis, S. E., Celniker, S. and Rubin, G. M.
BDGP/HMI AT Drosophila EST Project
TITLE Unpublished (2000)
JOURNAL On Dec 6, 2000 this sequence version replaced gi:11589485.
COMMENT Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST_estefruitfly.berkeley.edu
hit genomic AE003442: arm:x [7601669,7907935]
estimated-cyto:7C2-7D11: 04/07/2001
Plate: AT.85 row: H column: 4
High quality sequence stop: 616.
Location/Qualifiers
1..765
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="AT08588"
/clone_lib="AT Drosophila melanogaster adult testes POTB7"
/sex="male"
/dev_stage="0-3 day old Ore-R males"
/lab_host="Plates AT.10-AT.120: DH5-alpha. Plates AT.121-AT.319: DH5-alpha Tona"
/note="Organ: ADULT testes; Vector: POTB7; Site_1: EcoRI; Site_2: XhoI. The mRNA for the testis library was made from testes and seminal vesicles hand dissected from 0-3 day old Ore-R males. RNA kindly provided by the lab of Margaret Fuller. Sized fractionated cDNAs were directly ligated into POTB7. Plasmid cDNA library."

BASE COUNT 199 a 205 c 225 g 136 t
ORIGIN

alignment_scores:
Quality: 70.50 Length: 63
Ratio: 2.136 Gaps: 2
Percent Similarity: 52.381 Percent Identity: 34.921

alignment_block:
US-09-289-346a-9 x BF506184 ..
Align seg 1/1 to: BF506184 from: 1 to: 765

```

11 GYAGSerAlaArgGlyGlySerGlnThrSerAsnAspAlaAlaGcl 27
11 ::::: ||||| ::::: |||||
556 GCGCGCGGAGTGGCTGGCTACCAAGCAATTAACAAATGCTGCC... 603
27 uAlaLeuAnaIaSerSerLySGluAlaLeuGlnIleIleArgGlu 44
11 ::::: ||||| ::::: |||||
604 .GCCTTAGGCATGCTTTCCAAAGAGAGCGCGCGCATCCAAAGTGA 652
44 ySllePro..... 46
653 AGGCCAAAATCCGCGCGCAATTTAGTGAACCAAGTGAGAGACCTC 702
47 GluLySTyrLeuPheGlnPheHisAsnLeuAsnSerAsn 59
11 ::::: ||||| ::::: |||||
703 GAGCCCTTCCTCAAGATTTCTACAAACATTCATCCGAAT 741
seq_name: gb_est2:BE964992

```

seq_documentation_block:
LOCUS BE964992 1512 bp mRNA EST 14-DEC-2000
DEFINITION 601568769R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886169 3', mRNA sequence.
ACCESSION BE964992
VERSION BE964992.2 GI:11768902
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS 1 (bases 1 to 1512)
TITLE NIH-MGC <http://mhc.ncl.nih.gov/>.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
On Oct 3, 2000 this sequence version replaced gi:10575697.
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LMNL at: <http://image.llnl.gov>
Plate: LCM649 row: 1 column: 18
High quality sequence stop: 291.
Location/Qualifiers
1..1512
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3886169"
/clone_lib="NIH-MGC_69"
/tissue_type="large cell carcinoma, undifferentiated"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: oligo dT. Average insert size 1.1 kb. Library constructed by Life Technologies."

BASE COUNT 481 a 308 c 357 g 363 t 3 others
ORIGIN

alignment_scores:
Quality: 70.50 Length: 77
Ratio: 1.533 Gaps: 3
Percent Similarity: 59.740 Percent Identity: 31.169

alignment_block:
US-09-289-346a-9 x BE964992 ..
Align seg 1/1 to: BE964992 from: 1 to: 1512

```

4 TTPGlyGluPheGlnValAlaGlyArgSerAlaArgGlyGlySerGln 20
11 ::::: ||||| ::::: |||||
944 TGGGGGGGACACACACCGCGGGGCTTCTCTACCGTGGTGTGAAC 993
20 rSerAsnAsp...AlaAlaGlnAlaLeuAnaIaSerSerLySGlu 35
11 ::::: ||||| ::::: |||||
994 CATCAACACCCCTTATATCAACGAGGGCTTTCCACATGAATAAAGAG 1043
36 .GluAlaLeuGlnIleIle.....Arg 42
11 ::::: ||||| ::::: |||||
1044 CGCAAGCTTATATATGCTGGCTGCCACAAAGCGTGGGGGGAAC 1093
43 GluLySTyrLeuPheGlnPheHisAsnLeuAsnSerAsn 59
11 ::::: ||||| ::::: |||||
1094 GAAAAACAACCTTTAAAGAGACTCTTATCTTCACAAAGAGATTGTGA 1143
59 nLeuAspArgIlePheAspLysThrProGlu 69
11 ::::: ||||| ::::: |||||
1144 AGCGATCGTGTGTTGCAACACACACCTGAC 1174

```

```

seq_name: gb_est2:BG580771
seq_documentation_block: 487 bp mRNA EST 11-Apr-2001
LOCUS BG580771
DEFINITION EST482499 GVN Medicago truncatula cDNA clone pgvn-62el 5' end, mRNA
sequence.
ACCESSION BG580771
VERSION BG580771.1 GI:13595835
KEYWORDS EST.
SOURCE barrel medic.
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
Medicago.
1 (bases 1 to 487)
Fedorova,M., Plesion,B.L., Samac,D.A., Vance,C.P., Gantt,G.S., Town
,C.D., Van Aken,S., Uteck,T., Cho,J., and Fraser,C.M.
ESTs from one month old nitrogen-fixing root nodules of Medicago
truncatula, 2001
JOURNAL Unpublished (2001)
COMMENT Contact: Carroll P. Vance
Department of Agronomy and Plant Genetics
University of Minnesota
411 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108 USA
Tel: 612 625 5715
Fax: 651-649-5058
Email: vance004@maroon.tc.umn.edu
University of Minnesota name: M381825e TIGR sequence name:
MTCY575TK More information is available at: http://www.medicago.org
Seq primer: SKMD (CTA GAA CTA gtc gat CC).
FEATURES
Source
Location/Qualifiers
1..487
/organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon:3880"
/clone="pgvn-62el"
/clone_lib="GVN"
/tissue_type="N2-fixing root nodules"
/dev_stage="effective root nodules harvested one month
post inoculation with Sinorhizobium meliloti"
/lab_host="E. coli strain XL0LR"
/note="Vector: pBluescript SK-; Site.1: EcoRI; Site.2:
XhoI; cDNA was prepared from polyA+ enriched RNA from
effective root nodules harvested one month post
inoculation with Sinorhizobium meliloti. The cDNA was
directionally ligated into the uni-ZAP XR vector from
stratagene and packaged using GigaPack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-ZAP phage using Ex-Assist
helper phage and propagated in XL0LR cells."
BASE COUNT 153 a 83 c 104 g 137 t
ORIGIN
alignment_scores:
Quality: 69.00 Length: 64
Ratio: 1.683 Gaps: 2
Percent Similarity: 64.062 Percent Identity: 32.812
alignment_block:
US-09-289-346a-9 x BG580771 ..
Align seg 1/1 to: BG580771 from: 1 to: 487
4 TTPGlyGluPheGlnValAlaGlyArgSerAlaArgGlyGlyCysGlnPh 20
||||| |||||||:|||||:|||||:|||||:|||||:|||||:|||||:
153 TGGGGCTTTCAGTAGTCAACATGAGCGCCCTTTCAGATTAAGCA 202
20 rserAsnAspAlaAlaGluAlaLeuAsnAlaSerSerLysGluGlnA 37
||| |||||||:|||||:|||||:|||||:|||||:|||||:|||||:
203 AACACTGATGAGCTGCTAGATTGCTTCTCAAACTTGTGAGAGAGA 252

```

```

37 lAleuGlnIlelleArgGlyLysIle...ProGluLysTyrLeuPheGln 52
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
253 AATATGAGCTTCCAGATGATGATGATGATGATGATGATGATGATGAT 302
53 PheHisAsnLeuAsn...SerAsnLeuAspArgLysLeuAsp 65
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
303 GAGCACACCAAGATGATGATAAAGCTGATGATGATGATGATGAT 344
seq_name: gb_est1:A1959235
seq_documentation_block:
LOCUS A1959235 560 bp mRNA EST 20-AUG-1999
DEFINITION f425909.Y1 zebrafish Washu MPIMG EST Danio rerio cDNA 5' similar to
gb:x69150 40S RIBOSOMAL PROTEIN S18 (HUMAN);, mRNA sequence.
ACCESSION A1959235
VERSION A1959235.1 GI:5751948
KEYWORDS EST.
SOURCE zebrafish.
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Rasbora; Danio.
1 (bases 1 to 560)
Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy
,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wyllie,T., Underwood
,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,R.,
Swaller,T., Gibbons,M., Page,D., Harvey,N., Schuck,R., Ritter,E.,
Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R.,
and Wilson,R.
Washu zebrafish EST Project 1998
JOURNAL Unpublished (1998)
COMMENT Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: zbratfish@wustl.edu
cDNA Library Preparation: Matthew Clark, cDNA Library Arrayed by:
Matthew Clark, DNA Sequencing by: Washington University Genome
Sequencing Center Clone Distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
info@genomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@resgen.com) and
Resourcenzen@trumpet.franken.de, Berlin, Germany (web address:
www.trp.de)
Seq primer: T3 ET from Amersham
High quality sequence stop: 491.
FEATURES
Source
Location/Qualifiers
1..560
/organism="Danio rerio"
/db_xref="taxon:7955"
/clone_lib="zebrafish Washu MPIMG EST"
/sex="mixed"
/tissue_type="26 somite embryos, adult livers, shield
stage embryos"
/lab_host="XLI-blue MRF"
/note="Vector: pSPORT1; Site.1: NotI; Site.2: SalI; 1st
strand cDNA was primed with a Not I - oligo(dT)15 primer
[5' pGACTAGTCTTACATCGAGCGCGCCGCCCTTCTTTTCTTTTCTTTT3'];
double-stranded cDNA was ligated to Sal I adaptors (BRL),
digested with Not I and cloned into the Not I and Sal I
sites of the pSPORT1 vector (BRL). Library was constructed
by Matthew Clark (Lehrach lab, ICRF, London and Max Planck
institut fuer Molekulare Genetik, Berlin). cDNAs for EST
analysis were selected following oligonucleotide
hybridization fingerprinting of arrayed clones from
zebrafish late somitogenesis (26 ss), adult liver or
embryonic shield stage (5.6 h) libraries. Fingerprint
data were used to computationally cluster cDNAs, and a
single cDNA from each cluster was chosen for sequencing.
In some cases multiple members of the same cluster were
sequenced to assess clustering parameters or single clones

```


were sequenced additional times to assess quality

BASE COUNT 141 a 130 c 161 g 128 t
ORIGIN

alignment_scores:))
 Quality: 69.00 Length: 61
 Ratio: 1.917 Gaps: 2
 Percent Similarity: 59.016 Percent Identity: 31.148

alignment_block:
US-09-289-346a-9 x AI959235 ..

Align seg 1/1 to: AI959235 from: 1 to: 560

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1 ThrLeuValTrpGlyGluPheGlnValAlaGlyArgSerAlaArgGlyG1 17
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
22 ACATTGTGTGGGGG.....GGGGGTGTGGGGG 50

17 ycgsgtnttrserasnspalalalacilualaleuasnalasertl 34
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
51 GTGTACCCCTCTCTCCACGCCGCCGCCGCCGCCGCCGCCGATC 100

34 yscilualaleuGlnleileargGluGlylleProGluLysTrpLeu 50
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
101 AGATGTCTCTCTC.....GTCTGCCAGAGAGATTTCAG 135

51 PheGlnPheHisAsnLeuAsnSerAsnLeuAsp 61
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
136 CACATCTCTGTCTCTCAACAGCAAGCATTTGAT 168

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seq_name: gb_gss:AQ950848

seq_documentation_block:

LOCUS AQ950848 572 bp DNA GSS 27-JAN-2000
DEFINITION Sheared DNA-51M3.TF Sheared DNA Trypanosoma brucei genomic clone
ACCESSION AQ950848
VERSION AQ950848.1 GI:6774113
KEYWORDS GSS.
SOURCE Trypanosoma brucei.
ORGANISM Trypanosoma brucei.
Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;

REFERENCE
AUTHORS 1 (bases 1 to 572)
El-Sayed,N., Zhao,S., Zhao,H., Gill,S., Suh,E., Malek,J., Fujii,C.,
Gerrard,C., Leech,V., de Jong,P., Ullu,E., Melville,S., Donelson,J.,
Fraser,C. and Adams,M.
Determination of clone end sequences from Trypanosoma brucei GUTat
10.1 sheared DNA library
Unpublished (1999)
Other GSSs: Sheared DNA-51M3.TR
Contact: Najib M. El-Sayed
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: nelsayed@tigr.org

TITLE
JOURNAL
COMMENT
10.1 sheared DNA library
Unpublished (1999)
Other GSSs: Sheared DNA-51M3.TR
Contact: Najib M. El-Sayed
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: nelsayed@tigr.org

Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared
DNA library constructed at TIGR. Clones will be available for
distribution through ATCC. Sheared DNA end sequences search page:
<http://www.tigr.org/tldb/tldb/>
Seq primer: M13-Forward
Class: shotgun.

FEATURES
source

1. .572
Location/Qualifiers
/organism="Trypanosoma brucei"
/strain="TREU927/4 GUTat 10.1"
/db_xref="taxon:5691"
/clone="Sheared DNA-51M3"
/clone_lib="Sheared DNA"

/note="Vector: pUC18; Site_1: SmaI; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically
sheared to give a tight size distribution (approx 2 kb).
The v + i method used for the library construction is
described in detail in Smith, H.O. and Venter, J.C.
(Making small insert libraries for whole genome shotgun
sequencing projects. In Genome Sequencing: A Practical
Approach, eds. M. Vaudin and B. Barrel, Oxford University
press, 1999)."

BASE COUNT 115 a 118 c 180 g 159 t
ORIGIN

alignment_scores:))
 Quality: 69.00 Length: 32
 Ratio: 2.464 Gaps: 0
 Percent Similarity: 87.500 Percent Identity: 37.500

alignment_block:
US-09-289-346a-9 x AQ950848 ..

Align seg 1/1 to: AQ950848 from: 1 to: 572

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10 AlaGlyArgSerAlaArgGlyGlyGlnThrSerAsnspAlaAla1 26
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
288 AGGTGTCTCTCCGCGCATGGCGGTGTCCAAACGACAGATGATGATGT 337

26 acilualaleuasnalasertlscilualaleuGlnleile 41
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
338 TGAAGTGTCTCTCTCGGAGACTCTCCGACGCCGACGATTCAGTATCG 383

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seq_name: gb_gss:AQ947513

seq_documentation_block:

LOCUS AQ947513 587 bp DNA GSS 27-JAN-2000
DEFINITION Sheared DNA-49M17.TF Sheared DNA Trypanosoma brucei genomic clone
ACCESSION AQ947513
VERSION AQ947513.1 GI:6770778
KEYWORDS GSS.
SOURCE Trypanosoma brucei.
ORGANISM Trypanosoma brucei.
Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;

REFERENCE
AUTHORS 1 (bases 1 to 587)
El-Sayed,N., Zhao,S., Zhao,H., Gill,S., Suh,E., Malek,J., Fujii,C.,
Gerrard,C., Leech,V., de Jong,P., Ullu,E., Melville,S., Donelson,J.,
Fraser,C. and Adams,M.
Determination of clone end sequences from Trypanosoma brucei GUTat
10.1 sheared DNA library
Unpublished (1999)
Other GSSs: Sheared DNA-49M17.TR
Contact: Najib M. El-Sayed
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: nelsayed@tigr.org

TITLE
JOURNAL
COMMENT
10.1 sheared DNA library
Unpublished (1999)
Other GSSs: Sheared DNA-49M17.TR
Contact: Najib M. El-Sayed
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: nelsayed@tigr.org

Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared
DNA library constructed at TIGR. Clones will be available for
distribution through ATCC. Sheared DNA end sequences search page:
<http://www.tigr.org/tldb/tldb/>
Seq primer: M13-Forward
Class: shotgun.

FEATURES
source

1. .587
Location/Qualifiers
/organism="Trypanosoma brucei"
/strain="TREU927/4 GUTat 10.1"
/db_xref="taxon:5691"
/clone="Sheared DNA-49M17"

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days. Cells were induced six days after subculture"
/note=vector: lambda Zap. Cells were induced with yeast
cell wall extracts equivalent to 500ug/ml glucose in the
final concentration. Samples were taken at 0.5, 1, 12 and
24 hours after induction. Equal amounts of RNA from each
time point were pooled and used for mRNA isolation."

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BASE COUNT	214 a	117 c	140 g	178 t	1 others
ORIGIN					

alignment_scores:	Quality:	69.00	Length:	64
Ratio:	1.683		Gaps:	2
Percent Similarity:	64.062		Percent Identity:	32.812

alignment_block:
US-09-289-346A-9 x BF646894 ..

Align seg 1/1 to: BF646894 from: 1 to: 650

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4 TTPGIGLUPhGhGlnValA)aglyArgSerAlaArgGlyGlyCysGlnTh 20
||||| |||||||:|||||:|||||:|||||:|||||:|||||:
229 TGGGGCTTCTTTCAGTTACAAACCATGAGGTCCTTGGAGTATTAGGCA 278
20 rGersnAspAlaAla)agLlAlaLeuAsn)laseSerlyGluGlnA 37
||||| |||||||:|||||:|||||:|||||:|||||:
279 AAGACTTGATGAAGCTGAGTGTGTTCTTCTTCAAAATGTTGGAGGAA 328
37 lAlaGlnlIlelLeArgGlyLysIle...ProGlyLysIleuPheGln 52
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
329 AATGAGAGTTCACAGATGAGATCACCACCAATTCATTATTGATATAA 378
53 pHeiAsnLeuAsn...SerAsnLeuAspArgIlePheAsp 65
|||||:|||||:|||||:|||||:|||||:|||||:
379 GAGCACACCAAGAAATGTAAGAAACTGATGATGACTGTTGAT 420
seq_name: gb_est2:BF649762
seq_documentation_block:
LOCUS BF649762 654 bp mRNA EST 20-DEC-2000
DEFINITION NF083H056C1F1058 Elicited cell culture Medicago truncatula cDNA
clone NF083H056C 5', mRNA sequence.
ACCESSION BF649762
VERSION BF649762.1 GI:11914892
KEYWORDS EST.
SOURCE Medicago.
ORGANISM Medicago truncatula
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
1 (bases 1 to 654)
Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,
Flores,H.R., Iman,J.T., Weller,J.W. and May,G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Center for Medicago Genomics Research
Unpublished (2000)
Contact: Dixon RA
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7302
Fax: 580 221 7380
Email: radixon@noble.org
Insert length: 654 Std Error: 0.00
Plate: 083 row: H column: 06
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Location/Qualifiers
1..654
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/clone="NF083H056C"
/cclone_idb="Elicited cell culture"

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FEATURES	source
FEATURES	source

/tissue_type="Cell cultures derived from root tissues"
 /dev_stage="Cell suspensions were subcultured every 14
 days. Cells were induced six days after subculture"
 /note="Vector: Lambda Zap; Cells were induced with yeast
 cell wall extracts equivalent to 50ug/ml glucose in the
 final concentration. Samples were taken at 0.5, 1, 12 and
 24 hours after induction. Equal amounts of RNA from each
 time point were pooled and used for mRNA isolation."

BASE COUNT 207 a 117 c 143 g 186 t 1 others
 ORIGIN

alignment_scores:
 Quality: 69.00 Length: 64
 Ratio: 1.683 Gaps: 2
 Percent Similarity: 64.062 Percent Identity: 32.812

alignment_block:
 US-09-289-346a-9 x BF649762 ..

Align seg 1/1 to: BF649762 from: 1 to: 654

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195 TGGGCTTCTTCAAGTACAAACCATGAGTCCCTTGACTATTAGCA 244
20  rSerAsnAspAlaAlaGluAlaLeuAsnLaserLysGluGluA 37
||| ||||||| ||||||| ||||||| ||||||| |||||||
245 AAGACTTGATGAGCTGCTAGATGTCTTCTCATAAAGTTGGACGACA 294
37  lAlaGlnlIleleArgLysIle...ProGluLysTyrLeuPheGln 52
||||| ||||||| ||||||| ||||||| ||||||| |||||||
295 AATGACAGTTCAGAGATGATGATCACCACCAATGCTATTGTATATA 344
53  PheHisAsnLeuAsn...SerAsnLeuAspArgIlePheAsp 65
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
345 GAGCACACCAAGATGTAGAAACCTGATGATGATGAT 386

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seq_name: gb_gss:A2208697

seq_documentation_block:

LOCUS A2208697 910 bp DNA GSS 31-AUG-2000
 DEFINITION SP.0150. A2.C02.SP6 Strongylocentrotus purpuratus, purple sea
 urchin, sperm genomic BAC library Strongylocentrotus purpuratus
 genomic clone Plate-150 Col-4 Row-E, DNA sequence.

ACCESSION A2208697
 VERSION A2208697.1 GI:8421822

KEYWORDS GSS.
 ORGANISM Strongylocentrotus purpuratus.
 Strongylocentrotus purpuratus.

REFERENCE Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 Echinoida; Euechinoida; Echinacea; Echinoida;
 Strongylocentrotidae; Strongylocentrotus.
 1 (bases 1 to 910)

AUTHORS Cameron,R.A., Mahairas,G., Rast,J.P., Martinez,P., Biondi,T.R.,
 Swartzell,S., Wallace,J.C., Poustka,A.J., Livingston,B.T., Wray
 ,G.A., Ettensohn,C.A., Lehrach,H., Britten,R.J., Davidson,E.H. and
 Hood,L.

TITLE A sea urchin genome project: Sequence scan, virtual map, and
 additional resources
 JOURNAL Proc. Natl. Acad. Sci. U. S. A. 97 (17), 9514-9518 (2000)
 MEDLINE 20402566
 COMMENT Contact: Cameron, RA, Davidson, EH, Hood, L
 Division of Biology 156-29
 California Institute of Technology
 Pasadena California 91125, USA
 Tel: (626) 395-8421
 Fax: (626) 793-3047
 Email: acameron@caltech.edu
 Plate: 150 row: E column: 4
 Seq primer: SP6
 Class: BAC ends
 High quality sequence stop: 910.

FEATURES
 source location/Qualifiers
 1..910

/organism="Strongylocentrotus purpuratus"
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 urchin, sperm genomic BAC library"
 /note="Organ: sperm; Vector: BAC#3.6; BAC clones in E-Coli
 DH10B"

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 ORIGIN

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 Quality: 68.50 Length: 56
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 Percent Similarity: 62.500 Percent Identity: 35.714

alignment_block:
 US-09-289-346a-9 x A2208697 ..

Align seg 1/1 to: A2208697 from: 1 to: 910

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18  CysGlnThrSerAsnAspAlaAlaGlu...AlaLeuAsnLaserSe 33
||||| ||||||| ||||||| ||||||| ||||||| |||||||
604 TCGAACCTGCTACAGCGGCATCCCGGAAATGTTTAAACAATCTAT 653
33  rLysGluGluAlaLeuGlnIlele...ArgLysIleProGluL 48
||| ||||||| ||||||| ||||||| ||||||| |||||||
654 CTTTACTCCACACAGACAGCACTACGAAATATATGCAAACTAGCCGAA 703
48  yTyrLeuPheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePhe 64
||||| ||||||| ||||||| ||||||| ||||||| |||||||
704 AATGG.....CACTATTGGAATAAATATACCCGAGATTGG 741
65  AspLysThrProGluPro 70
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742 GGTAAACCCCTTCGCCG 759

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seq_name: gb_est2:W89594

seq_documentation_block:

LOCUS W89594 978 bp mRNA EST 12-SEP-1996
 DEFINITION mF3d09.r1 Soares mouse embryo NM063.5 14.5 Mus musculus cDNA
 clone IMAGE:419921 5', mRNA sequence.

ACCESSION W89594
 VERSION W89594.1 GI:1404927

KEYWORDS EST.
 ORGANISM house mouse.
 Mus musculus.

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus.
 1 (bases 1 to 978)

AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
 Geisell,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
 Phaisang,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
 Waterston,R.

TITLE The WashU-HMI Mouse EST Project
 JOURNAL Unpublished (1996)
 COMMENT Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810

Enail: mouseest@wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:254473
 Seq primer: -28M13 rev2 from Amersham
 High quality sequence stop: 474.
 location/Qualifiers

FEATURES


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KEYWORDS      GSS.
SOURCE         Saccharomyces castellii.
ORGANISM       Saccharomyces castellii.
REFERENCE      Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
AUTHORS        Saccharomycetales; Saccharomycetaceae; Saccharomyces.
TITLE          1 (bases 1 to 468)
JOURNAL        Clifton, P.F., Hillier, L.W., Fulton, L., Graves, T., Miner, T., Gish
COMMENT        W.R., Waterston, R.H. and Johnston, M.
                Surveying Saccharomyces genomes to identify functional elements by
                comparative DNA sequence analysis
                Unpublished (2001)
                Contact: Johnston M
                Department of Genetics
                Washington University Medical School
                Box 8232, 4566 Scott Ave., St. Louis, MO 63110, USA
                Tel: 314 362 2735
                Fax: 314 362 7855
                Email: mjgenetics.wustl.edu
                Class: random plasmid subclone.
FEATURES
  source
    1..468
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    /strain="NRRL Y-12630 (CBS 4309)"
    /db_xref="taxon:27288"
    /clone="476.d1041h1.s1"
    /clone_11b="Saccharomyces castellii NRRL Y-12630"
    /note="Random genomic sequence"
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alignment_block:
US-09-289-346a-9 x AZ926150/rev ..
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      201 CAATTAACGCGTCGTCGACTGGGTTCCCTAGACAAACATAAGATTA 152
          ::::|  ::::|  ::::|  ::::|  ::::|  ::::|  ::::|  ::::|
      24 aAlaAlaGluAlaLeuAsnAlaSerSerLysGluGluAlaLeuGlnIleI 41
          ::::|  ::::|  ::::|  ::::|  ::::|  ::::|  ::::|  ::::|
      151 TGTCAAAACGCTCTCAGATTACCATTAAGAAAGAGCTTGAAGATAC 102
          ::::|  ::::|  ::::|  ::::|  ::::|  ::::|  ::::|  ::::|
      41 leaArgGluLysIle.....ProGluLysTyrLeuPheGlnPhe 53
          ::::|  ::::|  ::::|  ::::|  ::::|  ::::|  ::::|  ::::|
      101 TTAGAGAGTAGTAGGTGACAGAAAGAAATCCAGATGAATAT.....TAC 61
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      54 HisAsnLeuAsnSer 58
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      60 CATGGATGCATTCA 46

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2216 AGCTAATGATGCTGCCGACAGGCGCTTAATGCGAGGTTCAGTGAAGCAG 2167
 37 lAeugInIleIleAArgGlulysIlleProGluIstYrleuPheGInPhe 53
 2166 CTTTACGATTAATTAAGGAAAACTCCCTTAAGATTTTATTTTCAATAT 2117
 54 HIsAnleuAsnSerAsnleuAspArgIlePheAspIlysthrPro 68
 2116 CATTAATTAAATGTAATTAGATAGCATTTT.....ACACCT 2078
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 ; Sequence 48, Application US/08838151A
 ; Patent No. 6291743
 ; GENERAL INFORMATION:
 ; APPLICANT: Stout, John T
 ; APPLICANT: Luu, Hang T
 ; APPLICANT: Maxwell, Douglas
 ; APPLICANT: Ahlgvist, Paul
 ; APPLICANT: Hanson, Steve
 ; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
 ; TITLE OF INVENTION: Genes
 ; NUMBER OF SEQUENCES: 63
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
 ; STREET: Two Prudential Plaza, Suite 4700
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: U.S.A.
 ; ZIP: 60601
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/838,151A
 ; FILING DATE:
 ; CLASSIFICATION: 800
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mueller, Lisa V
 ; REGISTRATION NUMBER: 38,978
 ; REFERENCE/DOCKET NUMBER: SYS3801P0260
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312-616-5400
 ; TELEFAX: 312-616-5460
 ; INFORMATION FOR SEQ ID NO: 48:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1062 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: circular
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: Bean Golden Mosaic Geminivirus
 ; STRAIN: Type II
 ; INDIVIDUAL ISOLATE: Guatemala
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 1..1059
 ; US-08-838-151A-48

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 Quality: 222.00 Length: 70
 Ratio: 3.700 Gaps: 0
 Percent Similarity: 85.714 Percent Identity: 60.000
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 US-09-289-346a-9 x US-08-838-151A-48

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 328 ACATCGAATGGGGACAAATTCGAAGTCGACGGCAGATCTGCAAGAGAG 377
 17 yCysGInThrSerAsnAspAlaIleAgluAlaIleAsnAlaSerSert 34
 378 TCAGCAGCTGCGCCACGACTCATATGCAAGGCAATTAAACGCCGATTCAA 427
 34 ySgInuAlaIleuGInIleIleAArgGlulysIlleProGluIstYrleu 50
 428 TTGAATCTCGCTTGACAAATATTGAGAGAGAACACCGAAAGATTCGTC 477
 51 PheGInPheHisAsnleuAsnSerAsnleuAspArgIlePheAspIlysthr 67
 478 CTTCAACATCACAACATCCGTTCTTAATCTCGAACGGATCTGTCGCAAGT 527
 67 rProGluPro 70
 528 GCCGGAACCA 537

seq_name: /cgn1_7/ptodata/1/ina/6B_COMP.seq:US-08-838-151A-51
 seq_documentation_block:
 ; Sequence 51, Application US/08838151A
 ; Patent No. 6291743
 ; GENERAL INFORMATION:
 ; APPLICANT: Stout, John T
 ; APPLICANT: Luu, Hang T
 ; APPLICANT: Maxwell, Douglas
 ; APPLICANT: Ahlgvist, Paul
 ; APPLICANT: Hanson, Steve
 ; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
 ; TITLE OF INVENTION: Genes
 ; NUMBER OF SEQUENCES: 63
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
 ; STREET: Two Prudential Plaza, Suite 4700
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: U.S.A.
 ; ZIP: 60601
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/838,151A
 ; FILING DATE:
 ; CLASSIFICATION: 800
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mueller, Lisa V
 ; REGISTRATION NUMBER: 38,978
 ; REFERENCE/DOCKET NUMBER: SYS3801P0260
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312-616-5400
 ; TELEFAX: 312-616-5460
 ; INFORMATION FOR SEQ ID NO: 51:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1062 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: circular
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: Bean Golden Mosaic Geminivirus
 ; STRAIN: Type II
 ; INDIVIDUAL ISOLATE: Guatemala


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FEATURE:
NAME/KEY: CDS
LOCATION: 1..1059
US-08-838-151A-51

alignment_scores:
Quality: 222.00 Length: 70
Ratio: 3.700 Gaps: 0
Percent Similarity: 85.714 Percent Identity: 60.000

alignment_block:
US-09-289-346A-9 x US-08-838-151A-51 ..

Align seg 1/1 to: US-08-838-151A-51 from: 1 to: 1062

1 ThrLeuValTrpGlyLuphGluValAlaGlyArgSerAlaArgGlyG1 17
||||| ||||||| ||||||| ||||||| ||||||| |||||||
328 ACAATCGAATGGGACAAATTCACAGTCGACGACGATCGCAAGAGGAG 377
17 yCysGlnThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerL 34
||||| ||||||| ||||||| ||||||| ||||||| |||||||
378 TCAGCAGTCTGCCAAGACTCATATGCAAGGCAATTAAAGCAGATTCAA 427
34 yGluGluAlaLeuGlnIleIleArgGluLysIleProGluLysTryLeu 50
||||| ||||||| ||||||| ||||||| ||||||| |||||||
428 TTGAATCTGCTTGCACAAATATGCAAGAGAACACCGAAGATTACGTC 477
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
||||| ||||||| ||||||| ||||||| ||||||| |||||||
478 CTTCAACATCACACACATCCGTTCTAATCTCGAAGCGATCTGTCMAAGT 527
67 rProGluPro 70
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528 GCCGGAACCA 537

seq_name: /cgnl_7/ptodata/1/ina/6A_COMB.seq:US-08-838-151A-54

seq_documentation_block:
Sequence 54, Application US/08838151A
Patent No. 6291743
GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminiivirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESSES:
ADDRESS: Dressler, Rockey, Milanow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838.151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SYS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
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INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 1062 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bean Golden Mosaic Geminiivirus
STRAIN: Type II
INDIVIDUAL ISOLATE: Guatemala
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1059
US-08-838-151A-54

alignment_scores:
Quality: 222.00 Length: 70
Ratio: 3.700 Gaps: 0
Percent Similarity: 85.714 Percent Identity: 60.000

alignment_block:
US-09-289-346A-9 x US-08-838-151A-54 ..

Align seg 1/1 to: US-08-838-151A-54 from: 1 to: 1062

1 ThrLeuValTrpGlyLuphGluValAlaGlyArgSerAlaArgGlyG1 17
||||| ||||||| ||||||| ||||||| ||||||| |||||||
328 ACAATCGAATGGGACAAATTCACAGTCGACGACGATCGCAAGAGGAG 377
17 yCysGlnThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerL 34
||||| ||||||| ||||||| ||||||| ||||||| |||||||
378 TCAGCAGTCTGCCAAGACTCATATGCAAGGCAATTAAAGCAGATTCAA 427
34 yGluGluAlaLeuGlnIleIleArgGluLysIleProGluLysTryLeu 50
||||| ||||||| ||||||| ||||||| ||||||| |||||||
428 TTGAATCTGCTTGCACAAATATGCAAGAGAACACCGAAGATTACGTC 477
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
||||| ||||||| ||||||| ||||||| ||||||| |||||||
478 CTTCAACATCACACACATCCGTTCTAATCTCGAAGCGATCTGTCMAAGT 527
67 rProGluPro 70
||||| |||||||
528 GCCGGAACCA 537

seq_name: /cgnl_7/ptodata/1/ina/6A_COMB.seq:US-08-809-103B-7

seq_documentation_block:
Sequence 7, Application US/08809103B
Patent No. 6133505
GENERAL INFORMATION:
APPLICANT: GRONENBORN, Bruno
TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESSES:
ADDRESS: YOUNG & THOMPSON
STREET: 745 South 23rd Street
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809.103B
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FILING DATE: 17-MAR-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94.11040
FILING DATE: 15-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR95/01192
FILING DATE: 15-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: PATCH, Andrew J.
REGISTRATION NUMBER: 32,925
REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 521-2297
TELEFAX: (703) 685-0573
TELEX: 248425 EMBON
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1145 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1077
US-08-809-103B-7

alignment_scores:
Quality: 222.00 Length: 69
Ratio: 3.828 Gaps: 0
Percent Similarity: 84.058 Percent Identity: 57.971

alignment_block:
US-09-289-346A-9 x US-08-809-103B-7 ..

Align seg 1/1 to: US-08-809-103B-7 from: 1 to: 1145

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2 LeuValTRpGlyGluPheGlnValAlaGlyArgSerAlaArgGlyGlyC 18
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331 CTTGAATGGGGTACTTCCAGATCGACGAGCATCTGCTAGGGGAGGACA 380
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
18 sGlnTrSerAsnAspAlaAlaIaGlnAlaLeuAsnAlaSerSerLysG 35
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
381 ACAGACAGCCACGACGCTTACGCAAGCAATTACGCGAGAGTAAGT 430
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
35 IuGlnAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeuPhe 51
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
431 CGCAGGCTCTGTGATTAATTAAGAAATTAGCCCTAGACATTACGTTCTA 480
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
52 GlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysThrPr 68
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
481 CATTTTCATATATATTAATAGTAAATTAGATTAGCTTTCCAGGCTCTCC 530
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
68 oGluPro 70
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531 GGCACCT 537
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seq_name: /cgn1_7/ptodata/1/ina/6A_COMB.seq:US-08-809-103B-1
seq_documentation_block:
Sequence 1, Application US/08809103B
Patent No. 6133505
GENERAL INFORMATION:
APPLICANT: GRONENBORN, Bruno
TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: YOUNG & THOMPSON
STREET: 745 South 23rd Street
CITY: Arlington

STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,103B
FILING DATE: 17-MAR-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94.11040
FILING DATE: 15-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR95/01192
FILING DATE: 15-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: PATCH, Andrew J.
REGISTRATION NUMBER: 32,925
REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 521-2297
TELEFAX: (703) 685-0573
TELEX: 248425 EMBON
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1148 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1077
US-08-809-103B-1

alignment_scores:
Quality: 222.00 Length: 69
Ratio: 3.828 Gaps: 0
Percent Similarity: 84.058 Percent Identity: 57.971

alignment_block:
US-09-289-346A-9 x US-08-809-103B-1 ..

Align seg 1/1 to: US-08-809-103B-1 from: 1 to: 1148

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331 CTTGAATGGGGTACTTCCAGATCGACGAGCATCTGCTAGGGGAGGACA 380
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
18 sGlnTrSerAsnAspAlaAlaIaGlnAlaLeuAsnAlaSerSerLysG 35
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
381 ACAGACAGCCACGACGCTTACGCAAGCAATTACGCGAGAGTAAGT 430
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
52 GlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysThrPr 68
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
481 CATTTTCATATATATTAATAGTAAATTAGATTAGCTTTCCAGGCTCTCC 530
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
68 oGluPro 70
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531 GGCACCT 537
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seq_name: /cgn1_7/ptodata/1/ina/6A_COMB.seq:US-08-809-103B-3
seq_documentation_block:
Sequence 3, Application US/08809103B

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: Patent No. 6133505
: GENERAL INFORMATION:
: APPLICANT: GROENENBORN, Bruno
: TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
: NUMBER OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
: NUMBER OF SEQUENCES: 17
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: YOUNG & THOMPSON
: STREET: 745 South 23rd Street
: CITY: Arlington
: STATE: Virginia
: COUNTRY: U.S.A.
: ZIP: 22202
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentln Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/809,103B
: FILING DATE: 17-MAR-1997
: CLASSIFICATION: 800
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: FR 94.11040
: FILING DATE: 15-SEP-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: WO PCT/FR95/01192
: FILING DATE: 15-SEP-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: PATCH, Andrew J.
: REGISTRATION NUMBER: 32,925
: REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (703) 521-2297
: TELEFAX: (703) 685-0573
: TELETYPE: 248425 EMBON
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1150 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..1077
: US-08-809-103B-3

alignment_scores:
      Quality: 222.00      Length: 69
      Ratio: 3.828      Gaps: 0
      Percent Similarity: 84.058      Percent Identity: 57.971

alignment_block:
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331 CTGATGGGGTACTTCCAGATCGACGACGATCTGCTAGGAGGAGACA 380
18 sGlnTrSerAsnAspAlaAlaGlnAlaLeuAsnAlaSerSerLysG 35
|||||: ||||| |||||: |||||: |||||: |||||:
381 ACAGACAGCGACGACGCTTACCGCAAGCAATTACGACGAGTAAGT 430.
35 lndUalaleuGlnlleleArGlnLyslleProGluysTyrlaunpe 51
: |||||: |||||: |||||: |||||: |||||: |||||:
431 CGAGGCTCTGATGTAAATTAAAGAAATTAGCGCTAGAGATTACGTTCTA 480
52 GlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysThrPr 68
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481 CATTTTCATATATATAATAGTATTAGATAGATTTCACAGGTGCTCC 530
68 oGluPro 70
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531 GGACCT 537

seq_name: /cgn1_7/plodata/1/ina/6A_COMB.seq:us-08-809-103B-5
seq_documentation_block:
: Sequence 5, Application US/08809103B
: Patent No. 6133505
: GENERAL INFORMATION:
: APPLICANT: GROENENBORN, Bruno
: TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
: NUMBER OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
: NUMBER OF SEQUENCES: 17
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: YOUNG & THOMPSON
: STREET: 745 South 23rd Street
: CITY: Arlington
: STATE: Virginia
: COUNTRY: U.S.A.
: ZIP: 22202
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentln Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/809,103B
: FILING DATE: 17-MAR-1997
: CLASSIFICATION: 800
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: FR 94.11040
: FILING DATE: 15-SEP-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: WO PCT/FR95/01192
: FILING DATE: 15-SEP-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: PATCH, Andrew J.
: REGISTRATION NUMBER: 32,925
: REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (703) 521-2297
: TELEFAX: (703) 685-0573
: TELETYPE: 248425 EMBON
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1150 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..1077
: US-08-809-103B-5

alignment_scores:
      Quality: 222.00      Length: 69
      Ratio: 3.828      Gaps: 0
      Percent Similarity: 84.058      Percent Identity: 57.971

alignment_block:
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331 CTGATGGGGTACTTCCAGATCGACGACGATCTGCTAGGAGGAGACA 380

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18 sGlnHrSerAsnAspAlaAlaAlaGluAlaLeuAsnAlaSerSerIysG 35
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35 LuGluAlaLeuGlnIleIleIleArgGluLysIleProGluLysTyrLeuPhe 51
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431 CCGAGCGCTCTTGATGTAATTAAGAAATTAAGCCGATTAACGTTCTCA 480
52 GlnPheAsnLeuAsnSerAsnLeuAspArgIlePheAspLysThrPr 68
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
481 CATTTCAATATATATATAGTAATTTAGATTAAGGTTTCAGGCTGCTCC 530
68 ocGluPro 70
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531 GGCACCT 537

seq_name: /cgn1_7/ptodata/1/ina/6B_COMB.seq:US-08-838-151A-43
seq_documentation_block:
: Sequence 43, Application US/08838151A
: Patent No. 6291743
: GENERAL INFORMATION:
: APPLICANT: Stout, John T
: APPLICANT: Luu, Hang T
: APPLICANT: Maxwell, Douglas
: APPLICANT: Ahlquist, Paul
: APPLICANT: Hanson, Steve
: TITLE OF INVENTION: Transgenic Plants Expressing Gemnivirus
: NUMBER OF SEQUENCES: 63
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Dressler, Rockey, Milnamow & Katz
: STREET: Two Prudential Plaza, Suite 4700
: CITY: Chicago
: STATE: Illinois
: COUNTRY: U.S.A.
: ZIP: 60601
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/838,151A
: FILING DATE:
: CLASSIFICATION: 800
: ATTORNEY/AGENT INFORMATION:
: NAME: Mueller, Lisa V
: REGISTRATION NUMBER: 38,978
: REFERENCE/DOCKET NUMBER: SVS3801P0260
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312-616-5400
: TELEFAX: 312-616-5460
: INFORMATION FOR SEQ ID NO: 43:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1183 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: circular
: MOLECULE TYPE: DNA (genomic)
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: ORIGINAL SOURCE:
: ORGANISM: Bean Golden Mosaic Gemnivirus
: STRAIN: Type II Isolates
: INDIVIDUAL ISOLATE: Guatemala
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..1059
: PUBLICATION INFORMATION:
: AUTHORS: Farla, JC
: AUTHORS: Gilbertson, RL
: AUTHORS: Hanson, SF

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: AUTHORS: Morales, FJ
: AUTHORS: Ahlquist, P
: AUTHORS: Loniello, AO
: AUTHORS: Maxwell, D
: TITLE: Bean Golden Mosaic Gemnivirus Type II
: TITLE: Isolates from the Dominican Republic and
: TITLE: Guatemala: Nucleotide Sequences, Infectious
: TITLE: Pseudorecombinants, and Phylogenetic Relationships
: JOURNAL: Phytopathology
: VOLUME: 84
: ISSUE: 3
: PAGES: 321-329
: DATE: 1994
: US-08-838-151A-43

alignment_scores:
Quality: 222.00 Length: 70
Ratio: 3.700 Gaps: 0
Percent Similarity: 85.714 Percent Identity: 60.000

alignment_block:
US-09-289-346a-9 x US-08-838-151A-43
Align seg 1/1 to: US-08-838-151A-43 from: 1 to: 1183

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17 yCysGlnHrSerAsnAspAlaAlaAlaGluAlaLeuAsnAlaSerSerL 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
378 TCAGCAGCTGTGCCAAGCACTCATATCCAAAGCATTAACGACATTCAA 427
34 ysgGluGluAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeu 50
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428 TTGAATCTGCTTGCACATATTTGAAGAGAACCAACCAAGATTACGTC 477
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
478 CTTCAACATCAACACATCCGTTCTAATCTCGAAGCATCTGCTCAAGT 527
67 rProGluPro 70
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528 GCCGACCA 537

seq_name: /cgn1_7/ptodata/1/ina/6B_COMB.seq:US-08-838-151A-45
seq_documentation_block:
: Sequence 45, Application US/08838151A
: Patent No. 6291743
: GENERAL INFORMATION:
: APPLICANT: Stout, John T
: APPLICANT: Luu, Hang T
: APPLICANT: Maxwell, Douglas
: APPLICANT: Ahlquist, Paul
: APPLICANT: Hanson, Steve
: TITLE OF INVENTION: Transgenic Plants Expressing Gemnivirus
: NUMBER OF SEQUENCES: 63
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Dressler, Rockey, Milnamow & Katz
: STREET: Two Prudential Plaza, Suite 4700
: CITY: Chicago
: STATE: Illinois
: COUNTRY: U.S.A.
: ZIP: 60601
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:

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Page 7

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1      CITY: Madison
2      STATE: WI
3      COUNTRY: US
4      ZIP: 53701-2113
5      COMPUTER READABLE FORM:
6      MEDIUM TYPE: Floppy disk
7      COMPUTER: IBM PC compatible
8      OPERATING SYSTEM: PC-DOS/MS-DOS
9      SOFTWARE: Patent in Release #1.0, Version #1.30
10     CURRENT APPLICATION DATA:
11     APPLICATION NUMBER: US/09/065,999
12     FILING DATE:
13     CLASSIFICATION:
14     ATTORNEY/AGENT INFORMATION:
15     NAME: Seay, Nicholas J.
16     REGISTRATION NUMBER: 27,386
17     REFERENCE/DOCKET NUMBER: 960296, 94754
18     TELECOMMUNICATION INFORMATION:
19     TELEPHONE: 608-251-5000
20     TELEFAX: 608-251-9166
21     INFORMATION FOR SEQ ID NO: 5:
22     SEQUENCE CHARACTERISTICS:
23     LENGTH: 1651 base pairs
24     TYPE: nucleic acid
25     STRANDEDNESS: single
26     TOPOLOGY: linear
27     MOLECULE TYPE: DNA (genomic)
28     OS-09-065-999-5

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alignment_scores:
  Quality: 222.00
  Ratio: 3.700
  Percent Similarity: 85.714
  Length: 70
  Gaps: 0
  Percent Identity: 50.000
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Align seg 1/1 to: US-09-065-999-5 from: 1 to: 1651

[illegible]

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seq_documentation_block:

; Sequence 6, Application US/09065995

Patent No. 6

APPLICANT: Hanson Stephen E

APPLICANT: Maxwell, Douglas B

TITLE OF INVENTION: TRANS-DOMINANT INHIBITION OF GEMINIVIRAL

; TITLE OF INVENTION: DI

; NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: Quarles & Brady ;

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STREET: One South Pinckney Street
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/065,999
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 960296,94754
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1651 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-065-999-6
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alignment_scores:
Quality: 222.00      Length: 70
Ratio: 3.700         Gaps: 0
Percent Similarity: 85.714   Percent Identity: 60.000
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alignment_block:

US-09-289-346a-9 x US-09-065-999-6 ..

Align seg 1/1 to: US-09-065-999-6 from: 1 to: 1651

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796 ACATTCGATCGGGACATTCGACATTCGACGAGATTCGACAGAGAG 845
17 yCysGlnThrSerAsnAspAlaAlaGlnAlaLeuAsnAlaSerSerL 34
|||||: ||||||: ||||||: ||||||: ||||||: ||||||: ||||||:
846 TCAGCAGCTCGCCACGACTCATATGCAAGGCAATTAAACCCGATTCAA 895
34 ysglGlnAlaLeuGlnIleIleArgGlnLysIleProGlnLysTyrLeu 50
|||||: ||||||: ||||||: ||||||: ||||||: ||||||: ||||||:
896 TTGCAATCTGCTTGACATATTGAAGAAACGAAACGAAAGATTACGTC 945
51 pheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
|||||: ||||||: ||||||: ||||||: ||||||: ||||||: ||||||:
946 CTTCAACATCACACATCCGTTCTATCTCGAAGCGATCTCTGTCAAAGT 995
67 rProGlnPro 70
|||||: ||||||: ||||||: ||||||: ||||||: ||||||: ||||||:
996 GCCGGAACCA 1005
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seq_name: /cgnl_7/ptodata/1/lna/6a_COMB.seq:US-09-065-999-8

seq_documentation_block:

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; Sequence 8, Application US/09065999
; Patent No. 6118048
; GENERAL INFORMATION:
; APPLICANT: Hanson, Stephen F.
; APPLICANT: Maxwell, Douglas P.
; TITLE OF INVENTION: TRANS-DOMINANT INHIBITION OF GEMINIVIRAL
; DNA REPLICATION BY GEMINIVIRUS REP GENE MUTANTS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
```

```
ADDRESSEE: Charles & Brady
STREET: One South Pinckney Street
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/065,999
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 960296,94754
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1894 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-065-999-8
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alignment_scores:
Quality: 222.00      Length: 70
Ratio: 3.700         Gaps: 0
Percent Similarity: 85.714   Percent Identity: 60.000
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alignment_block:

US-09-289-346a-9 x US-09-065-999-8 ..

Align seg 1/1 to: US-09-065-999-8 from: 1 to: 1894

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17 yCysGlnThrSerAsnAspAlaAlaGlnAlaLeuAsnAlaSerSerL 34
|||||: ||||||: ||||||: ||||||: ||||||: ||||||: ||||||:
846 TCAGCAGCTCGCCACGACTCATATGCAAGGCAATTAAACCCGATTCAA 895
34 ysglGlnAlaLeuGlnIleIleArgGlnLysIleProGlnLysTyrLeu 50
|||||: ||||||: ||||||: ||||||: ||||||: ||||||: ||||||:
896 TTGCAATCTGCTTGACATATTGAAGAAACGAAACGAAAGATTACGTC 945
51 pheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
|||||: ||||||: ||||||: ||||||: ||||||: ||||||: ||||||:
946 CTTCAACATCACACATCCGTTCTATCTCGAAGCGATCTCTGTCAAAGT 995
67 rProGlnPro 70
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996 GCCGGAACCA 1005
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seq_name: /cgnl_7/ptodata/1/lna/6a_COMB.seq:US-09-065-999-7

seq_documentation_block:

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; Sequence 7, Application US/09065999
; Patent No. 6118048
; GENERAL INFORMATION:
; APPLICANT: Hanson, Stephen F.
; APPLICANT: Maxwell, Douglas P.
; TITLE OF INVENTION: TRANS-DOMINANT INHIBITION OF GEMINIVIRAL
; DNA REPLICATION BY GEMINIVIRUS REP GENE MUTANTS
; NUMBER OF SEQUENCES: 8
```

```

CORRESPONDENCE ADDRESS:
ADDRESS: Quarles & Brady
STREET: One South Pluckney Street
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/065,999
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 960296.94754
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2072 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-065-999-7

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alignment_scores:
Quality: 222.00      Length: 70
Ratio: 3.700         Gaps: 0
Percent Similarity: 85.714   Percent Identity: 60.000

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alignment_block:

US-09-289-346a-9 x US-09-065-999-7 ..

Align seg 1/1 to: US-09-065-999-7 from: 1 to: 2072

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17 yCysGlnThrSerAsnAspAlaAlaAlaGlnAlaLeuAsnAlaSerS 34
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
846 TCAGCAGTGTGCCACAGCACTCATATCCAAAGCATTAAACGCAATT 895
34 ySGLuGlnAlaLeuGlnIleIleArgGluLysIleProGluLysTr 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
896 TTGAATCTGCTTGACATATATGAAGAGAACCAACGAAAGATTGCT 945
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAsp 67
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:
946 CTTCAACATCAGACATCCGTTCTAATCTCGAAGCATCTTCTCAAG 995
67 rProGluPro 70
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:
996 GCCGGACCA 1005

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seq_name: /cgn1_7/plodata/1/Ina/6b_COMB.seq:US-08-838-151A-1

seq_documentation_block:

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Sequence 1, Application US/08838151A
Patent No. 6291743
GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Luu, Hong T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul

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APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing GeminiVirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESS: Drossler, Rockey, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1162 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Tomato Mottle Gemini Virus
INDIVIDUAL ISOLATE: Florida
FEATURE:
NAME/KEY: CDS
LOCATION: 44..1127
PUBLICATION INFORMATION:
AUTHORS: Gilbertson, RL
AUTHORS: Hidayat, SH
AUTHORS: Paplomatas, EJ
AUTHORS: Rojas, MR
AUTHORS: Hou, YM
AUTHORS: Maxwell, DP
TITLE: Pseudorecombination between the infectious
TITLE: cloned DNA components of tomato mottle and bean
TITLE: dwarf mosaic geminiviruses.
JOURNAL: Jour. General Viro1.
VOLUME: 74
PAGES: 23-31
DATE: 1993
US-08-838-151A-1

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Quality: 220.00      Length: 70
Ratio: 3.667         Gaps: 0
Percent Similarity: 85.714   Percent Identity: 57.143

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alignment_block:

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Align seg 1/1 to: US-08-838-151A-1 from: 1 to: 1162

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|||||
51  PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspIySth 67
|||||
2121 TTTCAGTTCCACAACTTAATAGCAATTAGATAGCATATTGATAGAC 2072
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67  rProGluPro 70
|||||
2071 TCCTGAGCCA 2062
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seq_name: gb_v1:AY029750

seq_documentation_block: 2588 bp DNA circular VRL 08-MAY-2001
LOCUS AY029750
DEFINITION Tomato severe rugose virus DNA-A, complete sequence.
ACCESSION AY029750
VERSION AY029750.1 GI:14009278
KEYWORDS
SOURCE Tomato severe rugose virus.
ORGANISM Tomato severe rugose virus.
REFERENCE 1 (bases 1 to 2588)
VIRUSES: ssDNA viruses; Geminiviridae; begomovirus.
AUTHORS Rezende,W.L., Goulart,L.R., Parreira,K.S. and Figueiredo,J.E.F.
TITLE The full-length DNA-A nucleotide sequence of a novel
tomato-infecting begomovirus, Tomato severe rugose virus, in Brazil
JOURNAL Unpublished
2 (bases 1 to 2588)
AUTHORS Rezende,W.L., Goulart,L.R., Parreira,K.S. and Figueiredo,J.E.F.
TITLE Direct Submission
JOURNAL Submitted (03-APR-2001) Instituto de Genetica e Biologica,
Universidade Federal de Uberlandia, Av. Amazonas s/n, Bloco 2E,
Sala 24, Campus Umuarama, Uberlandia, Minas Gerais 38.400-000,
Brazil

FEATURES
source 1..2588
Location/Qualifiers
/organism="Tomato severe rugose virus"
/strain="Minas Gerais"
/db_xref="taxon:158463"
/country="Brazil"
/note="segment: DNA-A"
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305..1060
/gene="AV1"
305..1060
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/db_xref="GI:14009282"
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ATVKNDLRDREOVHMIFYAKYVGQYASNEQALVRFKVNNVVYNNHQEGKYNHT
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/protein_id="AAK50358.1"
/db_xref="GI:14009280"
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/translation="MRNSSSLTPPSIVQVRAAKRGIRRRRIDIEGCSLYVHIGCR
GHGTFHRCGTHHCTSGREMRILYLDIKSFLEPDROKSGCSNVHHBOSLRRPNVQQPEE
SIASQELHQJLPDWDPDFSFWDIK"
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complement(1533..2588)
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/db_xref="GI:14009279"
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IKVCRLEHENGEPHLAVILOPEGNVCRONREFPLVSPTRSTFRHPNIOAKSSDYK
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FOFHNLNSLDRITARADEPAPYPLSSFTNVFREMODNADYFGGARPERPISI
LIEGDSRTGKTMAARAFGANHYLSGHLDENFRVSNHYENVIDLIAPHYLIKHKME
LIGAKDMOSCKYKGPVQIKGIPCIELCNPEGCASYKVFRRKRNASLNNMTKHNA
KEVFLNPLYOGTOSC"
complement(2171..2434)
/gene="AC4"
complement(2171..2434)
/gene="AC4"
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/db_xref="GI:14009281"
/translation="MKMSGLISTCFPNKSLIAITAAKINDSSWSPQGOCHISIRFREL
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BASE COUNT 660 a 525 c 598 g 805 t
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alignment_scores:
Quality: 300.00 Length: 70
Ratio: 4.762 Gaps: 0
Percent Similarity: 90.000 Percent Identity: 78.571

alignment_block:
US-09-289-346a-10 x AY029750/rev ..
Align seg 1/1 to reverse of: AY029750 from: 1 to: 2588

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|||||
17 YCYSGIntThrSerAsnAspLeuLeuGlnUaIaLeuAsnAlaSerSerL 34
|||||
2208 TTGCCAGACAGCTACGATGCTGCCGAGAGAGCTTGAGACGACCTTCCA 2159
|||||
34 YSGIUGUAlaLeuGlnIleIleargGluIysIleProGluIuTyTyLeu 50
|||||
2158 AACACGCGCGCTTGCAATATCCGGAGAGAGCTACCGGAAAGTTT7TA 2109
|||||
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspIySth 67
|||||
2108 TTTCAGTTCCACAACTTAATAGTAATTAGATAGCATATTGCAAGGCG 2059
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67 rProGluPro 70
|||||
2058 TCAGGAGCCA 2049
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seq_name: gb_v1:AF291705

seq_documentation_block: 2622 bp DNA circular VRL 25-SEP-2000
LOCUS AF291705
DEFINITION Tomato mosaic virus DNA-A, complete sequence.
ACCESSION AF291705
VERSION AF291705.1 GI:10281644

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KEYWORDS Tomato rugose mosaic virus.
SOURCE Tomato rugose mosaic virus.
ORGANISM Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
REFERENCE 1 (bases 1 to 2622)
AUTHORS Fernandes,J.J., Fontes,E.P.B., Brommonschenkel,S.H., Carvalho,M.G., Zambolim,E.M. and Zerbini,F.M.
TITLE Molecular Cloning and Characterization of Tomato rugose mosaic virus (TRMV), a Begomovirus Isolated from Tomatoes at Triangulo Mineiro, Minas Gerais, Brazil
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2622)
AUTHORS Fernandes,J.J. and Zerbini,F.M.
TITLE Direct Submission
JOURNAL Submitted (31-JUL-2000) Dept. de Fitopatologia, Universidade Federal de Vicosa, Av. P.H. Rolfs, s/n - Centro, Vicosa, MG 36571-000, Brazil
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/villon
/db_xref="taxon:134599"
/country="Brazil: Uberlandia, Triangulo Mineiro, Mians Gerais"
/note="Previously referred to as Tomato geminivirus Uberlandia TRMV"
1. .227
/note="common region"
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/db_xref="GI:10281649"
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/gene="AC3"
/note="Rep"
/codon_start=1
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/protein_id="AA015548.1"
/db_xref="GI:10281648"
/translation="MDSRTGELLTAHQAEQNGVYTWETSNPLPYKMYNEDILYTRTV YHVOIRFNHNLRVGLGHKAYLNFQIMTSTSLRASQMTYLNRFKYLIMLYIDOLGVISV NNVIKAVFATDROVYNAVLENHSIKVLY"
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complement(1570. .2622,1. .6))
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complement(1570. .2622,1. .6))
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complement(1570. .2622,1. .6))
/note="Rep"
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/product="replication-associated protein"
/protein_id="AA015546.1"
/db_xref="GI:10281646"
/translation="MPSATRRFQIKAKNYLTYKCSISKEEALSQIKNLTPTNKR FKVCELEHNGEPLHVLQPEGNVCCONQFFDLVSPTRSTHHPNIOKASSSDVK SYVDKDTTTEMECFQIDGRSARGCCTANDAAEALNAPSKDALOIRKMEKFL FQPHNLNDRIFARAPPEWAPTFPISSFTNPREMODNADYEGRAARPERPIS IIRGDSRTGCKTMARALGANHYLSHGLDFPDRVYSNHYENVYIDDIAPHYLTKIWK ELICARBMQSNCKYKRPVQIKGCTPCIVLCNPEGASYKCFLDKEENSALSWTKIN AÖFIPLNSPLTÖSSTSGC"
BASE COUNT 684 a 562 c 600 g 776 t
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Quality: 298.00 Length: 70
Ratio: 4.730 Gaps: 0
Percent Similarity: 90.000 Percent Identity: 78.571
alignment_block:
US-09-289-346a-10 x AF291705/rev ..
Align seg 1/1 to reverse of: AF291705 from: 1 to: 2622
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2298 ACTATCGAATGAGGGGGAATTCGCAATCGACGACGAGAGTGTGAGGCGG 2249
17 YCYSGIntHrSerAsnAspLeuLeuGlnGlnAlaLeuAsnAlaSerSer 34
||||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
2248 TTGCCAGACAGCTAACGACGCTGCCGACGACGCTTGAACGACCTTCCA 2199
34 YSGlGlnAlaLeuGlnIleIleArgGlnIleProGlnIleProGlnIle 50
||::: ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
2198 AAGACATCGCCTTGCAAGATATCCGCGGACGACGACGAAAGTCTCTTA 2149
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAsnArgIlePheAspIle 67
||||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
2148 TTTCAGTTTCACATCTTAATAGTATTAGATGATTTGCCAAGGGC 2099
67 rProGluPro 70
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2098 TCCGACGCCA 2089
seq_name: gb_v1:LM092532
seq_documentation_block:
LOCUS LM092532 1193 bp DNA VRL 01-APR-1997
DEFINITION Leonurus mosaic virus Rep protein (rep) and coat protein (cp)
ACCESSION U92532
VERSION U92532.1 GI:1916344
KEYWORDS genes, partial cds.
SOURCE
ORGANISM Leonurus mosaic virus.
REFERENCE 1 (bases 1 to 1193)
AUTHORS Farfa,J.C. and Maxwell,D.P.
TITLE Variability in geminivirus associated with Phaseolus vulgaris in Brazil


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37 lalauGlnlleilleargIuLySllleProgluLyStyrlleuPheGlnThp 53
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2205 CCATGCAAAATATCAAGAAAGAACTACCGGAAAGTTTCTCTCCATATF 2156
54 HisAsnLeuAsnSerAsnLeuAsnPaArglllePheAspLyThrProGluPr 70
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2105 G 2105

seq_name: gb_v1:AF188708

seq_documentation_block: 1365 bp DNA VRL 07-NOV-1999
LOCUS AF188708
DEFINITION Cowpea golden mosaic geminivirus replication associated protein
(rep) and coat protein (cp) genes, partial cds.
ACCESSION AF188708
VERSION AF188708.1 GI:6273115
KEYWORDS
SOURCE .
ORGANISM cowpea golden mosaic geminivirus.
Virus(es): ssDNA viruses; Geminiviridae; Begomovirus.
REFERENCE
AUTHORS Farfa,J.C.
TITLE Partial nucleotide sequence of cowpea golden mosaic geminivirus
from Brazil
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1365)
AUTHORS Farfa,J.C.
TITLE Direct Submission
JOURNAL Submitted (21-SEP-1999) Biotechnology Laboratory, EMBRAPA, Caixa
Postal 179, Goiania, GO 75375, Brazil
FEATURES
source
1..1365
/organism="cowpea golden mosaic geminivirus"
/strain="CGMV-BR"
/specific_host="cowpea"
/db_xref="taxon:69263"
complement(<1..676)
/gene="rep"
complement(<1..676)
/gene="cp"
/feature="AC1"
/codon_start=1
/product="replication associated protein"
/protein_id="AAF06318.1"
/db_xref="GI:6273117"
/translation="MPPKRFKINAKNYFLTYPOCSIGKESAIPOLOTLQTPVKKYI
RVCREIHNGEPHLLHIOFGKQCTNCRFLPKHPTTSVSHNPITOSAKSSDYS
YIEKDGDIYEWGHPQIDGRSARGGQOTINDASALNANSSKEEMQIIEKLPKFLF
QYHNLSNLDRIFKRPPSPPOLSSFTVNPQOMDWDYFGROAAAPRPVSI
IIEEDSR"
rep_origin 674..820
gene 1021..>1365
/feature="subgenomic DNA"
/feature="cp"
/feature="AC1"
/codon_start=1
/product="coat protein"
/protein_id="AAF06317.1"
/db_xref="GI:6273116"
/translation="MVKRDAPWRHMSGTSKYSRTPNNSPRSGGPKYNAEWNRP
YRKPRIVMYRSRDVPRGCEGPKCVOSFEOKHDVSHIGKIVICLSDVTRGGGITRVRGK
RFQYKSVYITLKV"
BASE COUNT 339 a 259 c 332 g 435 t
ORIGIN
alignment_scores: 279.00 length: 67

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Ratio: 4.650 Gaps: 0
Percent Similarity: 89.552 Percent Identity: 77.612

alignment_block:
US-09-289-346a-10 x AF188708/rev ..
Align seg 1/1 to reverse of: AF188708 from: 1 to: 1365

4 TrpGlyLupheGlnValAspGlyATGserAlaArgGlyLysGlnThp 20
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
340 TGGGGTATTTCAAATCGACGAGATCTGCTAGAGAGGTCCACGAC 291
20 rSerAsnAspLeuLeuGluAlaLeuAsnAlaSerSerLysGlnThp 37
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
290 AATTATGATGATCGAGCATCGAGCGCTTAATGCTTCTTCAAGAAAG 241
37 lalauGlnlleilleargIuLySllleProgluLyStyrlleuPheGlnThp 53
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
240 CCATGCAAAATATCAAGAAAGAACTACCGAGAGAGTTCTCTCCAGTAT 191
54 HisAsnLeuAsnSerAsnLeuAsnPaArglllePheAspLyThrProGluPr 70
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
190 CACAAATTATTCAGTACCTGATAGAAATATTCAAAAGCTCCGAGAC 141
70 o 70
140 A 140

seq_name: gb_v1:AF288227

seq_documentation_block: 1383 bp DNA VRL 20-AUG-2000
LOCUS AF288227
DEFINITION Sweet potato leaf curl virus replication association protein (AC1)
and AC4 (AC4) genes, complete cds.
ACCESSION AF288227
VERSION AF288227.1 GI:9858125
KEYWORDS
SOURCE .
ORGANISM sweet potato leaf curl virus.
Virus(es): ssDNA viruses; Geminiviridae; Begomovirus.
REFERENCE
AUTHORS Lotrakul,P., Valverde,R.A., Clark,C.A., Sim,J. and De La Torre,R.
TITLE Detection of a geminivirus infecting sweet potato in the United
States
JOURNAL Plant Dis. 82, 1253-1257 (1998)
REFERENCE 2 (bases 1 to 1383)
AUTHORS Lotrakul,P. and Valverde,R.A.
TITLE Direct Submission
JOURNAL Submitted (18-JUL-2000) Plant Pathology and Crop Physiology,
Louisiana State University, 302 Life Sciences Bldg., Baton Rouge,
LA 70803, USA
FEATURES
source
1..1383
/organism="sweet potato leaf curl virus"
/db_xref="taxon:100755"
/feature="subgenomic DNA"
complement(285..1229)
/gene="AC1"
complement(285..1229)
/gene="AC1"
/feature="AC1"
/codon_start=1
/product="replication association protein"
/protein_id="AAG01006.1"
/db_xref="GI:9858126"
/translation="MAPPKRFKIDAKNYFLTYPRCSLSKEDCLAQLNLIQTPSNKKYI
HVARLEHDEPHLHVLYOPEGRKVCNNSPEFDVSNRSHNPHNPITOGAKSSDYS
YVOKDGLTITWGFQVDRGSRARGGQOTANAAALNAGSKKALQIIRKILPKRYLF
QFNHLYVNLDRITSPSPSYSSPPSSSSPFANVPIIISDMAENVMDSAAAPDRISIV
IEGFSRIICKTVMAKSLGPHNTLCGHLDLSRVVINSNMYNVIDOVNPOYLKHKREFWG
AOKDMOSNCKRYGKRPRIKGAVRPEGLAIVMVRCHTA"
complement(815..1072)
/gene="AC4"
gene

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CDS                                complement(815..1072)
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                                   /note="A14"
                                   /codon_start=1
                                   /product="AC4"
                                   /protein_id="AGG01007.1"
                                   /db_xref="GI:9658127"
                                   /translation="MGNUTSCWCCSSKANSQAQADSSIMSHRFDRIITFPTSRLENR
                                   APMSSPSIRGIPSPCVNSRSRTADLLEASRLLTTPORL"

BASE COUNT      359 a          296 c          327 g          401 t
ORIGIN

alignment_scores:
    Quality:     277.00           Length:         68
    Ratio:       4.617            Gaps:           0
Percent Similarity: 88.235        Percent Identity: 79.412

alignment_block:
US-09-289-346A-10 x AF288227/rev ..

Align seg 1/1 to reverse of: AF288227 from: 1 to: 1383

1 THrLeValTTrpGLyGlupheGInVAIsppGIYArgSerAlarGLyGI 17
|||||:::|||||||11111111111111111111111111111111
902 ACCATCACTCGGGGTGAATTCCAGGTCGACGGGAGATCTGTACAGACAG 853

17 yCSglnPTrSerAsnAspLeuLeuLeuUAlalaeuAnIasEserL 34
| | |||||:::||||| | |||||111111111111111111111111
852 CCAGCGACTGCTAACGACGACGCCGCAGAGGCTGTAAACGACGTTCTA 803

34 ySGLuGlualauEnGInIIeIleAYgluGluySTlleProGUluySTyrLeu 50
||||| | |||||11111111111111111111111111111111
802 AGGAACCTCGGTTGCAAATAATCACGAGACAACCTCCGTGAATAATTTTA 753

51 pHeGlnPhHisAsnLeuAsnSerAsnLeuAspARITlleheaspIlysrH 67
|||||111111111111111111111111111111111111111111111111111
752 YTYCAATTCATRAATTACTTAGTGATAATTGATGAGATTTTTTCTCTCTCC 703

67 rPro 68
|||
702 ACCT 699

seq_name: gb_v1:AF104036

seq_documentation_block:
LOCUS      AF104036             2828 bp      DNA      circular   VRL      05-AUG-1999
DEFINITION Sweet potato leaf curl virus DNA A, complete sequence.
ACCESSION  AF104036
VERSION    AF104036.1 GI:5702158
KEYWORDS
SOURCE     sweet potato leaf curl virus.
ORGANISM   sweet potato; leaf curl virus.
REFERENCE  Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
AUTHORS    Lotrakul,P., Valverde,R.A., Clark,C.A., Sim,J. and De La Torre,R.
TITLE      Lotrakul,P., Valverde,R.A., Clark,C.A., Sim,J. and De La Torre,R.
          Detection of a geminivirus infecting sweet potato in the United
          States
JOURNAL    Plant Dis. 82, 1253-1257 (1998)
REFERENCE  2 (bases 1 to 2828)
AUTHORS    Lotrakul,P. and Valverde,R.A.
TITLE      Cloning of a DNA-A-like genomic component of sweet potato leaf curl virus : nucleotide sequence and phylogenetic relationships
REMARK     Molecular Plant Pathology On-line (1999)
AUTHORS    http://www.bspp.org.uk/mpool/1999/0422lotrakul/
TITLE      3 (bases 1 to 2828)
REMARK     Lotrakul,P. and Valverde,R.A.
AUTHORS    Direct Submission
TITLE      Submitted (02-Nov-1998) Plant Pathology and Crop Physiology,
JOURNAL    Louisiana State University, 302 Life Sciences Bldg., LSU, Baton
          Rouge, LA 70803, USA
FEATURES
source      1..2828
Location/Qualifiers

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gene
CDS
/organism="sweet potato leaf curl virus"
/db_xref="taxon:100755"
/chromosome="DNA A"
/country="USA"
132..476
/gene="AV2"
132..476
/gene="AV2"
/note="AR2"
/codon_start=1
/product="precocut protein AV2"
/protein_id="AAD47169.1"
/db_xref="GI:5702159"
/translation="MAELMDPLQNPDLPTLVGFQMLSVKIQSLQSLKTYEPGTLGFEI
CSELIRIRFROYDRANARFAEIISSIMWGTETAEALIDSYRALHWECPCPCPCPC
GFKRRDEKEEG"
301..1065
/gene="AV1"
301..1065
/gene="AV1"
/note="AR1"
/codon_start=1
/product="coat protein AV1"
/protein_id="AAD47170.1"
/db_xref="GI:5702160"
/translation="MTGRMRVSPRPHPYGGAPRRRLNEFALIVPYTCNAVPLAARST
VPSVSNLKKRRRDRIRPGCGVPCVQDYEFKMDVPLHTGTFVCSDETRCTGLHRI
GRVYCSKSGIDGKVTAMDNDNAKRDHTNIITYWILRDRPNKDPINFQIITPMNDNEH
TPAKIRMDLRDMOVLKRESVYSGSPYSHEQALIRKFFGLVNHVITYNKEEAKYEE
NOLENALMLYSNASHASNPHYOTLRCRAIFYDSHNN"
complement(1081..1515)
/gene="AC3"
complement(1081..1515)
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complement(1081..1515)
/gene="AC3"
/note="AL3"
/codon_start=1
/product="AC3"
/protein_id="AAD47171.1"
/db_xref="GI:5702161"
/translation="MDSRTGESISHAQTTTAAVEEDTNPMSVGRTPAFLRLIMYHEST
OGRTILFQDLRVNERROLGFHKIFLQFRILITTLTGAIHSMTILERLKWRLCNEL
ANLGFSLVNLVEVIRYLPVCSMWIDELDTDCNDVAVLL"
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/gene="AC2"
complement(1232..1678)
/gene="AC2"
/note="AL2"
/codon_start=1
/product="transactivator protein AC2"
/protein_id="AAD47172.1"
/db_xref="GI:5702162"
/translation="MSNPISGYKRCPIOEPLHTEAKKAKRKVPEQPTRIWKGCGCC
ALTITCKXOHEFTHRGINKSCGYESSRIRHOPVCGSDCVPSQNNVCRREHTGEH
HQPIAEGEELQKEATGTFPQDLPTPLDLDDBSNMCTYSQLDMYFGTP"
complement(1587..2681)
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complement(1587..2681)
/gene="AC1"
complement(1587..2681)
/note="AL1; REP gene"
/codon_start=1
/product="replication initiation protein AC1"
/protein_id="AAD47173.1"
/db_xref="GI:5702163"
/translation="MAPPKRKIOAKNYFTYPRCSLSKEDCLAQILNIOGPSNNKY
HVAELHEDGEPHLHVLVQPECKFYCTNSRPFDLVSPKRSNHFEPNITQAGSSSVYK
VYDKGQDITWGEFQVQDGRSARGQQTANDAAEALNLGSKSEALQIIRKLPEKYLE
QHNIVSNIDRISPPSPSYSSPSSSSFNVPDITISMAAENWDSARADRPISIVIS
IGSPRICTWARSLEDPHNYLTCGLHDLSPKYSANAYNVIDVNPQYLHAKFEFQMG
AKQMSQNKYCKYPRVIGGPTIFLCMGSESSKWLMDKPEQALKNNMPTANAIPE
DYQSPFVQOEYSHSGATARHGEQESS"
complement(2267..2524)
/gene="AC4"
complement(2267..2524)

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/gene="AC4"
/feature="AC1"
/codon_start=1
/product="AC4"
/protein_id="AAD47174.1"
/db_xref="GI:5702164"
/translation="MGNLTSMCKSSKANSSNOIADSSIMSHRTRITFTPTSELN
APMSPSTIRGIPSPGVNSRSTADLEASRLTLTPQRRL"
BASE COUNT      741 a      606 c      675 g      806 t
ORIGIN

alignment_scores:
  Quality: 277.00      Length: 68
  Ratio: 4.617      Gaps: 0
  Percent Similarity: 88.235      Percent Identity: 79.412

alignment_block:
US-09-289-346A-10 x AF104036/rev ..

Align seg 1/1 to reverse of: AF104036 from: 1 to: 2828

1 ThrLeuValTrpGlyIuphGlnValAspGlyArgSerAlaArgGlyI 17
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2354 ACCATCAGTGGGGGTGATTCAGGTCGACGAGATCTGTAGAGAGG 2305
17 yCysGlnThrSerAsnAspLeuLeuGluAlaLeuAsnAlaSerSerL 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2304 CCACGACAGCTGCTACGACGACCCGACGAGGCTTAACGCAAGTTCVA 2255
34 ySgIuGluAlaLeuGlnIleIleArgGluIlyIleProGluIlyTyLeu 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2254 AAGAAGCTGCGTTCATATATATCATCGAGAGAACTCCCTGAATAATTTA 2205
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspIlysth 67
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2204 TTTCATTTTCATATATTAGTTAGTAATTAGATAGATTTTCTCTCCTCC 2155
67 rPro 68
|||||
2154 ACCT 2151

seq_name: gb_v1:SGU67926

seq_documentation_block:
LOCUS      SGU67926      554 bp      DNA
DEFINITION Sida golden mosaic geminivirus Rep protein (AC1) gene, partial cds.
ACCESSION  U67926
VERSION    067926.1 GI:1546801
KEYWORDS
SOURCE
ORGANISM   sida golden mosaic virus.
            Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
REFERENCE
AUTHORS   Roye,M.E., McLaughlin,W.A., Nakhla,N.K. and Maxwell,D.P.
TITLE     Genetic diversity among geminiviruses associated with the weed
            species Sida spp. Macroptilium lathyroides, and Wissadula
            amplissima from Jamaica
            Plant Dis. 81, 1251-1258 (1997)
JOURNAL
AUTHORS   Roye,M.E., McLaughlin,W.A. and Maxwell,D.P.
TITLE     Direct Submission
JOURNAL   Submitted (23-AUG-1996) Plant Pathology, University of Wisconsin,
            1630 Linden Drive, Madison, WI 53706-1598, USA
FEATURES
SOURCE
1..554
/organism="sida golden mosaic virus"
/strain="Jamaica"
/isolate="Jamaica, May 1993"
/db_xref="taxon:51034"
/note="DNA A component"
complement(1..554)
gene
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CDS
complement(1..554)
/gene="AC1"
/feature="replication-associated protein"
/codon_start=1
/product="Rep protein"
/protein_id="AAB97865.1"
/db_xref="GI:1546802"
/translation="SISKEEALSQLQTLKTPVNNKFKIKICRELHNGEPHLVLIQPE
GKVCNTNRPFDVSPTRSYVHFHNIGGAASSDPKSYVERKDGPTIEWGFQIDGRSA
RGGOOTANDAAEALNSGTRKEDALKITREKLPERYTLFOYHNLSSNIDRITSKPEPWS
HPFPLPSTVAVPGQMEADYFGR"
BASE COUNT      121 a      127 c      139 g      167 t
ORIGIN

alignment_scores:
  Quality: 274.00      Length: 70
  Ratio: 4.349      Gaps: 0
  Percent Similarity: 90.000      Percent Identity: 70.000

alignment_block:
US-09-289-346A-10 x SGU67926/rev ..

Align seg 1/1 to reverse of: SGU67926 from: 1 to: 554

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|||||:|||||:|||||:|||||:|||||:|||||:|||||:
290 ACCATCAGATGGGGGTGTTCCAGATGACGAGAGAGATGCTGTGGAAG 241
17 yCysGlnThrSerAsnAspLeuLeuGluAlaLeuAsnAlaSerSerL 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
240 TCAGCAACACAGACTAACGACGACCGCGAGCATGTGATTCGTGAAACA 191
34 ySgIuGluAlaLeuGlnIleIleArgGluIlyIleProGluIlyTyLeu 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
190 AGGAGATGCACTGAATAATCATCAGAGAGAGTACACAGAAATATCTC 141
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspIlysth 67
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
140 TTTCATATATCACAACCTATTCAGTATTCAGATAGATTTTCAGTAAACC 91
67 rProGluPro 70
|||||
90 TCCAGAACCG 81

seq_name: gb_v1:IEI132548

seq_documentation_block:
LOCUS      IEI132548      2763 bp      DNA      circular      VRL
DEFINITION Ipomoea yellow vein virus V2, V1, C3 and C2 genes.
ACCESSION  AJ132548
VERSION    AJ132548.1 GI:4210720
KEYWORDS   C2 gene; C2 protein; C3 gene; C3 protein; coat protein; V1 gene; V2
            gene; V2 protein.
SOURCE
ORGANISM   Ipomoea yellow vein virus.
            Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
REFERENCE
AUTHORS   Banks,G.K.
TITLE     Direct Submission
JOURNAL   Submitted (26-JAN-1999) Banks G.K., Virus Research, John Innes
            Centre, Norwich Research Park, Colney Lane, Norwich, NR4 6UL, UK
REFERENCE
AUTHORS   Banks,G.K., Bedford,I.D., Bellita,F.J., Cerzo,E.R. and Markham,P.G.
TITLE     A novel geminivirus of Ipomoea indica (Convolvulaceae) from southern
            Spain
JOURNAL
AUTHORS
JOURNAL   unpublished
FEATURES
SOURCE
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/location/Qualifiers
/organism="Ipomoea yellow vein virus"
/virion
/species="Ipomoea indica"
/db_xref="taxon:87832"
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/ gene="V2"
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/protein_id="CAI0695.1"
/db_xref="GI:4210721"
/translation="MTLLYKDDSDRCRAMCSTAEEMDPLONPJPDITLYGPRCMLSVKY
LOGLIKYERGTGTCFELCSGLTIRFVRODRANSRAELISLMGTEGKTESLDSY
RAUHWCCPNCCKRLCGFKRRPDEKEG"
gene      1215..1979
/ gene="V1"
CDS       1215..1979
/ gene="V1"
/codon_start=1
/product="coat protein"
/protein_id="CAI0696.1"
/db_xref="GI:4210722"
/translation="MTGRIVSPRPHPGGROVRSNLLEAIPTVYGNAPVPIARSY
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GKRYCTKSMTIDCKVMMDVNAKRDHTNITTYLIRPRPKDPLNFGQIFMTDNEP
TIAKIRMDLDRMOVLKRFSTVYSGPYSHKEQALIKFCKLYNHVYNHKEAKYE
NOLENALMLYSASSHASNPHYQTLRCRAVEYDSHK"
gene      complement(1976..2413)
CDS       complement(1976..2413)
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/protein_id="CAI0697.1"
/db_xref="GI:4210723"
/translation="MDSRTGESLSHAQITRAAEFFNNMVSIGTAPFHLRLMYHTNN
IDSKTINKVOLQVHNRNRPETGPKITLOERITPTRLIGALPNMTGTSNRLKMRIGCS
LASIGYSLNENYVIRHLPOCLWEVEVDIDCKDIKVLV"
gene      complement(2127..2576)
CDS       complement(2127..2576)
/ gene="C2"
/codon_start=1
/product="C2 protein"
/protein_id="CAI0698.1"
/db_xref="GI:4210724"
/translation="MSTAPSGYKRCPCAPQEPHAAKRRKRPPEPRRIYMKCGCS
AFITNDCKFOHGTGHRGVTSCGTDESSRLIQSHVCGSDCTIPSTIDVCPYKPRLK
DDEHSASSQPPBEGNMIPEDLPIDPHTNASWCYSQLDWYQSP"
BASE COUNT 734 a 570 c 671 g 788 t
ORIGIN

alignment_scores:
Quality: 273.00 Length: 68
Ratio: 4.627 Gaps: 0
Percent Similarity: 86.765 Percent Identity: 76.471

alignment_block:
US-09-289-346a-10 x IYE132548/rev ..
Align seg 1/1 to reverse of: IYE132548 from: 1 to: 2763
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469 ACCCTCATATGGGTGATTCAGATCGACGAGATCTGTAGAGAGAG 420
17 yCysGlnThrSerAsnAspLeuLeuLeuGluAlaLeuAsnAlaSerSerL 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
419 TCACGACGTCTGTACGACGACGCCGACGAGCGCTAAACGCATGTTCTA 370
34 ysgluGluAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeu 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
369 AAGAACCTGCGTTGCAAAATTAATCAGGAGAAACTCCCTGAAAAATTTTA 320
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysThr 67

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319 TTTCAATATCATTAATTTAGTAGTATTAGATAGATTTTCTCCGCC 270
67 IPro 68
|||
269 TCCCT 266

seq_name: gb_v1:MGU75278
seq_documentation_block:
LOCUS MGU75278 447 bp DNA VRL 27-NOV-1996
DEFINITION Macropitillium golden mosaic geminivirus replication-associated
protein (AC1) gene, partial cds.
ACCESSION U75278
VERSION U75278.1 GI:1688188
KEYWORDS
SOURCE
ORGANISM
Macropitillium golden mosaic geminivirus.
Macropitillium golden mosaic geminivirus
viruses; ssDNA viruses; Geminiviridae; Begomovirus.
REFERENCE
1 (bases 1 to 447)
Royer, M.E., McLaughlin, W.A. and Maxwell, D.P.
Diversity and phylogeny of whitefly-transmitted geminiviruses from
Jamaica
JOURNAL Theis (1996)
REFERENCE 2 (bases 1 to 447)
Royer, M.E., McLaughlin, W.A. and Maxwell, D.P.
Three distinct geminiviruses infecting M. lathyrifolides from Jamaica
but not BGWV
JOURNAL Unpublished (1996)
REFERENCE 3 (bases 1 to 447)
Royer, M.E., McLaughlin, W.A. and Maxwell, D.P.
Direct Submission
JOURNAL Submitted (17-OCT-1996) Biochemistry, University of the West
Indies, Mona, Kingston 7, Jamaica
FEATURES
source
1..447
/organism="Macropitillium golden mosaic geminivirus"
/strain="Jamaican"
/isolate="2"
/db_xref="taxon:51676"
/clone="pmcJRA2"
/complement(1..447)
/ gene="AC1"
/complement(<1..>447)
/ gene="AC1"
/codon_start=1
/product="replication-associated protein"
/protein_id="FAB36919.1"
/db_xref="GI:1688189"
/translation="HVLIOFGKFNCTNNRLFDLVSPRSAAHFHPNIOGAKSSSDVKS
YVEDGDPTIEMGVFOIDGRSARGGQOONSNDAAEALNSGTRKKAAMRTVKKELPEKFLF
QYHNUSSNLDRTFKDPKDPENAPPPPLSSFTINVPDENQENATNTFGRG"
BASE COUNT 97 a 112 c 110 g 128 t
ORIGIN

alignment_scores:
Quality: 266.00 Length: 70
Ratio: 4.361 Gaps: 0
Percent Similarity: 87.143 Percent Identity: 68.571

alignment_block:
US-09-289-346a-10 x MGU75278/rev ..
Align seg 1/1 to reverse of: MGU75278 from: 1 to: 447
1 TTTLeuValTTPGlyGluPheGlnValaSPGlyArgSerAlaArgSyl 17
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
294 ACCATGCAATGGGAGTGTTCAGATCGACGAGAGAGTGTCTGAGAGCGG 245
17 yCysGlnThrSerAsnAspLeuLeuLeuGluAlaLeuAsnAlaSerSerL 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
244 TCAGCAACATCATACGATCGACGCCGACGACATTAATTTCTGCAACA 195

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34  YSGIUGLUALALEUGINILEIARGLULYSILPROGILYSTYRLEU 50
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
194 AGAGCGCGCCATGAGATAGTCAAGAGAGAGTCCGGAAGATTCTC 145

51  PHEGIPHEHISASLEUASNSERASLEUASPARILPEHASPLYSTH 67
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
144 TTTCATATTCACAACTATCCATGACTGATAGATTTTCTATGAAGCA 95

67  rPROGILUPRO 70
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
94 TCCGGAACCA 85

seq_name: gb_v1:AF098940

seq_documentation_block:
LOCUS      AF098940      1405 bp      DNA      04-MAR-1999
DEFINITION Macropitilium golden mosaic geminivirus strain Jamaica strain 1
            replication associated protein (rep) and coat protein (cp) genes,
            partial cds.
ACCESSION  AF098940
VERSION    AF098940.1  GI:4336584
KEYWORDS   Macropitilium golden mosaic geminivirus.
            Macropitilium golden mosaic geminivirus.
            Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
ORGANISM   1 (bases 1 to 1405)
            Roye, M.E.
REFERENCE  1
AUTHORS    Roye, M.E.
TITLE      Genetic diversity and phylogeny of whitefly-transmitted
            geminiviruses from Jamaica
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 1405)
AUTHORS    Roye, M.E., McLaughlin, W.A. and Maxwell, D.P.
TITLE      Molecular characterization of two distinct geminiviruses infecting
            M. lathyroides from Jamaica
JOURNAL    Unpublished
REFERENCE  3 (bases 1 to 1405)
AUTHORS    Roye, M.E., McLaughlin, W.A. and Maxwell, D.P.
TITLE      Direct Submission
JOURNAL    Submitted (14-OCT-1998) Biotechnology Centre, University of the
            West Indies, Mona, Kingston 7, Jamaica
FEATURES   Location/Qualifiers
            1..1405
             /organism="Macropitilium golden mosaic geminivirus"
             /strain="Jamaica strain 1"
             /specific_host="Macropitilium lathyroides"
             /db_xref="taxon:51676"
             /country="Jamaica"
             /clone="pmGUA3"
             /complement(<1..701)
             /gene="rep"
             /complement(<1..701)
             /gene="cp"
             /codon_start=1
             /product="replication associated protein"
             /protein_id="AAD17850.1"
             /db_xref="GI:4336586"
             /translation="MPKRGSPSIRKKNVFLTYPOCSILTKREALSOLTNLMPVKKPFI
            KICREPHEDGQPHLHLIOFGKFNENNRLLFDLVSPSRSAHFHNPLOGAKSSDVAS
            YVNDGDTIENGVIQIDGRSRGSGOOTSNDAAALNSGTREAMRIYKEKLPKFLF
            OYHNDSSMDRITFMKDPMPVAPPPPLSSFTVPEMOMADYFGRSAAAPERPMISI
            IVEGDSRTGKTMAC"
            702..1030
             /note="intergenic region"
             /length=1031..>1405
             /gene="cp"
             /db_xref="taxon:51676"
             /db_xref="GI:4336587"
             /codon_start=1
             /product="coat protein"
             /protein_id="AAD17849.1"
             /db_xref="GI:4336585"
             /translation="MPKRDGSMWRTTPGAVKVRRLNYSPPRGYGFPSNKAQEWVNRPM

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RRKRIYRLTSPDVRGCEGPCCKVOSYEQRRHDSHVGVKWCISDVTGCVITHRVK
RFCVKFYLIGKIMDENINCS"
BASE COUNT      328 a      333 c      357 g      386 t      1 others
ORIGIN

alignment_scores:
    Quality:      266.00      Length:      70
    Ratio:        4.361      Gaps:      0
    Percent Similarity: 87.143      Percent Identity: 68.571

alignment_block:
US-09-289-346a-10 x AF098940/rev ..

Align seg 1/1 to reverse of: AF098940 from: 1 to: 1405

1  ThrLeuValTrpGlyGluPheGlnValAspGlyArgSerAlaArgGly 17
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
374 ACCATCGAATGGGAGGTGTTCCAGATCGACGAGAGAGAGTCTCGAGCGG 325

17  ycygginphrserasnaspheuleuleuleuglualeuasnalserserl 34
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
324 TCAGCAACATCTTAACGATGCAGCCGCCGACACATTAATTCTGGAACAA 275

34  YSGIUGLUALALEUGINILEIARGLULYSILPROGILYSTYRLEU 50
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
274 AGAGCGCGCCATGAGATAGTCAAGAGAGAGTCCGGAAGATTCTC 225

51  PHEGIPHEHISASLEUASNSERASLEUASPARILPEHASPLYSTH 67
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
224 TTTCATATTCACAACTATCCATGACTGATAGATTTTCTATGAAGCA 175

67  rPROGILUPRO 70
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
174 TCCGGAACCA 165

seq_name: gb_v1:AB001315

seq_documentation_block:
LOCUS      AB001315      570 bp      DNA      13-FEB-1999
DEFINITION Tobacco leaf curl virus CI and C4 genes, clone YOKOHAMA3-1, partial
            and complete cds.
ACCESSION  AB001315
VERSION    AB001315.1  GI:3798714
KEYWORDS   Tobacco leaf curl virus
            Tobacco leaf curl virus
            Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
ORGANISM   1 (bases 1 to 570)
            Ooi, K.
REFERENCE  1
AUTHORS    Ooi, K.
TITLE      Direct Submission
JOURNAL    Submitted (19-FEB-1997) to the DDBJ/EMBL/Genbank databases.
            Kazuyuki Ooi, Kyushu University, Department of Biology, 6-10-1
            Hakozaki Higashi-ku, Fukuoka, Fukuoka 812, Japan
            (E-mail: kooi@scdbbox.nc.kyushu-u.ac.jp, Tel: +81-92-642-2624,
            Fax: +81-92-642-2645)
            2 (bases 1 to 570)
            Ooi, K., Ohshita, S., Ishii, I. and Yahara, T.
            Molecular phylogeny of geminiviruses infecting wild plants in Japan
            J. Plant Res. 110, 247-257 (1997)
FEATURES   Location/Qualifiers
            1..570
             /organism="tobacco leaf curl virus"
             /isolate="YOKOHAMA3"
             /specific_host="Eupatorium makinoi"
             /db_xref="taxon:67762"
             /clone="YOKOHAMA3-1"
             /complement(1..570)
             /gene="CI"
             /complement(<1..>570)
             /gene="CI"
             /codon_start=1

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```

/protein_id="BA34033.1"
/db_xref="GI:4426541"
/translation="EALISOLQNIPTNKLTKICRELHDDGSPHLVLLQEGKVK
CONRRPFDIVSPTRSAHPHIOGAKSSSVKSYIDKDGTLPMGTFOIDGRSARGC
ONANDACAEALNMSKAEALATIREKLPKPIFYQYHNLSNLDRIAPLPLEVVCPT
ASSFDQVPEELEWASENVMSAPARWRP"
gene
complement(231..488)
/feature="C4"
complement(231..488)
CDS
complement(231..488)
/feature="C4"
/codon_start=1
/protein_id="BA34034.1"
/db_xref="GI:3798715"
/translation="MEALISMCFSCSSKANTNAKITDSWTYPOPDHISIRPRELNP
APTSPTSTETIRSNCEHSRSTEEVELEAARMLTTHVQR"
BASE COUNT      141 a      121 c      126 g      182 t
ORIGIN

alignment_scores:
Quality: 261.00      Length: 85
Ratio: 4.279      Gaps: 1
Percent Similarity: 71.765      Percent Identity: 60.000

alignment_block:
US-09-289-346A-10 x AB001315/rev ..

Align seg 1/1 to reverse of: AB001315 from: 1 to: 570

1 ThrLeuValTTPGlyGluPheGlnValAlaSpGlyArgSerAlaArgGly 17
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
318 ACGCTCGAATGGGGAACATTCAGATCGACGAGAGAGTCTAAGAGAGG 269
17 yGysGlnThrSerAsnAspLeuLeuLeuGluAlaLeuAsnAlaSerSerL 34
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
268 CTGCCAGAAATGCTAACGACGATGTCAGAGGCGTTAAATGCAAGTCTTA 219
34 yGluGluAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeu 50
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
218 AGCGACAGACCATTTAGCAATATTAGGAGAAAGCTCCCTTAAGATTATTA 169
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIle..... 63
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
168 TTTCATATATCAATATTAAATAGTATTAGATAGGATTTTTCCTCTCC 119
64 ..... PheAspLysThrP 68
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
118 GTTGGAGGTTTGTGCTTTCACAGCCTCATCTTTCATCAAGTTC 69
68 roGlu 69
|||||
68 CAGAA 64

seq_name: gb_v1:AB001318
seq_documentation_block:
LOCUS AB001318 570 bp DNA VRL 13-FEB-1999
DEFINITION Tobacco leaf curl virus C1 and C4 genes, clone YOKOHAMA5-2, partial
and complete cds.
ACCESSION AB001318
VERSION AB001318.1 GI:3798720
KEYWORDS tobacco leaf curl virus (isolate:YOKOHAMA5,
specific_host:Eupatorium makinoi) DNA, clone:YOKOHAMA5-2,
tobacco leaf curl virus
Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
ORGANISM
Ooi,K.
REFERENCE
Submitted (19-FEB-1997) to the DDBJ/EMBL/GenBank databases.
AUTHORS Kazuyuki Ooi, Kyushu University, Department of Biology, 6-10-1
Hakozaki Higashi-ku, Fukuoka 812, Japan
JOURNAL (E-mail:kooi@scbembex.nc.kyushu-u.ac.jp, Tel:+81-92-642-2624,

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REFERENCE
2 (bases 1 to 570)
AUTHORS Ooi,K., Ohshita,S., Ishii,I. and Yahara,T.
TITLE Molecular phylogeny of geminiviruses infecting wild plants in Japan
JOURNAL J. Plant Res. 110, 247-257 (1997)
FEATURES
Location/Qualifiers
1..570
/organism="tobacco leaf curl virus"
/isolate="YOKOHAMA5"
/specific_host="Eupatorium makinoi"
/db_xref="taxon:67762"
/clone="YOKOHAMA5-2"
complement(1..570)
/gene="C1"
complement(<1..>570)
CDS
complement(1..570)
/gene="C1"
/codon_start=1
/protein_id="BA34039.1"
/db_xref="GI:4426544"
/translation="EALISOLQNIPTNKLTKICRELHDDGSPHLVLLQEGKVK
CONRRPFDIVSPTRSAHPHIOGAKSSSVKSYIDKDGTLPMGTFOIDGRSARGC
ONANDACAEALNMSKAEALATIREKLPKPIFYQYHNLSNLDRIAPLPLEVVCPT
ASSFDQVPEELEWASENVMSAPARWRP"
gene
complement(231..488)
/feature="C4"
complement(231..488)
CDS
complement(231..488)
/feature="C4"
/codon_start=1
/protein_id="BA34040.1"
/db_xref="GI:3798721"
/translation="MEALISMCFSCSSKANTNAKITDSWTYPOPDHISIRPRELNP
APTSPTSTETIRSNCEHSRSTEEVELEAARMLTTHVQR"
BASE COUNT      140 a      121 c      129 g      180 t
ORIGIN

alignment_scores:
Quality: 261.00      Length: 85
Ratio: 4.279      Gaps: 1
Percent Similarity: 71.765      Percent Identity: 60.000

alignment_block:
US-09-289-346A-10 x AB001318/rev ..

Align seg 1/1 to reverse of: AB001318 from: 1 to: 570

1 ThrLeuValTTPGlyGluPheGlnValAlaSpGlyArgSerAlaArgGly 17
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
318 ACGCTCGAATGGGGAACATTCAGATCGACGAGAGAGTCTAAGAGAGG 269
17 yGysGlnThrSerAsnAspLeuLeuLeuGluAlaLeuAsnAlaSerSerL 34
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
268 CTGCCAGAAATGCTAACGACGATGTCAGAGGCGTTAAATGCAAGTCTTA 219
34 yGluGluAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeu 50
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
218 AGCGACAGACCATTTAGCAATATTAGGAGAAAGCTCCCTTAAGATTATTA 169
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIle..... 63
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
168 TTTCATATATCAATATTAAATAGTATTAGATAGGATTTTTCCTCTCC 119
64 ..... PheAspLysThrP 68
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
118 GTTGGAGGTTTGTGCTTTCACAGCCTCATCTTTCATCAAGTTC 69
68 roGlu 69
|||||
68 CAGAA 64

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```

alignment_scores:      Quality: 235.00      Length: 85
                       Ratio: 3.852      Gaps: 1
Percent Similarity: 71.765      Percent Identity: 54.118

alignment_block:
US-09-289-346a-10 x AA084371 ..

Align seg 1/1 to: AA084371 from: 1 to: 434

1 ThleuValTrpGlyLupheGlnValAspGlyArgSerAlaArgGlyG1 17
||||| ||||||| ||||||| ||||||| ||||||| |||||||
95 ACCCTGCAATGGGAGAGTTTACGATCGAGCATCTGCAGAGGGG 144
17 YCysGlnThrSerAsnAspleuLeuGluAlaLeuAsnAlaSerSerL 34
||||| ||||||| ||||||| ||||||| ||||||| |||||||
145 ACAACAAATCAGCCATGACGCTTACGCCCGCTTACACATCGAAGTA 194
34 YsgGluAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeu 50
||||| ||||||| ||||||| ||||||| ||||||| |||||||
195 AGTCAGAGGCTTTACGCTTTAGGGAATTAGCCCTTAAGAGATTATGTT 244
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIle..... 63
||||| ||||||| ||||||| ||||||| ||||||| |||||||
245 TTACAATTTCATATTAATTAATAGTAATTTAGATAGATTTTACACCTCC 294
64 ..... PheAspLysThrP 68
||||| ||||||| ||||||| ||||||| ||||||| |||||||
295 GTTGGAGGTTTATGTTTCCTTTTATCTCTTCTTTGATGACGAGTTC 344
68 roglu 69
|||||
345 CAGAA 394

seq_name: /cgnl_8/gcgdata/geneseq/geneseqn/NA1995.DAT:AA084372
seq_documentation_block:
ID AA084372 standard: DNA; 479 BP.

XX AC AA084372;
XX AC 19-AUG-1995 (first entry)
XX DE Gemini virus-specific poly(ribozyme)-F target sequence.
XX KW ribozyme target sequence: poly(ribozyme)-F;
XX KW tomato leaf curl virus; RNA cleavage; tomato transgenic plant;
XX KW virus disease-resistance; ss.
XX OS Tomato leaf curl virus.
XX FH Key Location/Qualifiers
FH FT misc_feature 46..96
FT FT misc_feature /tag= a
FT FT misc_feature /note= "ribozyme R4-R5 target sequence"
FT FT misc_feature 58..60
FT FT misc_feature /tag= b
FT FT misc_feature /note= "ribozyme R4 cleavage site"
FT FT misc_feature 81..83
FT FT misc_feature /tag= c
FT FT misc_feature /note= "ribozyme R5 cleavage site"
FT FT misc_feature 356..386
FT FT misc_feature /tag= d
FT FT misc_feature /note= "ribozyme R2 target sequence"
FT FT misc_feature 370..372
FT FT misc_feature /tag= c
FT FT misc_feature /note= "ribozyme R2 cleavage site"
FT FT misc_feature 429..459
FT FT misc_feature /tag= e
FT FT misc_feature /note= "ribozyme R3 target sequence"
FT FT misc_feature 442..444

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```

FT FT /*tag= d
FT FT /note= "ribozyme R3 cleavage site"
XX XX
XX XX MO9503404-A.
XX XX 02-FEB-1995.
XX XX 22-JUL-1993; 93WO-EP01946.
XX XX 22-JUL-1993; 93AU-0047014.
XX XX 22-JUL-1993; 93WO-EP01946.
XX XX
XX XX (BIOC-) BIOCEM SA.
XX XX (CSTR ) COMMONWEALTH SCI & IND RES ORG.
XX XX Baudino S, Comeau D, Dry IB, Gruber V, Lenee P;
XX XX Mason J, Rezalan MA, Rlyden JE, Rezalan MA.
XX XX WPI: 1995-075232/10.
XX XX
XX XX Synthetic DNA virus ribozyme(s) - reduce replication, infection
XX XX and/or assembly of viruses by cleaving target virus sequence,
XX XX useful for preparing resistant plants, esp tomatoes.
XX XX
XX XX Example 10: Fig 11c: 90pp: English.
XX XX
XX XX The sequence is a tomato leaf curl virus target sequence for
XX XX poly(ribozyme)-F, which hybridizes to and cleaves the sequence and
XX XX thereby reduces replication, infection and/or assembly of the virus
XX XX CC substantially. The ribozyme may be expressed in a transgenic plant,
XX XX CC e.g. tomato, to confer virus disease-resistance.
XX XX
XX XX Sequence 479 BP; 145 A; 95 C; 97 G; 142 T; 0 other;

alignment_scores:      Quality: 235.00      Length: 85
                       Ratio: 3.852      Gaps: 1
Percent Similarity: 71.765      Percent Identity: 54.118

alignment_block:
US-09-289-346a-10 x AA084372 ..

Align seg 1/1 to: AA084372 from: 1 to: 479

1 ThleuValTrpGlyLupheGlnValAspGlyArgSerAlaArgGlyG1 17
||||| ||||||| ||||||| ||||||| ||||||| |||||||
140 ACCCTGCAATGGGAGAGTTTACGATCGAGCATCTGCAGAGGGG 189
17 YCysGlnThrSerAsnAspleuLeuGluAlaLeuAsnAlaSerSerL 34
||||| ||||||| ||||||| ||||||| ||||||| |||||||
190 ACAACAAATCAGCCATGACGCTTACGCCCGCTTACACATCGAAGTA 239
34 YsgGluAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeu 50
||||| ||||||| ||||||| ||||||| ||||||| |||||||
240 AGRCAAGAGGCTTTACGCTTACGGAATTAGCCCTTAAGATTTATGTT 289
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIle..... 63
||||| ||||||| ||||||| ||||||| ||||||| |||||||
290 TTACAATTTCATATTAATTAATAGTAATTTAGATAGATTTTACACCTCC 339
64 ..... PheAspLysThrP 68
||||| ||||||| ||||||| ||||||| ||||||| |||||||
340 GTTGGAGGTTTATGTTTCCTTTTATCTCTTCTTTGATGACGAGTTC 389
68 roglu 69
|||||
390 CAGAA 394

seq_name: /cgnl_8/gcgdata/geneseq/geneseqn/NA1995.DAT:AA084375
seq_documentation_block:
ID AA084375 standard: DNA; 550 BP.

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XX AA084375;
AC
XX
XX 19-AUG-1995 (first entry)
DT
XX Tomato leaf curl virus Australian strain DNA sequence.
DE
XX Tomato leaf curl virus; Australia strain; plant disease; ds.
KM
XX Tomato leaf curl virus (Australia).
OS
XX WO9503404-A.
PN
XX 02-FEB-1995.
PD
XX 22-JUL-1993; 93WO-EP01946.
PF
XX 22-JUL-1993; 93AU-0047014.
PR
XX 22-JUL-1993; 93WO-EP01946.
XX
XX (BIOC-) BIOCEM SA.
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX
XX Baugino S, Comeau D, Dry IB, Gruber V, Lence P;
PI Mason J, Rezaiian MA, Rigden JE, Rezaiian MA;
XX
XX WPI: 1995-075232/10.
DR
XX
XX Synthetic DNA virus ribozyme(s) - reduce replication, infection
PT and/or assembly of viruses by cleaving target virus sequence,
PT useful for preparing resistant plants, esp tomatoes.
XX
XX Disclosure: Fig 1: 90pp; English.
XX
CC The sequence represents the complementary sense DNA strand of an
CC Australian strain of tomato leaf curl virus. Ribozymes specific
CC for this sequence may be used in generation of transgenic plants
CC with disease-resistance.
XX
XX Sequence 550 BP; 148 A; 120 C; 134 G; 142 T; 6 other;
SQ
alignment_scores:
Quality: 234.50 Length: 86
Ratio: 3.844 Gaps: 1
Percent Similarity: 70.930 Percent Identity: 53.488
alignment_block:
US-09-289-346A-10 x AA084375 ..
Align seg 1/1 to: AA084375 from: 1 to: 550
1 ThleuValtTrrpGlyGluPheGlnValAspGlyArgSerAlaArgGlyGly 17
||||| ||||||||| ||||||||| ||||||||| |||||||||
201 ACCCTCGAATGGGGAGAGTTTCAGATCGATGAGATCTCCAGAGGGG 250
17 YCYGlnThrSerAsnAspLeuLeuGlnAlaLeuAsnAlaSerSerL 34
| ||||| ||||| ||||| ||||| ||||| ||||| |||||
251 ACACACATTCAGCCATGACGCTTACGCCCGCTTAACACATGGAAGTA 300
34 ysglGlnAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeu 50
| ||||| ||||| ||||| ||||| ||||| ||||| |||||
301 AGTCAGAGCGCTTAAGCTCTTAGGAATTTACCCCTAAGATTATGTT 350
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIle..... 63
| ||||| ||||| ||||| ||||| ||||| ||||| |||||
351 TTACAATTTCATTAATTAAATAGTAATTAGATGATTTNNNTACACC 400
64 ..... PheAspLysT 67
401 TCCGTTGAGAGTTTATGTTCTTCCTTTTATCTCTTCTTTGATCGAG 450
67 hrProGlu 69

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451 TTCCAGAA 458
::|||
seq_name: /cgnl_8/gcgdata/geneseq/geneseqn/NA1997.DAT:AA793317
seq_documentation_block:
ID AA793317 standard: DNA: 2744 BP.
XX
XX AA793317;
XX
XX 27-APR-1998 (first entry)
DT
XX Tomato leaf curl virus from Southern India (stem-loop begin).
DE
XX Geminiivirus; TLGV-IND; AC1 gene; transdominant mutation;
XX transgenic plant; disease resistance; ss; cyclic; circular.
XX
XX Tomato leaf curl virus from Southern India.
OS
XX WO9739110-A1.
PN
XX 23-OCT-1997.
PD
XX 15-APR-1997; 97WO-US06300.
PF
XX 16-APR-1996; 96US-0015517.
PR
XX
XX (SEMI-) SEMINIS VEGETABLE SEEDS INC.
PA (WISC) WISCONSIN AUTOMNI RES FOUND.
XX
XX Ahlquist PG, Hanson SF, Luu HT, Maxwell DP, Stout JT;
XX
XX WPI: 1997-526447/48.
DR
XX
XX Transgenic plants expressing geminivirus AC1 and CI wild-type and
PT mutant genes - have increased resistance to geminivirus infection
PT e.g. tomato mottle virus, tomato yellow leaf curl virus or bean
XX golden mosaic geminivirus
XX
XX Disclosure: Page 119-121; 132pp; English.
XX
CC This genomic DNA sequence comprises a full-length sequence
CC (stem-loop begin) from a tomato leaf curl virus from Southern
CC India. The invention involves production of transgenic plants
CC containing DNA comprising geminivirus AC1 or CI wild-type or mutant
CC sequences (see AA793282-93) that negatively interfere in trans with
CC geminiviral replication during infection. Such transgenic plants
CC are resistant to viral infection. The AC1/CI genes are especially
CC from tomato mottle virus, tomato yellow leaf curl virus or bean
CC golden mosaic virus.
XX
XX Sequence 2744 BP; 742 A; 539 C; 637 G; 826 T; 0 other;
SQ
alignment_scores:
Quality: 232.00 Length: 65
Ratio: 4.296 Gaps: 1
Percent Similarity: 83.077 Percent Identity: 69.231
alignment_block:
US-09-289-346A-10 x AA793317/rev ..
Align seg 1/1 to reverse of: AA793317 from: 1 to: 2744
4 TrrpGlyGlnPheGlnValAspGlyArgSerAlaArgGlyGlyCysGlnTh 20
||||| ||||||||| ||||||||| ||||||||| ||||
2266 TGGGGTGGAGTTTCAGATCGATGAGATCTCCAGAGAGTCACACAGAC 2217
20 rSerAsnAspLeuLeuGlnAlaLeuAsnAlaSerSerLysGluGluA 37
| ||||| ||||| ||||| ||||| ||||| |||||
2216 ACCTAATGATGCTCCGCGAGAGCCCTTAATGACAGTTCAAGCTGAAGC 2167
37 lalGlnIleIleArgGluLysIleProGluLysTyrLeuPheGlnPhe 53

```



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1 ThrLeuValTrpGlyGluPheGlnValAspGlyArgSerAlaArgGly 17
||||| ||||||| ||||||| ||||||| ||||||| |||||||
328 ACNATCGATGGGACATTCACAGTCGACGCGACATCTGCCAAGAGG 377
17 yCysGlnThrSerAsnAspLeuLeuGlnAlaLeuAsnAlaSerSer 34
||||| ||||||| ||||||| ||||||| ||||||| |||||||
378 TCAGCAGTCTGCCACGACTCATATGCAAGCATTAACGCGATTTCAA 427
34 ySgLUAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeu 50
||||| ||||||| ||||||| ||||||| ||||||| |||||||
428 TTGAATCTGCTTGACAAATATGAAAGAACACACCAAGATTACGTC 477
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLys 67
||||| ||||||| ||||||| ||||||| ||||||| |||||||
478 CTTCAACATCACAACATCCGTTCTATCTCGAAGCATCTTCGTCNAA 527
67 rProGluPro 70
||||| |||||||
528 GCCGGAACCA 537

seq_name: /cgnl_8/gcgdata/geneseq/geneseq/NA1997.DAT:AA193292
seq_documentation_block:
ID AA193292 standard; DNA; 1062 BP.
XX
AC AA193292:
XX
XX 27-APR-1998 (first entry)
XX
XX Bean golden mosaic geminivirus CI mutant ORF BGAC228.
XX
XX Geminivirus; BGWV; CI gene; transdominant mutation;
XX transgenic plant; disease resistance; ss: cyclic; circular.
XX
XX Bean golden mosaic virus type II isolate Guatemala.
XX
XX WO9739110-A1.
XX
XX 23-OCT-1997.
XX
XX 15-APR-1997; 97WO-US06300.
XX
XX 16-APR-1996; 96US-0015517.
XX
XX (SEMI-) SEMINIS VEGETABLE SEEDS INC.
XX (WISC ) WISCONSIN ALUMNI RES FOUND.
XX
XX Ahlquist PG, Hanson SF, Luu HT, Maxwell DP, Stout JT;
XX
XX WPI: 1997-526447/48.
XX P-PSDB: AAW34334.
XX
XX Transgenic plants expressing geminivirus AC1 and CI wild-type and
XX mutant genes - have increased resistance to geminivirus infection
XX e.g. tomato mottle virus, tomato yellow leaf curl virus or bean
XX golden mosaic geminivirus
XX
XX Claim 13; Page 111-112; 132pp; English.
XX
XX This DNA sequence comprises construct BGAC228 that codes for a
XX transdominant lethal mutant (see AAW34334) of the CI protein (see
XX AAW34338) of bean golden mosaic virus (BGWV). It was obtained by
XX Kunkel mutagenesis of the wild-type CI gene (see AA193314). CI is
XX required for replication. The invention involves production of
XX transgenic plants containing DNA comprising geminivirus CI or AC1
XX wild-type or mutant sequences that negatively interfere in trans
XX with geminiviral replication during infection. Such transgenic
XX plants are resistant to viral infection. The AC1/CI genes are
XX especially from BGWV, tomato mottle virus or tomato yellow leaf
XX curl virus (see AA193282-93) and encode polypeptides (see AAW34324-35)
XX that have mutations in the highly conserved DNA-nicking and/or the
XX NTP-binding domains.

```

```

XX
SQ Sequence 1062 BP; 338 A; 247 C; 218 G; 259 T; 0 other;

alignment_scores:
Quality: 223.00 Length: 70
Ratio: 3.780 Gaps: 0
Percent Similarity: 84.286 Percent Identity: 60.000

alignment_block:
US-09-289-346A-10 x AA193292 ..
Align seg 1/1 to: AA193292 from: 1 to: 1062

1 ThrLeuValTrpGlyGluPheGlnValAspGlyArgSerAlaArgGly 17
||||| ||||||| ||||||| ||||||| ||||||| |||||||
328 ACNATCGATGGGACATTCACAGTCGACGCGACATCTGCCAAGAGG 377
17 yCysGlnThrSerAsnAspLeuLeuGlnAlaLeuAsnAlaSerSer 34
||||| ||||||| ||||||| ||||||| ||||||| |||||||
378 TCAGCAGTCTGCCACGACTCATATGCAAGCATTAACGCGATTTCAA 427
34 ySgLUAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeu 50
||||| ||||||| ||||||| ||||||| ||||||| |||||||
428 TTGAATCTGCTTGACAAATATGAAAGAACACACCAAGATTACGTC 477
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLys 67
||||| ||||||| ||||||| ||||||| ||||||| |||||||
478 CTTCAACATCACAACATCCGTTCTATCTCGAAGCATCTTCGTCNAA 527
67 rProGluPro 70
||||| |||||||
528 GCCGGAACCA 537

seq_name: /cgnl_8/gcgdata/geneseq/geneseq/NA1997.DAT:AA193293
seq_documentation_block:
ID AA193293 standard; DNA; 1062 BP.
XX
AC AA193293:
XX
XX 27-APR-1998 (first entry)
XX
XX Bean golden mosaic geminivirus CI mutant ORF BGAC262.
XX
XX Geminivirus; BGWV; CI gene; transdominant mutation;
XX transgenic plant; disease resistance; ss: cyclic; circular.
XX
XX Bean golden mosaic virus type II isolate Guatemala.
XX
XX WO9739110-A1.
XX
XX 23-OCT-1997.
XX
XX 15-APR-1997; 97WO-US06300.
XX
XX 16-APR-1996; 96US-0015517.
XX
XX (SEMI-) SEMINIS VEGETABLE SEEDS INC.
XX (WISC ) WISCONSIN ALUMNI RES FOUND.
XX
XX Ahlquist PG, Hanson SF, Luu HT, Maxwell DP, Stout JT;
XX
XX WPI: 1997-526447/48.
XX P-PSDB: AAW34335.
XX
XX Transgenic plants expressing geminivirus AC1 and CI wild-type and
XX mutant genes - have increased resistance to geminivirus infection
XX e.g. tomato mottle virus, tomato yellow leaf curl virus or bean
XX golden mosaic geminivirus
XX
XX Claim 13; Page 115-116; 132pp; English.
XX

```

CC This DNA sequence comprises construct BGAC262 that codes for a
 CC transdominant lethal mutant (see AAM34335) of the CI protein (see
 CC AAM34338) of bean golden mosaic virus (BGMV). It was obtained by
 CC Kunzel mutagenesis of the wild-type CI gene (see AAT93314). CI is
 CC required for replication. The invention involves production of
 CC transgenic plants containing DNA comprising geminivirus CI or AC1
 CC wild-type or mutant sequences that negatively interfere in trans
 CC with geminiviral replication during infection. Such transgenic
 CC plants are resistant to viral infection. The AC1/CI genes are
 CC especially from BGMV, tomato mottle virus or tomato yellow leaf
 CC curl virus (see AAT93282-93) and encode polypeptides (see AAM34324-35)
 CC that have mutations in the highly conserved DNA-nicking and/or the
 CC NTP-binding domains.

XX Sequence 1062 BP: 340 A; 245 C; 219 G; 258 T; 0 other:

alignment_scores:

Quality:	223.00	Length:	70
Ratio:	3.780	Gaps:	0
Percent Similarity:	84.286	Percent Identity:	60.000

alignment_block:

US-09-289-346A-10 x AAT93293 ..

Align seg 1/1 to: AAT93293 from: 1 to: 1062

```

1  ThrleuValTTPGlyGluPheGlnValAspGlyValArgSerAlaArgGlyG1 17
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
328 ACAATCGAATGGGACATTCGACGCGCATTCGCAAGGAGG 377
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17  YCysGlnThrSerAsnSpleuLeuGluAlaLeuAsnAlaSerSerL 34
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
378 TCACGACGTCGCCAACGACATCATGCAAGGACATTAACCGACAGTTCAA 427
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
34  YSGluGluAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeu 50
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
428 TTGATATCGCTTGACATATTGAAGGAAGAACCAAGCAATTAACGTC 477
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
51  PheGlnPheHisAsnLeuAsnSerAsnLeuAsnSparGlyIlePheAspLysTh 67
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
478 CTTCAACATCCACACATCCGTTCTAATCTCGAACGGATCTTCGTCAGAGT 527
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
67  rProGluPro 70
   |||:|||||:
528 GCCGGAACCA 537

```

seq_name: /cgml_8/gcgcdata/geneseq/geneseqn/NA1997.DAT:AAT93314

seq_documentation_block:

ID AAT93314 standard; DNA: 1183 BP.

XX AAT93314:

DT 27-APR-1998 (first entry)

XX Bean golden mosaic geminivirus CI open reading frame.

XX Geminivirus; BGMV; CI gene; transdominant mutation;

XX transgenic plant; disease resistance; ss; cyclic; circular.

XX Bean golden mosaic virus type II isolate Guatemala.

XX Key Location/Qualifiers

FT CDS 1..1062

XX MO9739110-A1.

XX 23-OCT-1997.

PF 15-APR-1997; 97WO-US06300.

XX

PR 16-APR-1996; 96US-0015517.

XX (SEMT-) SEMINIS VEGGETABLE SEEDS INC.

PA (WISC) WISCONSIN ALUMNI RES FOUND.

PI Ahlquist PG, Hanson SF, Lou HT, Maxwell DP, Stout JT;

DR WPI: 1997-526447/48.

XX P-PSDB; AAM34338.

XX Transgenic plants expressing geminivirus AC1 and CI wild-type and

PT mutant genes - have increased resistance to geminivirus infection

PT e.g. tomato mottle virus, tomato yellow leaf curl virus or bean

PT golden mosaic geminivirus

XX Example 5; Page 100-102; 132pp; English.

CC This genomic DNA sequence includes the open reading frame (ORF) of
 CC the wild-type CI gene of bean golden mosaic virus (BGMV), a
 CC geminivirus that has a monopartite genome. The CI protein (see
 CC AAM34338) is required for replication. The wild-type CI ORF was
 CC subjected to Kunzel mutagenesis (see AAT93290-93). The invention
 CC involves production of transgenic plants containing DNA comprising
 CC CI or AC1 wild-type or mutant sequences that negatively interfere
 CC in trans with geminiviral replication during infection. Such
 CC transgenic plants are resistant to viral infection. The AC1/CI
 CC genes are especially from BGMV, tomato mottle virus or tomato
 CC yellow leaf curl virus (see AAT93282-93) and encode polypeptides
 CC (see AAM34324-35) that have mutations in the highly conserved
 CC DNA-nicking domain and/or the NTP-binding domains.

XX Sequence 1183 BP: 372 A; 276 C; 248 G; 287 T; 0 other:

alignment_scores:

Quality:	223.00	Length:	70
Ratio:	3.780	Gaps:	0
Percent Similarity:	84.286	Percent Identity:	60.000

alignment_block:

US-09-289-346A-10 x AAT93314 ..

Align seg 1/1 to: AAT93314 from: 1 to: 1183

```

1  ThrleuValTTPGlyGluPheGlnValAspGlyValArgSerAlaArgGlyG1 17
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
328 ACAATCGAATGGGACATTCGACGCGCATTCGCAAGGAGG 377
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17  YCysGlnThrSerAsnSpleuLeuGluAlaLeuAsnAlaSerSerL 34
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
378 TCACGACGTCGCCAACGACATCATGCAAGGACATTAACCGACAGTTCAA 427
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
34  YSGluGluAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeu 50
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
428 TTGATATCGCTTGACATATTGAAGGAAGAACCAAGCAATTAACGTC 477
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
51  PheGlnPheHisAsnLeuAsnSerAsnLeuAsnSparGlyIlePheAspLysTh 67
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
478 CTTCAACATCCACACATCCGTTCTAATCTCGAACGGATCTTCGTCAGAGT 527
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
67  rProGluPro 70
   |||:|||||:
528 GCCGGAACCA 537

```

seq_name: /cgml_8/gcgcdata/geneseq/geneseqn/NA1997.DAT:AAT93290

seq_documentation_block:

ID AAT93290 standard; DNA: 1183 BP.

XX AAT93290:

DT 27-APR-1998 (first entry)

XX

```

DE  Bean golden mosaic geminivirus CI mutant gene.
XX
XX  Geminivirus; BGMV; CI gene; transdominant mutation;
KW  transgenic plant; disease resistance; ss: cyclic; circular.
XX
OS  Bean golden mosaic virus type II isolate Guatemala.
XX
XX  Key      Location/Qualifiers
FH  CDS      1..1062
FT          /*tag= a
XX
XX  WO9739110-A1.
XX
XX  23-OCT-1997.
XX
XX  15-APR-1997; 97WO-US06300.
XX
XX  16-APR-1996; 96US-0015517.
XX
XX  (SEMI-) SEMINIS VEGETABLE SEEDS INC.
PA  (MISC) WISCONSIN ALUMNI RES FOUND.
XX
XX  Ahlquist PG, Hanson SF, Luu HT, Maxwell DP, Stout JT;
PI  WPI; 1997-526447/48.
XX  P-PSDB; AAW34332.
XX
XX  Transgenic plants expressing geminivirus AC1 and CI wild-type and
PT  mutant genes - have increased resistance to geminivirus infection
PT  e.g. tomato mottle virus, tomato yellow leaf curl virus or bean
XX  golden mosaic geminivirus
XX
XX  Claim 13; Page 103-105; 132pp; English.
XX
XX  This DNA sequence comprises construct BGAC190 that codes for a
CC  control mutant (see AAW34332) of the CI protein (see AAW34338) of bean
CC  golden mosaic virus (BGMV). It was obtained by Kunkel mutagenesis
CC  of the wild-type CI gene (see AAT93314). CI is required for
CC  replication. The invention involves production of transgenic
CC  plants containing DNA comprising geminivirus CI or AC1 wild-type or
CC  mutant sequences that negatively interfere in trans with
CC  geminiviral replication during infection. Such transgenic plants
CC  are resistant to viral infection. The AC1/CI genes are especially
CC  from BGMV, tomato mottle virus or tomato yellow leaf curl virus (see
CC  AAT93282-93) and encode polypeptides (see AAW34324-35) that have
CC  mutations in the highly conserved DNA-nicking and/or the NTP-binding
CC  domains.
XX
XX  Sequence 1183 BP; 371 A; 277 C; 249 G; 286 T; 0 other;
SO

```

```

alignment_scores:      Quality: 223.00      Length: 70
                        Ratio: 3.780      Gaps: 0
Percent Similarity: 84.286      Percent Identity: 60.000

```

alignment_block:

US-09-289-346a-10 x AAT93290 ..

Align seg 1/1 to: AAT93290 from: 1 to: 1183

```

1  ThtleuValTrpGlyGluPheGlnValAspGlyArgSerAlaArgGlyG1 17
   |||::: |||:::|||||:::|||||:::|||||:::|||||:::|||||
328 ACAATCGAATGGGGACATTCACAAAGTCGACGCCAGATCTCCAAAGAGG 377
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
17  yCySgIaThSerAsnAspLeuLeuGluAlaLeuAsnAlaSerSerL 34
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
378 TCAGCACTGTGCCAAGCATATGCAAGCAAGCATTAACGACAGATTCAA 427
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
34  ySgIuGluAlaLeuGlnIleleArgGluLysIleProGluLysTyrLeu 50
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
428 TTGAATCTGCTTGACAAATATTCAGAGGAAGAACCCGAAAGATTACGTC 477

```

```

51  PheGlnPheHisAlaLeuAsnSerAsnLeuAspArgIlePheAspLysrh 67
   ::||| |||:::|||||:::|||||:::|||||:::|||||:::|||||
478 CTTCAACATCGACACACATCCGTTTAATCTGCAACGATCTTCGCAAGT 527
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
67  rProGluPro 70
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
528 GCCCGAACCA 537

```

seq_name: /cgnl_8/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA94700

seq_documentation_block:

ID AAA94700 standard; DNA; 1651 BP.

AC AAA94700;

DT 15-JAN-2001 (first entry)

DE PMRG 2288 35S-rep gene cassette.

XX Geminivirus; DNA-A; geminivirus replication inhibition; ac3 gene;

KW transgenic plant; antiviral; gene therapy; bean golden mosaic virus;

KW BGMV; alfalfa mosaic virus; AMV; cauliflower mosaic virus; CaMV; ds.

XX Bean golden mosaic virus.

OS Cauliflower mosaic virus.

OS Alfalfa mosaic virus.

OS Synthetic.

XX US6118048-A.

XX 12-SEP-2000.

XX 24-APR-1998; 98US-0065999.

XX 25-APR-1997; 97US-0044925.

XX (MISC) WISCONSIN ALUMNI RES FOUND.

XX WPI; 2000-610861/58.

XX Genetic construct comprising a mutant geminiviral rep gene, useful for

PT producing a plant resistant to geminiviral infection.

XX Example; Column 15-16; 14pp; English.

XX The present sequence is a 35S-rep gene cassette comprising the rep gene

CC of bean golden mosaic virus (BGMV)-GA cloned downstream of the CamV

CC 35S promoter and an alfalfa mosaic virus (AMV) leader sequence. The

CC sequence was integrated into pBSII-KS+ to produce a rep gene expression

CC vector. DNA-nicking domain mutations may be incorporated into rep gene

CC to produce a genetic construct that acts as a transdominant inhibitor

CC of geminiviral replication. When expressed in a plant cell, this

CC inhibitor is able to dramatically reduce replication of geminivirus.

CC Genetic constructs that include sequences containing a portion of the

CC ac3 gene in addition to the trans-dominant inhibitor exhibit increased

CC efficiency and broadened specificity of inhibition of geminiviral

CC replication. Geminiviruses are one of the greatest constraints on

CC production of important crops, including cassava, beans, cowpeas,

CC peppers, tomatoes and cotton. The effects of the virus can be overcome

CC by using the genetic construct.

SO Sequence 1651 BP; 517 A; 393 C; 342 G; 399 T; 0 other;

alignment_scores: Quality: 223.00 Length: 70

Ratio: 3.780 Gaps: 0

Percent Similarity: 84.286 Percent Identity: 60.000

alignment_block:

US-09-289-346a-10 x AAA94700 ..

Align seg 1/1 to: AAA94700 from: 1 to: 1651

```

1 ThrleuValTrpGluGluPheGlnValAspGlyArgSerAlaArgGly1 17
|||||
796 ACAATCGAATGGGAGCATTCCTCAAGTCAGCGAGATCTGCAAGAGGAGG 845
17 yCysGlnThrSerAsnAspLeuLeuGluAlaLeuAsnAlaSerSerL 34
|||||
846 TCACGAGTCTGCCAAGCAGCTATATGCAAAAGCATTTAAACCCAGATTCGA 895
34 ySGluGluAlaLeuGlnIleIleArgGluLysIleProGluLysTrpLeu 50
|||||
896 TTGAATCTGCCCTTGACAAATATTGAAGAGAAACAACCGAAAGATTACGTC 945
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
|||||
946 CTTCACATCAACACATCCGTTCTAATCTCGAACGATCTTCGTCAAAGT 995
67 rProGluPro 70
|||||
996 GCCGGAACCA 1005

seq_name: /cgml_8/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA94701
seq_documentation_block:
ID AAA94701 standard; DNA: 1651 BP.
XX
XX AAA94701;
XX
XX 15-JAN-2001 (first entry)
XX
XX pTrepN nucleotide sequence.
XX
XX Geminivirus; DNA-A: geminivirus replication inhibition; ac3 gene;
XX transgenic plant; antiviral; gene therapy; bean golden mosaic virus;
XX BGWV; alfalfa mosaic virus; AMV; cauliflower mosaic virus; CaMV; ds.
XX
XX Bean golden mosaic virus.
XX Cauliflower mosaic virus.
XX Alfalfa mosaic virus.
XX Synthetic.
XX
XX US6118048-A.
XX
XX 12-SEP-2000.
XX
XX 24-APR-1998; 98US-0065999.
XX
XX 25-APR-1997; 97US-0044925.
XX
XX (WISC ) WISCONSIN ALUMNI RES FOUND.
XX
XX WPI; 2000-610861/58.
XX
XX Genetic construct comprising a mutant geminiviral rep gene, useful for
XX producing a plant resistant to geminiviral infection -
XX
XX Example; Column 17-18; 14pp; English.
XX
XX The present sequence is pTrepN, a vector containing a CaMV-35S
XX promoter-driven rep gene derived from bean golden mosaic virus (BGWV)-GA.
XX Site-directed mutagenesis was used to engineer an NcoI site in the start
XX codon of the rep gene to facilitate cloning of DNA-nicking domain
XX mutants. The resulting genetic constructs act as trans-dominant
XX inhibitors of geminiviral replication. When expressed in a plant cell,
XX these inhibitors are able to dramatically reduce replication of
XX geminivirus. Genetic constructs that include sequences containing a
XX portion of the ac3 gene in addition to the trans-dominant inhibitor
XX exhibit increased efficiency and broadened specificity of inhibition of
XX geminiviral replication. Geminiviruses are one of the greatest
XX constraints on production of important crops, including cassava, beans,
XX cowpeas, peppers, tomatoes and cotton. The effects of the virus can be
XX overcome by using the genetic construct.

```

```

SQ Sequence 1651 BP; 517 A; 392 C; 343 G; 399 T; 0 other;
alignment_scores:
Quality: 223.00 Length: 70
Ratio: 3.780 Gaps: 0
Percent Similarity: 84.286 Percent Identity: 60.000
alignment_block:
US-09-289-346a-10 x AAA94701 ..
Align seg 1/1 to: AAA94701 from: 1 to: 1651

1 ThrleuValTrpGluGluPheGlnValAspGlyArgSerAlaArgGly1 17
|||||
796 ACAATCGAATGGGAGCATTCCTCAAGTCAGCGAGATCTGCAAGAGGAGG 845
17 yCysGlnThrSerAsnAspLeuLeuGluAlaLeuAsnAlaSerSerL 34
|||||
846 TCACGAGTCTGCCAAGCAGCTATATGCAAAAGCATTTAAACCCAGATTCGA 895
34 ySGluGluAlaLeuGlnIleIleArgGluLysIleProGluLysTrpLeu 50
|||||
896 TTGAATCTGCCCTTGACAAATATTGAAGAGAAACAACCGAAAGATTACGTC 945
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
|||||
946 CTTCACATCAACACATCCGTTCTAATCTCGAACGATCTTCGTCAAAGT 995
67 rProGluPro 70
|||||
996 GCCGGAACCA 1005

seq_name: /cgml_8/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA94703
seq_documentation_block:
ID AAA94703 standard; DNA: 1894 BP.
XX
XX AAA94703;
XX
XX 15-JAN-2001 (first entry)
XX
XX pTrep3deltaE/CX nucleotide sequence.
XX
XX Geminivirus; DNA-A: geminivirus replication inhibition; ac3 gene;
XX transgenic plant; antiviral; gene therapy; ds.
XX
XX Synthetic.
XX
XX US6118048-A.
XX
XX 12-SEP-2000.
XX
XX 24-APR-1998; 98US-0065999.
XX
XX 25-APR-1997; 97US-0044925.
XX
XX (WISC ) WISCONSIN ALUMNI RES FOUND.
XX
XX WPI; 2000-610861/58.
XX
XX Genetic construct comprising a mutant geminiviral rep gene, useful for
XX producing a plant resistant to geminiviral infection -
XX
XX Example; Column 19-22; 14pp; English.
XX
XX The present sequence is pTrep3deltaE/CX. It contains a mutated
XX geminivirus rep gene sequence. Genetic constructs containing DNA-nicking
XX domain mutants in the rep gene may be used as trans-dominant inhibitors
XX of geminiviral replication. When expressed in a plant cell,
XX these inhibitors are able to dramatically reduce replication of
XX geminivirus. Genetic constructs that include sequences containing a
XX portion of the ac3 gene in addition to the trans-dominant inhibitor

```

CC exhibit increased efficiency and broadened specificity of inhibition of
 CC geminiviral replication. Geminiviruses are one of the greatest
 CC constraints on production of important crops, including cassava, beans,
 CC cowpeas, peppers, tomatoes and cotton. The effects of the virus can be
 CC overcome by using the genetic construct.

Sequence 1894 BP; 604 A; 421 C; 388 G; 481 T; 0 other;

alignment_scores:

Quality:	223.00	Length:	70
Ratio:	3.780	Gaps:	0
Percent Similarity:	84.286	Percent Identity:	60.000

alignment_block:

US-09-289-346a-10 x AAA94703 ..

Align seg 1/1 to: AAA94703 from: 1 to: 1894

```

1 ThleuValTrpGlyGluPheGlnValAspGlyArgSerAlaArgGlyI 17
||||| ||||||||| ||||||||| ||||||||| |||||||||
796 ACAATGCATGGGGACAAATTCACAGTCGACGGCAGATCTGCCAAGAGS 845
17 yCysGlnThrSerAsnAspLeuLeuGluAlaLeuAsnAlaSerSerL 34
| ||||| ||||| ||||| ||||| ||||| ||||| |||||
846 TCAGCAGCTGCGCAACGACTCATATGCACAAAGCATTAACGCAATTCAM 895
34 ySgUGluAlaLeuGlnIleIleArgGluIlyStleProGluIlyTyLeu 50
||||| ||||| ||||| ||||| ||||| ||||| |||||
896 TTGAATCTGCTTGACAAATATTCAGAGAACACCGAAAGATTACGTC 945
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysThr 67
||||| ||||| ||||| ||||| ||||| ||||| |||||
946 CTTCACATCACAACATCCGCTTCTAATCTCGAACGATCTTCTCAAACT 995
67 rProGluPro 70
: |||||
996 GCCGGAACCA 1005

```

seq_name: /cgnl_8/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA94702

seq_documentation_block:

ID AAA94702 standard; DNA; 2072 BP.

AC AAA94702;

DE 15-JAN-2001 (first entry)

DE pTrep23 nucleotide sequence.

KW Geminivirus; DNA-A; geminivirus replication inhibition; ac3 gene;
 KW transgenic plant; antiviral; gene therapy; ds.

OS Synthetic.

PN US6118048-A.

PD 12-SEP-2000.

PF 24-APR-1998; 98US-0065999.

PR 25-APR-1997; 97US-0044925.

PA (WISC) WISCONSIN ALUMNI RES FOUND.

DR WPI; 2000-610861/58.

PT Genetic construct comprising a mutant geminiviral rep gene, useful for
 PT producing a plant resistant to geminiviral infection -
 PS Example: Column 17-20; 14pp: English.

CC The present sequence is pTrep23. It contains the wild type geminivirus

CC rep gene sequence. Genetic constructs containing DNA-licking domain
 CC mutants in the rep gene may be used as trans-dominant inhibitors
 CC of geminiviral replication. When expressed in a plant cell,
 CC these inhibitors are able to dramatically reduce replication of
 CC geminiviruses. Genetic constructs that include sequences containing a
 CC portion of the ac3 gene in addition to the trans-dominant inhibitor
 CC exhibit increased efficiency and broadened specificity of inhibition of
 CC geminiviral replication. Geminiviruses are one of the greatest
 CC constraints on production of important crops, including cassava, beans,
 CC cowpeas, peppers, tomatoes and cotton. The effects of the virus can be
 CC overcome by using the genetic construct.

Sequence 2072 BP; 661 A; 467 C; 421 G; 523 T; 0 other;

alignment_scores:

Quality:	223.00	Length:	70
Ratio: <td>3.780</td> <td>Gaps:</td> <td>0</td>	3.780	Gaps:	0
Percent Similarity:	84.286	Percent Identity:	60.000

alignment_block:

US-09-289-346a-10 x AAA94702 ..

Align seg 1/1 to: AAA94702 from: 1 to: 2072

```

1 ThleuValTrpGlyGluPheGlnValAspGlyArgSerAlaArgGlyI 17
||||| ||||||||| ||||||||| ||||||||| |||||||||
796 ACAATGCATGGGGACAAATTCACAGTCGACGGCAGATCTGCCAAGAGS 845
17 yCysGlnThrSerAsnAspLeuLeuGluAlaLeuAsnAlaSerSerL 34
| ||||| ||||| ||||| ||||| ||||| ||||| |||||
846 TCAGCAGCTGCGCAACGACTCATATGCACAAAGCATTAACGCAATTCAM 895
34 ySgUGluAlaLeuGlnIleIleArgGluIlyStleProGluIlyTyLeu 50
||||| ||||| ||||| ||||| ||||| ||||| |||||
896 TTGAATCTGCTTGACAAATATTCAGAGAACACCGAAAGATTACGTC 945
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysThr 67
||||| ||||| ||||| ||||| ||||| ||||| |||||
946 CTTCACATCACAACATCCGCTTCTAATCTCGAACGATCTTCTCAAACT 995
67 rProGluPro 70
: |||||
996 GCCGGAACCA 1005

```

seq_name: /cgnl_8/gcgdata/geneseq/geneseqn/NA1996.DAT:AA12904

seq_documentation_block:

ID AA12904 standard; DNA; 1080 BP.

AC AA12904;

DE 07-NOV-1996 (first entry)

DE Sardinian tomato yellow leaf curl virus mutated C1 gene (K227A).

KW Nucleotide triphosphate binding site; DNA helicase; RNA helicase;
 KW modification; mutation; viral replication; deficient; inhibition;
 KW viral resistance; geminivirus; tomato yellow leaf curl virus;
 KW Sardinian isolate; STYLCV; transgenic plant; P-loop; C1 gene;
 KW A11 gene; dominant negative phenotype; ss.

OS Sardinian tomato yellow leaf curl virus.

PN Key Location/Qualifiers

FT CDS 1..1080

FT /*tag= a

FT /product= Rep.(K227A)
 FT /note= "encodes Rep protein in which wild-type lys
 FT at position 227, i.e. within the NTP-
 FT binding site, is replaced by Ala"

PN W09608573-A1.

```
XX 21-MAR-1996.
PD
XX 15-SEP-1995; 95MO-FR01192.
XX
XX 15-SEP-1994; 94FR-0011040.
XX
XX (CNRS ) CENT NAT RECH SCI.
XX
XX Gronenborn B;
XX
XX WPI: 1996-179947/18.
XX P-PSDB; AAR88870.
XX
XX Prodn. of virus-resistant transgenic plants - using mutated genomic
XX sequence from phytopathogenic DNA virus
XX
XX Disclosure: Fig 13; 93pp; French.
XX
XX Mutation of consensus amino acids in the NTP-binding site of
XX geminivirus Rep protein is used to produce replication deficient
XX viruses. The mutated viral nucleic acid is used for producing
XX transgenic plants that are resistant to, or tolerant of, the native
XX virus. The present sequence encodes a mutant form of the Rep (or C1)
XX protein from the Sardinian isolate of tomato yellow leaf curl virus
XX (STYLCV) in which the wild-type Lys227 residue has been changed to an
XX Ala residue; transgenic Nicotiana benthamiana plants generated by
XX transformation with the mutated virus were found to be resistant to
XX STYLCV, i.e the mutation results in a dominant negative phenotype.
XX
XX Sequence 1080 BP; 355 A; 248 C; 210 G; 267 T; 0 other;
SQ
```

```
alignment_scores:
  Quality: 221.00      Length: 69
  Ratio: 3.877        Gaps: 0
  Percent Similarity: 82.609   Percent Identity: 56.522
```

```
alignment_block:
US-09-289-346a-10 x AAT12904
```

```
Align seg 1/1 to: AAT12904 from: 1 to: 1080
```

```
2 LeuValITRpGIygluphegInValaspIyargSeraIaArgIyGlyCy 18
   ||| ||||| |||||::||| ||||| ||||| ||||| |||||
331 CTTGAATGGGCTACTTCAGATCGACGACGATCTGCTAGCGAGACA 380
   |||||::||| |||::|||::|||::|||::|||::|||::|||::
18 sGInThSerAsnAspleuLeuLeuGluAlaLeuAsnAlaSerSerIySG 35
   |||||::||| |||::|||::|||::|||::|||::|||::|||::
381 ACACACAGCCACACGCGCTTACGCCAAGCAATTAACCAAGAGTAAGT 430
   |||||::||| |||::|||::|||::|||::|||::|||::|||::
35 LucIuAlaLeuGluInleIleArgGluIySilePogIuIyTyrlLeuPhe 51
   ::|||::|||::|||::|||::|||::|||::|||::|||::|||::
431 CGCAGGCTCTTGATGTAATTAAGATTAGCGCTTACGATTTACGTTCTA 480
   |||||::||| |||::|||::|||::|||::|||::|||::|||::
52 GluPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspIySthPr 68
   ::|||::|||::|||::|||::|||::|||::|||::|||::|||::
481 CATTTCATATATAATAGTAATTTAGATAGGTTTCCAGCGTCCCTCC 530
   |||||::||| |||::|||::|||::|||::|||::|||::|||::
68 oGluPro 70
   |||
531 GGCACCT 537
```



```

614 AGATACCAACAAAAAACACAAAAAAC 643
seq_name: gb_est2:BE964992

```

```

seq_documentation_block:
LOCUS      BE964992      1512 bp      mRNA      EST      14-DEC-2000
DEFINITION 601658769R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886169 3',
            mRNA sequence.
ACCESSION  BE964992
VERSION    BE964992.2  GI:11768902
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE  1 (bases 1 to 1512)
            NIH-MGC http://mcc.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            JOURNAL
            Unpublished (1999)
            On Oct 3, 2000 this sequence version replaced gi:10575697.
            Contact: Robert Strausberg, Ph.D.
            Email: cga@rsi.femail.nih.gov
            Tissue Procurement: DCTD/DTP/Gazdar
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: L1CM649 row: 1 column: 18
            High quality sequence stop: 291.
FEATURES
    source
        1..1512
            location/Qualifiers
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="IMAGE:3886169"
                /clone_1ib="NIH_MGC_69"
                /tissue_type="large cell carcinoma, undifferentiated"
                /lab_host="DH10B (phage-resistant)"
                /note="Organ: lung; Vector: pCMV-SORT6; Site_1: NotI;
                Site_2: SalI; Cloned unidirectional. Primer: Oligo dT.
                Average insert size 1.1 kb. Library constructed by Life
                Technologies."
BASE COUNT      481 a      308 c      357 g      363 t      3 others
ORIGIN

```

```

alignment_scores:
    Quality: 74.50      Length: 77
    Ratio: 1.656      Gaps: 3
    Percent Similarity: 58.442      Percent Identity: 32.468

```

alignment_block:

US-09-289-346A-10 x BE964992 ..

Align seg 1/1 to: BE964992 from: 1 to: 1512

```

4  TrrglgtlupheglnvalaspGlyArgSerAlaArglyGlyCysGlnTh 20
|||||
944 TGGGGGGGGCACACACCGGGGGGTTCTCTACCGGTGTGTGAGAAAC 993
|||||
20 rserAspAspLeuLeu...LeuGlAlaLeuAsnAlaSerSerlyGlu 35
|||||
994 CATCAACACCCCTTATATCAACACGAGGTCTTCCACATAAAAAAGAGG 1043
|||||
36 ..GluAlaLeuGlnIleIle.....Arg 42
|||||
1044 CGGAAGGTATATATGTCGCGCCACAAAGGCTGGGGGGGCAAC 1093
|||||
43 GlulysIleProGluysTyrlleupheglnpheHisAsnLeuAsnSerAs 59
|||||
1094 GAAAAACACACCTTTAAAGAGCTCTTATCTTCACAGAAAGATTCTGA 1143
|||||

```

```

59 nleuAspArgIlePheAspLyThrProGlu 69
: |||||:
1144 AGGCGATCGTGTGTTCCAAACACACCTGAC 1174
seq_name: gb_gss:A0950848

```

```

seq_documentation_block:
LOCUS      A0950848      572 bp      DNA      GSS      27-JAN-2000
DEFINITION Sheared DNA-SIM3.TF Sheared DNA Trypanosoma brucei genomic clone
            Sheared DNA-SIM3, DNA sequence.
ACCESSION  A0950848
VERSION    A0950848.1  GI:6774113
KEYWORDS   GSS.
SOURCE     Trypanosoma brucei.
            Trypanosoma brucei.
            Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE  1 (bases 1 to 572)
            El-Sayed,N., Zhao,H., Gili,S., Suh,E., Malek,J., Fujii,C.,
            Gerrard,C., Leech,V., de Jong,P., Ullu,E., Melville,S., Donelson,J.,
            Fraser,C. and Adams,M.
            Determination of clone end sequences from Trypanosoma brucei GUTat
            10.1 sheared DNA library
            Unpublished (1999)
            Other_GSSs: Sheared DNA-SIM3.TF
            Contact: Najib M. El-Sayed
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: nelsayed@tigr.org
            Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared
            DNA library constructed at TIGR. Clones will be available for
            distribution through ATCC. Sheared DNA end sequences search page:
            http://www.tigr.org/tdb/mbd/tbdb/.
            Seq primer: M13-Forward
            Class: Shotgun.
FEATURES
    source
        1..572
            location/Qualifiers
                /organism="Trypanosoma brucei"
                /strain="TREU927/4 GUTat 10.1"
                /db_xref="taxon:5691"
                /clone="Sheared DNA-SIM3"
                /clone_1ib="Sheared DNA"
                /note="Vector: pUC18; Site_1: SmaI; Constructed at The
                Institute for Genomic Research (TIGR), Rockville, MD.
                Genomic DNA isolated from a cloned population of
                Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically
                sheared to give a tight size distribution (approx 2 kb).
                The v + i method used for the library construction is
                described in detail in Smith, H.O. and Venter, J.C.
                (Making small insert libraries for whole genome shotgun
                sequencing projects. In Genome Sequencing: A Practical
                Approach, eds. M. Vaundin and B. Barrel, Oxford University
                Press, 1999)."
BASE COUNT      115 a      118 c      180 g      159 t
ORIGIN

```

```

alignment_scores:
    Quality: 69.00      Length: 31
    Ratio: 2.556      Gaps: 0
    Percent Similarity: 87.097      Percent Identity: 38.710

```

alignment_block:

US-09-289-346A-10 x A0950848 ..

Align seg 1/1 to: A0950848 from: 1 to: 572

```

11 GlyArgSerAlaArglyGlyCysGlnThSerAspAspLeuLeuGln 27
|||||

```


alignment_scores: Quality: 68.50 Length: 54
Ratio: 1.903 Gaps: 3
Percent Similarity: 66.667 Percent Identity: 35.185

alignment_block:

US-09-289-346a-10 x BG595046/rev ..

Align seg 1/1 to reverse of: BG595046 from: 1 to: 732

```

11 GYATGSeRAlArGlyGlyCysGlnThrsSerAsnAsp.....LeuLe 25
|||||
408 GGAAGGTGGCTGCTAGCAGATCTTAGACGAGTAATGCAATAGACCTTG 359
25 uLeuGluAlaLeuAsnAlaSerSerLysGluGluAlaLeuGlnLeuLea 42
|||||
358 TATTACAGACCAAAATAGCAAACTCTTACATCTTATCCAAAGTTAGCA 309
42 rGluLysLleProGluLysTyrLeuPheGlnPheHisAsn...LeuAsn 57
|||||
308 AATAAAGATT.....CTTCACCTGTTCAGATTCCCAATAGCCTCAAC 265
58 SerAsnLeuAsp 61
|||||
264 AACATATCAAC 253

```

seq_name: gb_est2:BF544043

seq_documentation_block:

LOCUS BF544043 297 bp mRNA EST 11-DEC-2000
DEFINITION UI-R-E0-cl-e-12-0-UI-r1 UI-R-E0 Rattus norvegicus cDNA clone
UI-R-E0-cl-e-12-0-UI 5', mRNA sequence.

ACCESSION BF544043
VERSION BF544043.1 GI:11635150
KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 297)

REFERENCE 1 (bases 1 to 297)
AUTHORS Ronald,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtracction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)

MEDLINE 97044477
COMMENT Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa

451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250

Fax: 319 335 9565
Email: mscoares@blue.weeg.uiowa.edu

CDNA Library Preparation: M.B. Soares Lab Clone distribution:
clones will be available through Research Genetics (www.resgen.com)

This clone is also available through the I.M.A.G.E. Consortium at
LNLN (info@image.llnl.gov). IMAGE ID- I792063

Seq primer: M13 forward.

FEATURES
source Location/Qualifiers

```

1..297
/oiganism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-E0-cl-e-12-0-UI"
/clone_lib="UI-R-E0"
/dev_stage="embryonic"
/lab_host="DH10B (Life Technologies)"
/Note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: NotI; Site_2: EcoRI; This library
consists of a mixture of individually tagged normalized
libraries constructed from 8, 12 and 18-day embryo. The
tag is a string of 3-5 nucleotides present between the
```

NOT I site and the oligo-dT track which allows
identification of the library of origin of a clone within
the mixture."

BASE COUNT 70 a 65 c 87 g 75 t
ORIGIN

alignment_scores: Quality: 68.00 Length: 59
Ratio: 2.125 Gaps: 2
Percent Similarity: 54.237 Percent Identity: 37.288

alignment_block:

US-09-289-346a-10 x BF544043 ..

Align seg 1/1 to: BF544043 from: 1 to: 297

```

6 GluPheGlnValAspGlyArgSerAlaArgGlyGlyCysGlnThrsSerAs 22
|||||
69 GACTTAGGGTGGAGTGCAGAGTATA.....TGTCACACCTCTGA 109
22 nAspLeuLeuGluAlaLeuAsnAlaSerSerLysGluGluAlaLeuG 39
|||||
110 AGCTTGCCTTTGGGTGCCGAGACGACGAGGAGGAGAGACA... 155
39 lIlelIeArGluLysLleProGluLysTyrLeuPheGlnPheHisAsn 55
|||||
156 .....AAT 158
56 LeuAsnSerAsnLeuAspArgLlePhe 64
|||||
159 CTCGAATGCCATCTCTGCGAGAAATCTTC 185

```

seq_name: gb_est1:AA729985

seq_documentation_block:

LOCUS AA729985 396 bp mRNA EST 22-JAN-1998
DEFINITION nx34b10.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1257979 3',
mRNA sequence.

ACCESSION AA729985
VERSION AA729985.1 GI:2751344
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 396)

REFERENCE 1 (bases 1 to 396)
AUTHORS NCI-CGAP htcp://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:

www.bio.llnl.gov/bbrp/image/image.html

Insert Length: 551 Std Error: 0.00

Seq primer: -40m13 fwd. ET from Amersham

High quality sequence stop: 380.

FEATURES
source Location/Qualifiers

```

1..396
/oiganism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1257979"
/clone_lib="NCI CGAP GC4"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/Note="Vector: pT73D-Pac (Pharmacia) with a modified
```

polylinker; 1st strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I - RI adaptor primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p773 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo.

BASE COUNT 68 a 119 c 117 g 92 t
ORIGIN

alignment_scores:
Quality: 67.50 Length: 81
Ratio: 1.467 Gaps: 2
Percent Similarity: 56.790 Percent Identity: 25.926

alignment_block:
US-09-289-346a-10 x AA729985/rev ..

Align seg 1/1 to reverse of: AA729985 from: 1 to: 396

```

1  ThrleuValTrpGlyIupheGlnVal.....AspGlyAr 12
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
384 ACCCTGATCTACGGGCGACTGGAGCATATGAGTGAACCTGACGGCAG 335
12  gSerAlaArgGlyGlyCysGlnThrSerAsnAspLeuLeuGluAla 29
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
334 GCGCTCAAAATCGAGGACTCGAGGCGCATGCCGCTGTGGCAGCTGT 285
29  euAsnAlaSerSerLysGluGluAlaLeuGlnIleIleArgGluLysIle 45
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
284 TACAGGCGAAGAACCGACCGAGCCTTCGATGCTTCGGAGAACCTGT 235
46  ProGluLysTyrLeu.....ProGluLysTyrLeuPheGlnPhe 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
234 GAGGAGGAGCGCATCATCATGACGACCTGCCGACTGGAGTGGGGA 185
51  ....PheGlnPheHisAsnLeuAsnSerAsnLeuAspArg 62
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
184 GTCTGTGTTCCACACACGACGATGCGTCCCTTCATGCTG 142
seq_name: gb_gss: A2926150

```

seq_documentation_block:

LOCUS A2926150 468 bp DNA GSS 01-APR-2001
DEFINITION 476.d1041h1.sl Saccharomyces castellii NRRL Y-12630 Saccharomyces
castellii genomic clone 476.d1041h1.sl, DNA sequence.

ACCESSION A2926150
VERSION A2926150.1 GI:13497051

KEYWORDS GSS.
SOURCE Saccharomyces castellii.
ORGANISM Saccharomyces castellii
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.

REFERENCE 1 (bases 1 to 468)

AUTHORS Clifton, P.F., Hillier, L.W., Fulton, L., Graves, T., Miner, T., Gish, W.R., Waterston, R.H. and Johnston, M.
TITLE Surveying Saccharomyces genomes to identify functional elements by comparative DNA sequence analysis
JOURNAL unpublished (2001)

COMMENT Contact: Johnston M
Department of Genetics
Washington University Medical School
Box 8232, 4566 Scott Ave., St. Louis, MO 63110, USA
Tel: 314 362 2735
Fax: 314 362 7855
Email: mjgenetics.wustl.edu
Class: Random plasmid subclone.
Location/Qualifiers
1..468

FEATURES
source
/organism="Saccharomyces castellii"
/strain="NRRL Y-12630 (CBS 4309)"
/db_xref="taxon:27288"

/clone-lib="476.d1041h1.sl"
/note="Random genomic sequence"
BASE COUNT 131 a 94 c 76 g 167 t
ORIGIN

alignment_scores:
Quality: 67.50 Length: 55
Ratio: 1.929 Gaps: 2
Percent Similarity: 63.636 Percent Identity: 30.909

alignment_block:
US-09-289-346a-10 x A2926150/rev ..

Align seg 1/1 to reverse of: A2926150 from: 1 to: 468

```

8  GluValAspGlyArgSerAlaArgGlyGlyGlnThrSerAsnAspLe 24
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
201 CAATTAAACGGTCTTCGAGACTGGCTTTCCTAGAGAACTAAAGATT 152
24  uLeuLeuGluAlaLeuAsnAlaSerSerLysGluGluAlaLeuGlnIle 41
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
151 TGTCAACGTCCTCAGCATTAACATAGAAAGAGCTACTTGAAGATTAC 102
41  leArgGluLysIle.....ProGluLysTyrLeuPheGlnPhe 53
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
101 TTGAGACTAAGGTGACGAAAGAAATCCAGATGAATAT.....TAC 61
54  HisAsnLeuAsnSer 58
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
60 CATGGAGATGATTTCA 46
seq_name: gb_est1:AM677682

```

seq_documentation_block:

LOCUS AM677682 571 bp mRNA EST 19-JUL-2000
DEFINITION WS1_10.B06.d1.A002 Water-stressed 1 (WS1) Sorghum bicolor cDNA,
mRNA sequence.

ACCESSION AM677682
VERSION AM677682.1 GI:751387

KEYWORDS EST.

SOURCE sorghum.

ORGANISM sorghum bicolor

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Sorghum.

REFERENCE 1 (bases 1 to 571)
AUTHORS Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C., Sudman, M. and Pratt, L.H.

TITLE An EST database from Sorghum: water-stressed plants
JOURNAL unpublished (2000)
COMMENT Contact: Cordonnier-Pratt MM
Department of Botany
The University of Georgia
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 542 1805
Email: emprat@uga.edu

Sequences have been trimmed to exclude polyA, vector and regions below Phred quality 16. The threshold for highest quality sequence is 20.
Seq primer: JEN REV
High quality sequence stop: 541
POLYA-No.

FEATURES
source
Location/Qualifiers
1..571

/organism="Sorghum bicolor"
/db_xref="taxon:4558"
/clone-lib="Water-stressed 1 (WS1)"
/note="Organ: Mix of 5-week old plants on days 7 & 8 after water was withheld; Vector: Lambda Zap; Site_1: XhoI; Site_2: EcoRI; The library was made from poly-A RNA in the

cloning vector lambda ZAP II. Clones to be sequenced were prepared by mass excision.

BASE COUNT 150 a 130 c 135 g 156 t

ORIGIN

alignment_scores:

Quality:	67.50	Length:	61
Ratio:	1.824	Gaps:	2
Percent Similarity:	60.656	Percent Identity:	31.148

alignment_block:

US-09-289-346a-10 x AM677682 ..

Align seg 1/1 to: AM677682 from: 1 to: 571

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14 AAlaArgGLyGLyCysGlnThrSerAsnAspLeuLeuLeuGlnAlaLeuAs 30
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  1 GCACGAGGAGCATGC...ATAGAGCAGCAGCTGCTCAGCCAAACACTTA 47
30 nAlaSerLysGluGluAlaLeuGlnIleIleArgGluLysIle.... 45
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
  48 CAGATTTCAGAGCTACTACGCTATGATCTGCATTCAGCATGCTCTG 97
46 .....ProGluLysTyrLeuPheGlnPheHisAsnLeuAsn 57
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
  98 CTTTATGTGCGCAACCTGCCGAATCTCTTTCAGCAGCATGTGTCTCA 147
58 SerAsnLeuAspArgIlePheAspLysThrPro 68
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 148 AATGCATTCATGACTGCTGTTCACAGACTCCT 180

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seq_name: gb_est1:BE470391

seq_documentation_block:

LOCUS BE470391 777 bp mRNA EST 28-JUL-2000

DEFINITION IPHdk01397 Head kidney cDNA library Ictalurus punctatus cDNA 5', mRNA sequence.

ACCESSION BE470391

VERSION BE470391.1 GI:9560882

KEYWORDS EST.

SOURCE channel catfish.

ORGANISM Ictalurus punctatus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi; Siluriformes; Ictaluridae; Ictalurus.

REFERENCE 1 (bases 1 to 777)

CAO, D., KOCABAS, A., JU, Z., KARSLI, A., LI, P., PATTERSON, A. and LIU, Z. J.

TITLE Transcriptome analysis of channel catfish (*Ictalurus punctatus*): Gene cataloging and profiling from the head kidney

JOURNAL Unpublished (2000)

COMMENT The Fish Molecular Genetics and Biotechnology Laboratory, Department of Fisheries and Allied Aquacultures and Program of Cell and Molecular Biosciences

Auburn University
203 Swingle Hall, Auburn University, Auburn, AL 36849, USA
Tel: 334 844 4054
Fax: 334 844 9208
Email: zliu@cesag.auburn.edu

Seq primer: M13 Reverse

FEATURES

source 1..777

/organism="Ictalurus punctatus"

/db_xref="taxon:7998"

/clone_lib="Head kidney cDNA library"

/note="Organ: Head kidney; Vector: pSport1; Site_1: NotI; Site_2: SalI"

BASE COUNT 210 a 184 c 194 g 189 t

ORIGIN

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Quality:	67.50	Length:	48
Ratio:	2.250	Gaps:	2
Percent Similarity:	62.500	Percent Identity:	39.583

alignment_block:

US-09-289-346a-10 x BE470391 ..

Align seg 1/1 to: BE470391 from: 1 to: 777

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  49 TCCATTCAGACTCTCTTACAGGCTTAATGCCAGACAGAGACAGCTC 98
31 aSerLysGluGluAlaLeuGlnIleIleArgGluLysIle..... 45
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  99 TCACAGCACAACAGAAACAGTCCAGTACCAAGAGAGATCAGCAAA 148
46 .....ProGluLysTyrLeuPheGlnPheHisAsnLeuAsn 57
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seq_name: gb_gss:AQ367423

seq_documentation_block:

LOCUS AQ367423 705 bp DNA GSS 07-MAR-2000

DEFINITION toxb0001E09r CUGI Tomato BAC library Lycopersicon esculentum genomic clone toxb0001E09r, DNA sequence.

ACCESSION AQ367423

VERSION AQ367423.1 GI:4220937

KEYWORDS GSS.

SOURCE tomato.

ORGANISM Lycopersicon esculentum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; eustersid II; Solanales; Solanaceae; Solanum;

Lycopersicon.

REFERENCE 1 (bases 1 to 705)

BUDIMAN, M. A., MAO, L., WOOD, T. C. and WING, R. A.

A deep-coverage tomato BAC library and prospects toward development of an STC framework for genome sequencing

JOURNAL Genome Res. 10 (1), 129-136 (2000)

MEDLINE 20113122

COMMENT Contact: Wing RA

Clemson University Genomics Institute

100 Jordan Hall, Clemson, SC 29634, USA

Tel: 864 656 7288

Fax: 864 656 4293

Email: rwing@clemson.edu

Seq primer: GGAAACAGCTATGACCATG

Class: BAC ends

High quality sequence stop: 375.

FEATURES

source 1..705

/organism="Lycopersicon esculentum"

/cultivar="Heinz 1706"

/db_xref="taxon:4081"

/clone="toxb0001E09r"

/clone_lib="CUGI Tomato BAC library"

/tissue_type="Nuclei preparation from leaf"

/lab_host="E. coli DH10B"

/note="Vector: pBeloBAC 11; Site_1: HindIII; Site_2: HindIII; Tomato is a vegetable crop that ranks second only to potatoes in value and importance. Among plant geneticists and physiologists, tomato represents an ideal dicot model beside Arabidopsis and monocot rice to derive genomic information from. To facilitate the genome analysis of tomato, we have constructed a tomato BAC library that is suitable for positional cloning, physical mapping, and genome sequencing. The library contains 129 ,000 clones and a random sampling of 498 clones indicated an average insert size of 117.5 kb. With 15X haploid

genome equivalents (1C equals 953 Mb) (Arumuganathan and Earle, 1991), the probability to recover any particular sequence is greater than 99%. High stability, large insert and ease in manipulation make BAC libraries the choice for genome sequencing. Pre characterization of a few hundred bases of insert ends will make BAC clones extremely useful for rapid contig assembly (Venter, Smith, and Hood, 1996). Here we present the construction, characterization of the tomato BAC library, and preliminary analysis of the 1536 tomato BAC end sequences."

BASE COUNT 215 a 176 c 116 g 198 t
ORIGIN

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Quality: 67.00 Length: 99
Ratio: 1.367 Gaps: 4
Percent Similarity: 49.495 Percent Identity: 23.232

alignment_block:
US-09-289-346A-10 x A0367423 ..

Align seg 1/1 to: A0367423 from: 1 to: 705

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13 .....S 13
291 GTCTCGAAGCATAAGCAATCATCTTCTCTTGCAATGACATGCACCC 340
13 eAlaATGAGlyGlyCysGlnThrSerAsnAspLeuLeu..... 26
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341 AAACCAATTAAGATGATGCATCAATTAACATGATGATCTTACCTCTAT 390
27 ..GluAlaLeuAsnAlaSerSerLySGluGlnAlaLeuGlnIleLeu 42
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391 GGCGAAGATGAGAACCGGTGGTGGTACGACAAAGCTTGAGCTTGAA 440
42 gGluGlyLe.....ProGluLySyr.....LeuPheG 52
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441 AGCTATTCTCACACTCATCCGACCATTAACAATGAGACATTTGGTATGTC 490
52 lnpheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLySthr 67
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491 AAGTTCATCTCAGTTGGGAGACATATAGGACATCCCTTGACAAATCG 537

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seq_name: gb_est1:BB448215

seq_documentation_block:

LOCUS BB448215 315 bp mRNA EST 19-JUL-2000
DEFINITION BB448215 RIKEN full-length enriched, 9 days embryo Mus musculus
CDNA clone D030065H24 3', mRNA sequence.

ACCESSION BB448215
VERSION BB448215.1 GI:9290827

KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 315)
Kono, H., Aizawa, K., Akahira, S., Akiyama, J., Atakawa, T., Carninci
P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,
Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,
Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,
Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M.,
Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,
Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata
Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, T., Sugahara, Y.,
Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tomimaga, N., Toya
T., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yamazaki, I.,
Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino

TITLE
JOURNAL
COMMENT
M., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Kono, H., et al.)
Unpublished (2000)
Contact: Yoshinobu Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suenho-cho, Tsunumi-Ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@sc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki
N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Thermotabilization and thermocycling of thermostable enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh, M., Katsunagi, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki
Y. and Hayashizaki, Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)
Please visit our web site (http://genome.riken.go.jp) for
further details.

FEATURES

source

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1..315
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="D030065H24"
/clone_lib="RIKEN full-length enriched, 9 days embryo"
/seq_stage="9 days embryo"
/lab_host="DH10B"
/note="Site-1: SalI; Site-2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN, Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer 15'
GAGAGAGAGAGCGCCGACACTCGAGTGTGTTTTTTTTTTTTTTVN 3', cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. Second strand cDNA was prepared with the
primer adapter of sequence 15'
GAGACAGAGATTTCGAGCTTAATTAATTAATCCGCCGCCGCC 3'. cDNA
was cleaved with BamHI and XhoI. Vector: a modified
pBluescript KS(+) after bulk excision from Lambda fLc I."
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BASE COUNT 83 a 84 c 68 g 80 t
ORIGIN

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Ratio: 1.847 Gaps: 3
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alignment_block:
US-09-289-346A-10 x BB448215 ..

Align seg 1/1 to: BB448215 from: 1 to: 315

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134 GGAGGATTAATGATCGCTCGCACTGAGTTAGAGGGTGTGAGACATC 183
21 rAsnAspLeuLeuLeuGlnAlaLeuAsnAlaSerSerLySGluGlnAla 38
||||:|||||:|||||:|||||:|||||:
184 TAGGTGATTTCTG.....GCAACTGCAACTTCGCTCTTGAAAGACAG 227
38 eudInIleIleArgGluLySyr.....IleProGluLySyr.....LeuPhe 51

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228  TAGGATCATCTCCCTTAACACACTCCCATGCTACTCCCTTTAAA  277
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52  GlnPheHis  54
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278  CAGTTTCAC  286

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Fri Jan 4 09:37:09 2002

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Page 10



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2216 AGCTAATGATGCTGCCGACAGCCCTTAARGCAGTTTCAGCTGACGAC 2167
37 lalenglnllellearglulyslleprogluyslyrleuphglmphe 53
2166 CTTTAGCAATAATTAGGAAAACTCTAAAGATTTTATTATTTCATAT 2117
54 HisanleuAsnSerAsnLeuAspArglleAspIleAspIleThrPro 68
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seq_name: /cgn1_7/ptodata/1/lna/6B.COMB.seq:US-08-838-151A-48

seq_documentation_block:
; Sequence 48, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Lau, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Gemnivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1062 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bean Golden Mosaic Gemivirus
; STRAIN: Type II
; INDIVIDUAL ISOLATE: Guatemala
; NAME/KEY: CDS
; LOCATION: 1..1059
; US-08-838-151A-48

alignment_scores:
; Quality: 223.00 length: 70
; Ratio: 3.780 Gaps: 0
; Percent Similarity: 84.286 Percent Identity: 60.000

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378 TCACAGCTCTGCCACAGCATCATGCAAGGCAATTAACCGCATTCAA 427
34 ysgluAlaleuGlullellearglulyslleprogluyslyrleu 50
428 TTGAATCTGCTTGACAATATTGAAGGAGAACACGAAAGATTACCTC 477
51 PheglInPheHisAsnLeuAsnSerAsnLeuAspArglleAspIle 67
478 CTTCAACATCAACAACATCGCTTAATCTCGAACGATCTCGTCAAGT 527
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528 GCCGGAGACA 537

seq_name: /cgn1_7/ptodata/1/lna/6B.COMB.seq:US-08-838-151A-51

seq_documentation_block:
; Sequence 51, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Lau, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Gemnivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
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; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
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; STRAIN: Type II
; INDIVIDUAL ISOLATE: Guatemala

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? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/838,151A
? FILING DATE:
? CLASSIFICATION: 800
? ATTORNEY/AGENT INFORMATION:
? NAME: Mueller, Lisa V
? REGISTRATION NUMBER: 38,978
? REFERENCE/DOCKET NUMBER: SVS3801P0260
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 312-616-5400
? TELEFAX: 312-616-5460
? INFORMATION FOR SEQ ID NO: 43:
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? LENGTH: 1183 base pairs
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? ORGANISM: Bean Golden Mosaic Geminivirus
? STRAIN: Type II Isolates
? INDIVIDUAL ISOLATE: Guatemala
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? PUBLICATION INFORMATION:
? AUTHORS: Farfa, JC
? AUTHORS: Gilbertson, RL
? AUTHORS: Hanson, SF
? AUTHORS: Morales, FJ
? AUTHORS: Ahlquist, P
? AUTHORS: Lonleillo, AO
? AUTHORS: Maxwell, D
? TITLE: Bean Golden Mosaic Geminivirus Type II
? TITLE: Isolates from the Dominican Republic and
? TITLE: Guatemala: Nucleotide Sequences, Infectious
? TITLE: Pseudorecombinants, and Phylogenetic Relationships
? JOURNAL: Phytopathology
? VOLUME: 84
? ISSUE: 3
? PAGES: 321-329
? DATE: 1994
? US-08-838-151A-43

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? Quality: 223.00 Length: 70
? Ratio: 3.780 Gaps: 0
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? US-09-289-346A-10 x US-08-838-151A-43 ..

Align seg 1/1 to: US-08-838-151A-43 from: 1 to: 1183

1 ThrleuValTrpGlyGluPheGlnValAspGlyArgSerAlaArgGlyG1 17
  |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
328 ACAATCGAATGGGAGCAATTCACGACGCGAGATCTGCAAGAGGAGG 377
  |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
17 YCYGSLThSerAsnSpleuLeuLeuGluAlaLeuAsnAlaSerSerL 34
  |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
378 TCACAGCTCTCCACACGACTCATATGCAAGCGATTAAACCGACATTCAA 427
  |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
34 YSGlGluAlaLeuGlnLlelleArgGluLysIleProGluLysTyrLeu 50
  |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
428 TTGAATCTGCGCTTGACAATATTGANAAGAACACGAAAGATTACGTC 477
  |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
  |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::

```

```

478 CTTCACATCAACACATCGTTCTAATCTCGAACGATCTTCGCAAGGT 527
67 rProGluPro 70
  |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
528 GCCGGAACCA 537

seq_name: /cgnl_7/plodata/1/lna/5h_comb.seq:us-08-838-151A-45

seq_documentation_block:
? Sequence 45, Application US/08838151A
? Patent No. 6291743
? GENERAL INFORMATION:
? APPLICANT: Stout, John T
? APPLICANT: Luu, Hang T
? APPLICANT: Maxwell, Douglas
? APPLICANT: Ahlquist, Paul
? APPLICANT: Hanson, Steve
? TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
? NUMBER OF SEQUENCES: 63
? CORRESPONDENCE ADDRESS:
? ADDRESS: Dressler, Rocky, Milnamow & Katz
? STREET: Two Prudential Plaza, Suite 4700
? CITY: Chicago
? STATE: Illinois
? COUNTRY: U.S.A.
? ZIP: 60601
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/838,151A
? FILING DATE:
? CLASSIFICATION: 800
? ATTORNEY/AGENT INFORMATION:
? NAME: Mueller, Lisa V
? REGISTRATION NUMBER: 38,978
? REFERENCE/DOCKET NUMBER: SVS3801P0260
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 312-616-5400
? TELEFAX: 312-616-5460
? INFORMATION FOR SEQ ID NO: 45:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1183 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: circular
? MOLECULE TYPE: DNA (genomic)
? HYPOTHETICAL: NO
? ANTI-SENSE: NO
? ORIGINAL SOURCE:
? ORGANISM: Bean Golden Mosaic Geminivirus
? STRAIN: Type II
? INDIVIDUAL ISOLATE: Guatemala
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 1..1059
? US-08-838-151A-45

alignment_scores:
? Quality: 223.00 Length: 70
? Ratio: 3.780 Gaps: 0
? Percent Similarity: 84.286 Percent Identity: 60.000

alignment_block:
? US-09-289-346A-10 x US-08-838-151A-45 ..

Align seg 1/1 to: US-08-838-151A-45 from: 1 to: 1183

1 ThrleuValTrpGlyGluPheGlnValAspGlyArgSerAlaArgGlyG1 17

```

```
||||: ||||:|||||||
328 ACAATCGAATGGGACAAATTCAGTCAGCGAGATCTGCAAGAGAGAG 377
17 yCysGlnThrSerAsnAspLeuLeuLeuGluAlaLeuAsnAlaSerSerL 34
378 TACAGCATCTGCCAACGACTCATATGCAAGCAAGCATTAACGCAGATTCAA 427
34 yGluGluAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeu 50
428 TTGATCTCTGCTTGACATATTTGAAGAAAGAACACCGAAGATTACGTC 477
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
478 CTTCAAACATCAACAACATCCGTTCTATCTGAACGAGATCTGCTCAAGT 527
67 rProGluPro 70
528 GCCGGAACCA 537
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seq_name: /cgnl_7/ptodata/1/ina/6A_COMB.seq:us-09-065-999-5

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seq_documentation_block:
; Sequence 5, Application US/09065999
; Patent No. 6118048
; GENERAL INFORMATION:
; APPLICANT: Hanson, Stephen F.
; TITLE OF INVENTION: TRANS-DOMINANT INHIBITION OF GEMINIVIRAL
; TITLE OF INVENTION: DNA REPLICATION BY GEMINIVIRUS REP GENE MUTANTS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: One South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/065,999
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27,386
; REFERENCE/DOCKET NUMBER: 960296.94754
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-251-5000
; TELEFAX: 608-251-9166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1651 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-065-999-5
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alignment_scores:

Quality:	223.00	Length:	70
Ratio:	3.780	Gaps:	0
Percent Similarity:	84.286	Percent Identity:	60.000

alignment_block:

US-09-289-346a-10 x US-09-065-999-5 ..

Align seg 1/1 to: US-09-065-999-5 from: 1 to: 1651

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1 ThrLeuValTrpGluPheGlnValAspGlyArgSerAlaArgGlyL 17
||||: ||||:|||||||
796 ACAATCGAATGGGACAAATTCAGTCAGCGAGATCTGCAAGAGAGAG 845
17 yCysGlnThrSerAsnAspLeuLeuLeuGluAlaLeuAsnAlaSerSerL 34
846 TCAGCATCTGCCAACGACTCATATGCAAGCAAGCATTAACGCAGATTCAA 895
34 yGluGluAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeu 50
896 TTGAATCTGCTTGACATATTTGAAGAAAGAACACCGAAGATTACGTC 945
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
946 CTTCAAACATCAACAACATCCGTTCTATCTGAACGAGATCTGCTCAAGT 995
67 rProGluPro 70
996 GCCGGAACCA 1005
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seq_name: /cgnl_7/ptodata/1/ina/6A_COMB.seq:US-09-065-999-6

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seq_documentation_block:
; Sequence 6, Application US/09065999
; Patent No. 6118048
; GENERAL INFORMATION:
; APPLICANT: Hanson, Stephen F.
; APPLICANT: Maxwell, Douglas P.
; TITLE OF INVENTION: TRANS-DOMINANT INHIBITION OF GEMINIVIRAL
; TITLE OF INVENTION: DNA REPLICATION BY GEMINIVIRUS REP GENE MUTANTS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: One South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/065,999
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27,386
; REFERENCE/DOCKET NUMBER: 960296.94754
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-251-5000
; TELEFAX: 608-251-9166
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1651 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-065-999-6
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alignment_scores:

Quality:	223.00	Length:	70
Ratio:	3.780	Gaps:	0
Percent Similarity:	84.286	Percent Identity:	60.000

alignment_block:

US-09-289-346a-10 x US-09-065-999-6 ..

Align seg 1/1 to: US-09-065-999-6 from: 1 to: 1651

Align seg 1/1 to: US-09-065-999-7 from: 1 to: 2072

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1  ThleuValTrpGlyGluPheGlnValAspGlyArgSerIleArgGlyGly 17
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
796 ACAATCTGGCTGACATATTTGAGAGAGACACCGCAAGATTACGTC 845
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17  yCysGlnThrSerAsnAspLeuLeuGlnAlaLeuAsnAlaSerSerL 34
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
846 TCAGCACTCTGCCACGACGCTCATATGCAAGCGATTAAACGCGATTCA 895
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
34  ySGLuGlnAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeu 50
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
896 TTGAATCTGGCTGACATATTTGAGAGAGACACCGCAAGATTACGTC 945
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
51  PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
946 CTTCACATCTCACACATCCGCTTAATCTGCAACGCGATCTTCGTCAAAGT 995
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
67  rProGluPro 70
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996 GCCGGAACCA 1005

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seq_name: /cgn1_7/ptodata/1/lna/6A.COMB.seq:US-08-809-103B-7

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seq_documentation_block:
; Sequence 7, Application US/08809103B
; Patent No. 6133505
; GENERAL INFORMATION:
; APPLICANT: GRONENBORN, Bruno
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,103B
; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94.11040
; FILING DATE: 15-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR95/01192
; FILING DATE: 15-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: US94AL CNR TOM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 685-0573
; TELELEX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1145 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1077

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US-08-809-103B-7

alignment_scores:
 Quality: 221.00 Length: 69
 Ratio: 3.877 Gaps: 0
 Percent Similarity: 82.609 Percent Identity: 56.522

alignment_block:

US-09-289-346a-10 x US-08-809-103B-7 ..

Align seg 1/1 to: US-08-809-103B-7 from: 1 to: 1145

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2  leuValTrpGlyGluPheGlnValAspGlyArgSerIleArgGlyGly 18
   ||| ||||| |||||:|||||:|||||:|||||:|||||:|||||:
331 CTGAATGGGCTACTTCACATGCGAGCGAGCTCTGAGGGAGACA 380
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
18  sGlnThrSerAsnAspLeuLeuGlnAlaLeuAsnAlaSerSerLys 35
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
381 ACAGACAGCCGACGCGCTTACGCAAGCGCATTAACCGCAGAGTAAGT 430
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
35  lGlnAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeuPhe 51
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
431 CGCAGCGCTTGATGATTAATAACGATTACGCGCTTACGATTACGTTCTA 480
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
52  GlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysThrPr 68
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
481 CATTTTCATATATTAATAATTAATAAGGTTTCAGCGCTCC 530
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68  oGluPro 70
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531 GGCACCT 537

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seq_name: /cgn1_7/ptodata/1/lna/6A.COMB.seq:US-08-809-103B-1

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seq_documentation_block:
; Sequence 1, Application US/08809103B
; Patent No. 6133505
; GENERAL INFORMATION:
; APPLICANT: GRONENBORN, Bruno
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,103B
; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94.11040
; FILING DATE: 15-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR95/01192
; FILING DATE: 15-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: US94AL CNR TOM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 685-0573
; TELELEX: 248425 EMBON

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; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1148 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1077
; US-08-809-103B-1

alignment_scores:
    Quality: 221.00      Length: 69
    Ratio: 3.877        Gaps: 0
Percent Similarity: 82.609   Percent Identity: 56.522

alignment_block:
US-09-289-346A-10 x US-08-809-103B-1

Align seg 1/1 to: US-08-809-103B-1 from: 1 to: 1148

2 LeuValTrpGlyGluPheGlnValAspGlyArgSerAlaArgGlyGlyCys 18
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331 CTTGAATGGGCTGATGATTAATTAAGACGCTAGAGATTACGTTCTA 480
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
18 sGlnThrSerAsnLeuLeuGlnAlaLeuAsnAlaSerSerIysG 35
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
381 ACACACAGCCACGACGCTTACGCCAAGGCAATTACGACGAGTAAGT 430
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
35 LngLAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeuPhe 51
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431 CGCAGGCTCTGATGATTAATTAAGACGCTAGAGATTACGTTCTA 480
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
52 GlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysThrPr 68
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
481 CATTTTCATATATATAATAGTAATTAGATTAGGTTTCCAGGTGCTCC 530
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
68 oGluPro 70
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
531 GGCACCT 537

seq_name: /cgn1_7/plodata/1/lna/6A.COMB.seq:US-08-809-103B-3

seq_documentation_block:
; Sequence 3, Application US/08809103B
; Patent No. 6133505
; GENERAL INFORMATION:
; APPLICANT: GROENENBORN, Bruno
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,103B
; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94.11040
; FILING DATE: 15-SEP-1994
; PRIOR APPLICATION DATA:
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```

; APPLICATION NUMBER: WO PCT/FR95/01192
; FILING DATE: 15-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: US94AL CNR TOM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 685-0573
; TELEEX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1150 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1077
; US-08-809-103B-3

alignment_scores:
    Quality: 221.00      Length: 69
    Ratio: 3.877        Gaps: 0
Percent Similarity: 82.609   Percent Identity: 56.522

alignment_block:
US-09-289-346A-10 x US-08-809-103B-3

Align seg 1/1 to: US-08-809-103B-3 from: 1 to: 1150

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||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
18 sGlnThrSerAsnLeuLeuGlnAlaLeuAsnAlaSerSerIysG 35
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
381 ACACACAGCCACGACGCTTACGCCAAGGCAATTACGACGAGTAAGT 430
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
35 LngLAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeuPhe 51
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
431 CGCAGGCTCTGATGATTAATTAAGACGCTAGAGATTACGTTCTA 480
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
52 GlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysThrPr 68
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
481 CATTTTCATATATATAATAGTAATTAGATTAGGTTTCCAGGTGCTCC 530
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
68 oGluPro 70
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
531 GGCACCT 537

seq_name: /cgn1_7/plodata/1/lna/6A.COMB.seq:US-08-809-103B-5

seq_documentation_block:
; Sequence 5, Application US/08809103B
; Patent No. 6133505
; GENERAL INFORMATION:
; APPLICANT: GROENENBORN, Bruno
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,103B
FILING DATE: 17-MAR-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94.11040
FILING DATE: 15-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR95/01192
FILING DATE: 15-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: PATCH, Andrew J.
REGISTRATION NUMBER: 32,925
REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 521-2297
TELEFAX: (703) 685-0573
TELEX: 248425 EMBON
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1150 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1077
US-08-809-103B-5

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alignment_scores:
Quality: 221.00      Length: 69
Ratio: 3.877         Gaps: 0
Percent Similarity: 82.609   Percent Identity: 56.522

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alignment_block:
US-09-289-346A-10 x US-08-809-103B-5

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Align seg 1/1 to: US-08-809-103B-5 from: 1 to: 1150

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2 LeuValTrpGlyGluPheGlnValAlaSpGlyArgSerAlaArgGlyGlyc 18
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331 CTGGAATGGGGTACTTCCAGATCGAGCGATCTGCTAGGGAGAGACA 380
18 sGlnThrSerAsnAspLeuLeuGluAlaLeuAsnAlaSerSerlysg 35
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381 ACAGACAGCCACGACGCTTACGCAAGCAATTAACGCAAGTAAGT 430
35 IuGluAlaLeuGlnIleLeuArgGluLysIleProGluLysTyrLeuPhe 51
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431 CGAGGCTCTGATGTAATTAAGCAATTAACGCTAGAGATTACGTTCTA 480
52 GlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysThrPr 68
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481 CATTTCATATATATAATAGTATTAGATAGAGTTTCCAGATGCCCTCC 530
68 oGluPro 70
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seq_documentation_block:
Sequence 1, Application US/08838151A
Patent No. 6291743
GENERAL INFORMATION:

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APPLICANT: Stout, John T
APPLICANT: Lou, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul

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APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing GeminiVirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESS: Dressler, Rockey, Milamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1162 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Tomato Mottle Gemini Virus
INDIVIDUAL ISOLATE: Florida
FEATURE:
NAME/KEY: CDS
LOCATION: 44..1127
PUBLICATION INFORMATION:
AUTHORS: Gilbertson, RL
AUTHORS: Hidayat, SH
AUTHORS: Paplomatas, EJ
AUTHORS: Rojas, MR
AUTHORS: Hou, YM
AUTHORS: Maxwell, DP
TITLE: Pseudorecombination between the infectious
TITLE: cloned DNA components of tomato mottle and bean
TITLE: dwarf mosaic geminiviruses.
JOURNAL: Jour. General Virol.
VOLUME: 74
PAGES: 23-31
DATE: 1993
US-08-838-151A-1

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Ratio: 3.746         Gaps: 0
Percent Similarity: 84.286   Percent Identity: 57.143

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1 ThrLeuValTrpGlyGluPheGlnValAlaSpGlyArgSerAlaArgGly 17
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371 ACATCGAATGGGAGATTTCAGATCGACGCAAGATCTGCCAGAGAGG 420

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